# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/04 04:53:13*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717077.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_SRR9717077 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717077.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Sep 04 04:53:12 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9717077.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 899,217 |
| Mapped reads | 821,284 / 91.33% |
| Unmapped reads | 77,933 / 8.67% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,635 / 0.18% |
| Read min/max/mean length | 30 / 76 / 76.06 |
| Duplicated reads (estimated) | 19,488 / 2.17% |
| Duplication rate | 1.77% |
| Clipped reads | 820,730 / 91.27% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 11,739,201 / 24.66% |
| Number/percentage of C's | 8,799,778 / 18.49% |
| Number/percentage of T's | 15,388,070 / 32.33% |
| Number/percentage of G's | 11,668,418 / 24.52% |
| Number/percentage of N's | 489 / 0% |
| GC Percentage | 43% |

## 2.3. Coverage

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

| | |
|---|---|
| Standard Deviation | 0.1643 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.46 |

## 2.5. Mismatches and indels

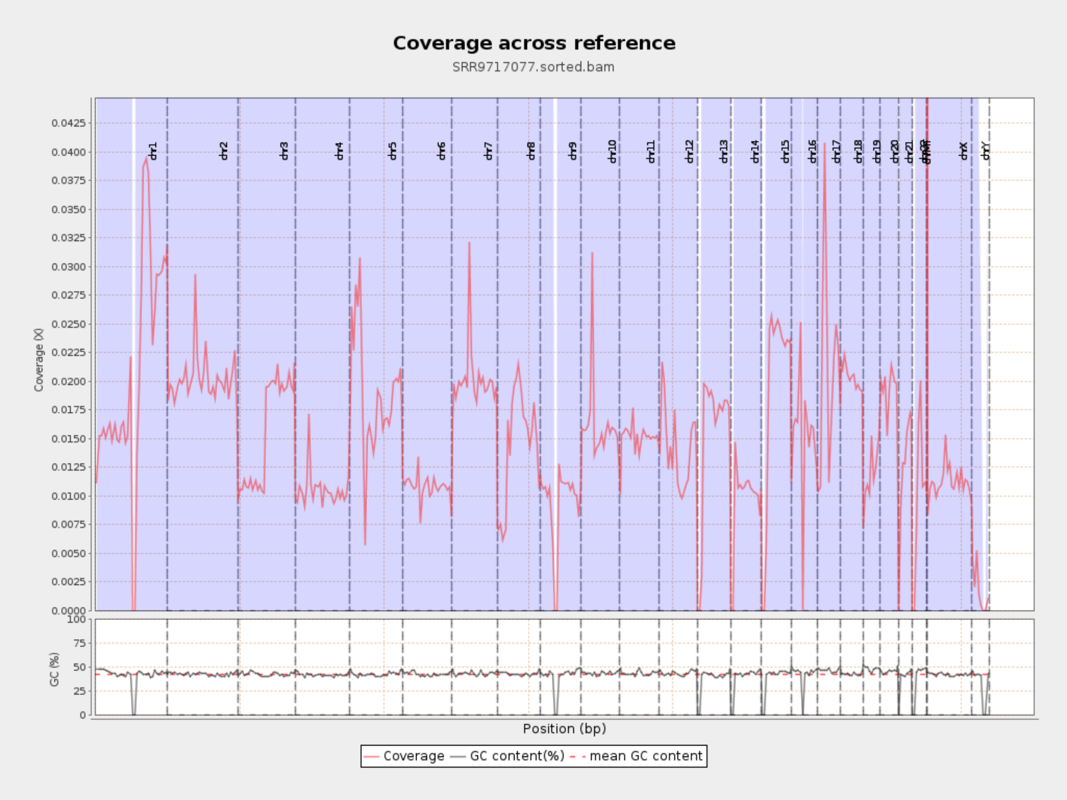
| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 228,327 |
| Insertions | 3,707 |
| Mapped reads with at least one insertion | 0.45% |
| Deletions | 9,340 |
| Mapped reads with at least one deletion | 1.13% |
| Homopolymer indels | 41.35% |

## 2.6. Chromosome stats

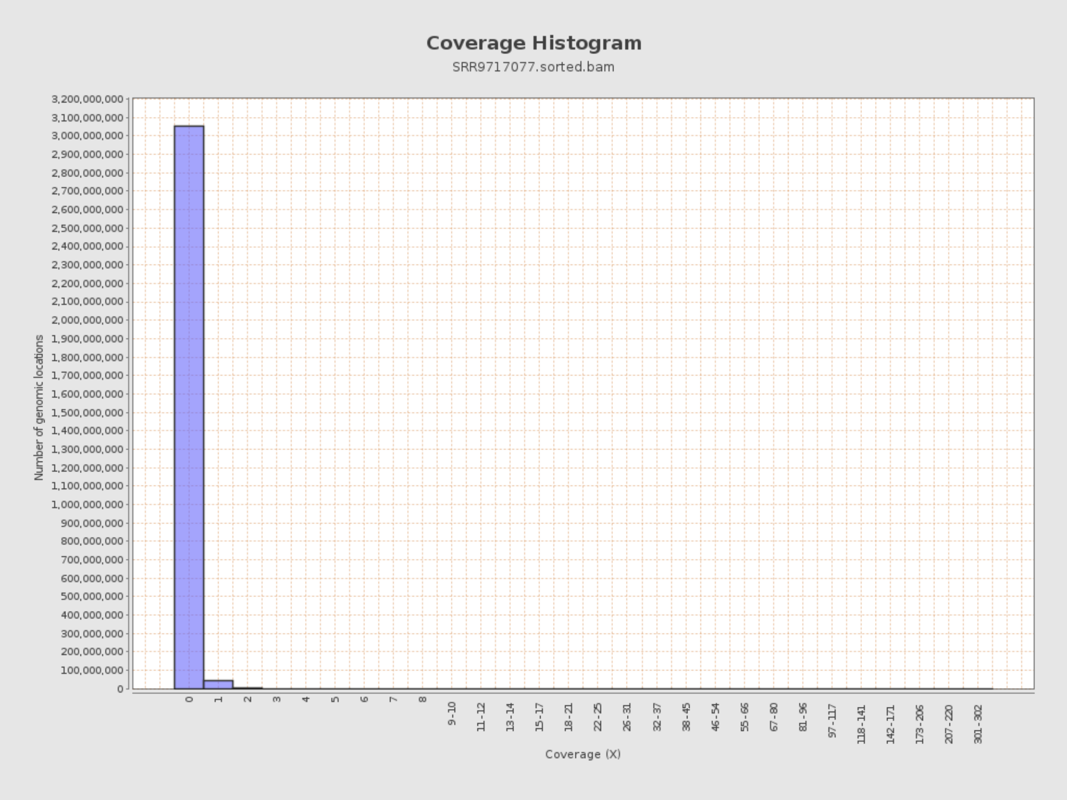
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5128432 | 0.0206 | 0.2163 |
| chr2 | 243199373 | 4927173 | 0.0203 | 0.2148 |
| chr3 | 198022430 | 3057874 | 0.0154 | 0.1324 |
| chr4 | 191154276 | 2012138 | 0.0105 | 0.1117 |
| chr5 | 180915260 | 3449752 | 0.0191 | 0.1453 |
| chr6 | 171115067 | 1847537 | 0.0108 | 0.1204 |
| chr7 | 159138663 | 3219033 | 0.0202 | 0.2661 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2151542 | 0.0147 | 0.1425 |
| chr9 | 141213431 | 1310326 | 0.0093 | 0.126 |
| chr10 | 135534747 | 2199523 | 0.0162 | 0.1915 |
| chr11 | 135006516 | 2043985 | 0.0151 | 0.1582 |
| chr12 | 133851895 | 1888843 | 0.0141 | 0.1259 |
| chr13 | 115169878 | 1744250 | 0.0151 | 0.1294 |
| chr14 | 107349540 | 1017367 | 0.0095 | 0.106 |
| chr15 | 102531392 | 1997912 | 0.0195 | 0.1474 |
| chr16 | 90354753 | 1361314 | 0.0151 | 0.1402 |
| chr17 | 81195210 | 1735199 | 0.0214 | 0.1602 |
| chr18 | 78077248 | 1589162 | 0.0204 | 0.2652 |
| chr19 | 59128983 | 720411 | 0.0122 | 0.1702 |
| chr20 | 63025520 | 1201835 | 0.0191 | 0.1461 |
| chr21 | 48129895 | 605103 | 0.0126 | 0.1218 |
| chr22 | 51304566 | 523815 | 0.0102 | 0.1057 |
| chrMT | 16571 | 23179 | 1.3988 | 1.5353 |
| chrX | 155270560 | 1753049 | 0.0113 | 0.121 |
| chrY | 59373566 | 101923 | 0.0017 | 0.0517 |

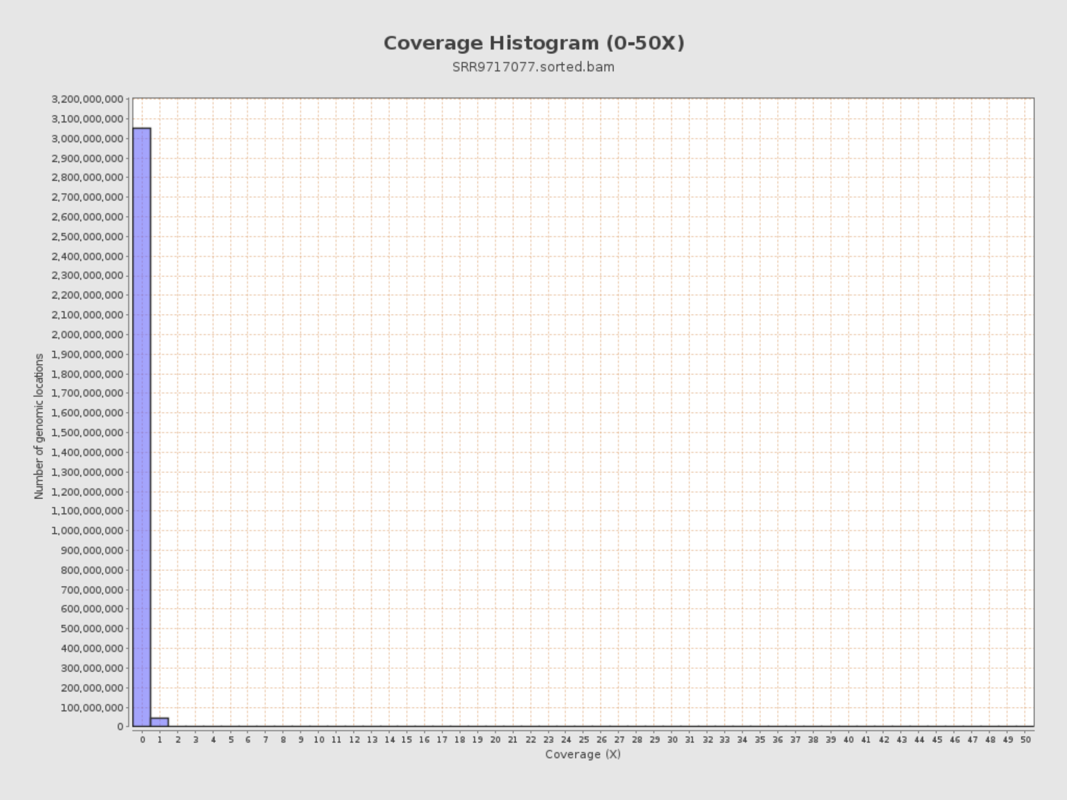
# 3. Results : Coverage across reference



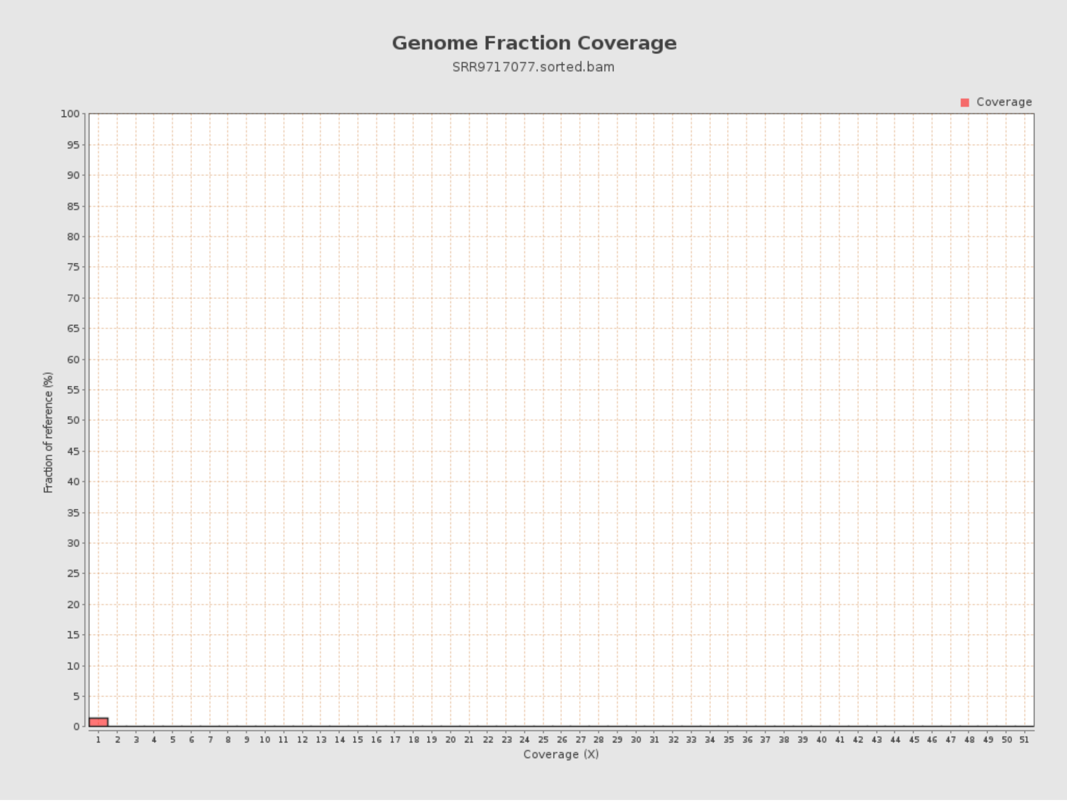
# 4. Results : Coverage Histogram



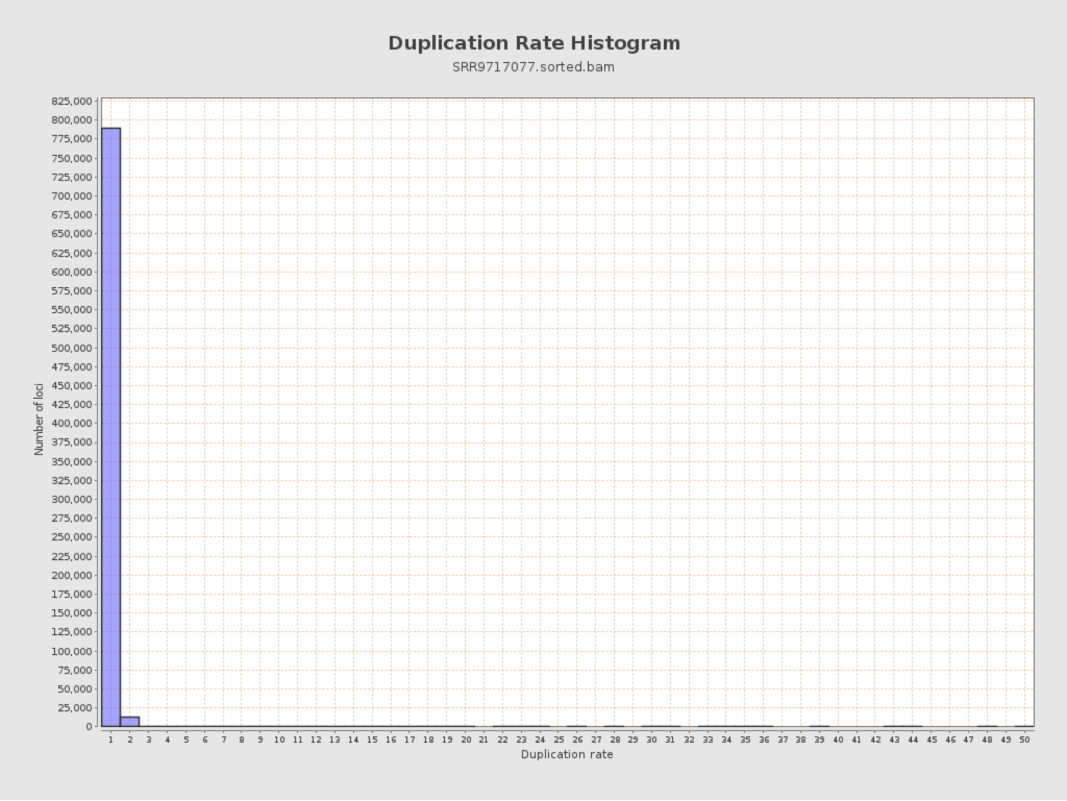
# 5. Results : Coverage Histogram (0-50X)



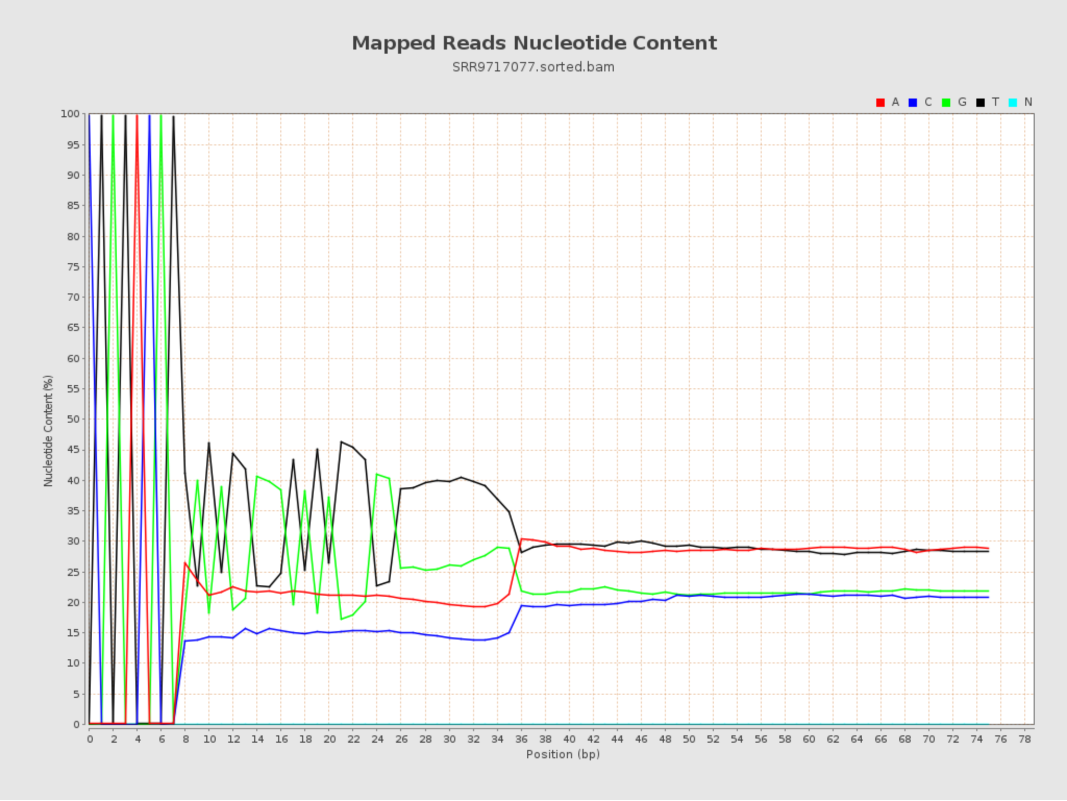
# 6. Results : Genome Fraction Coverage



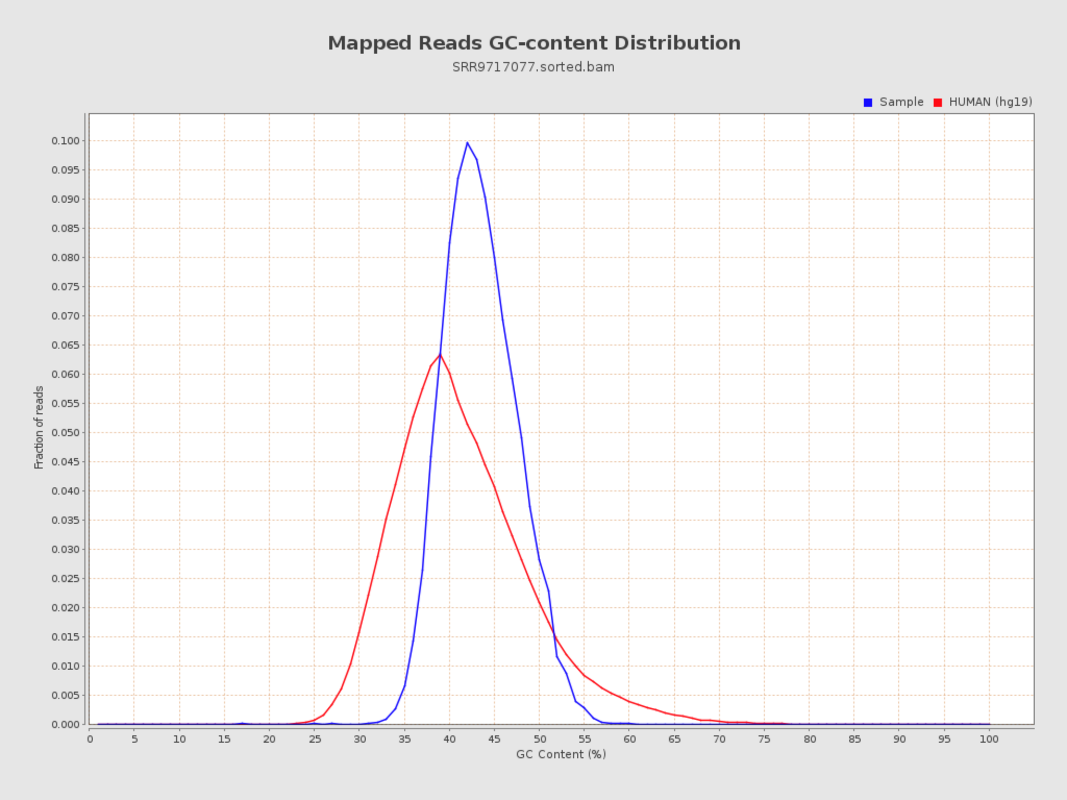
# 7. Results : Duplication Rate Histogram



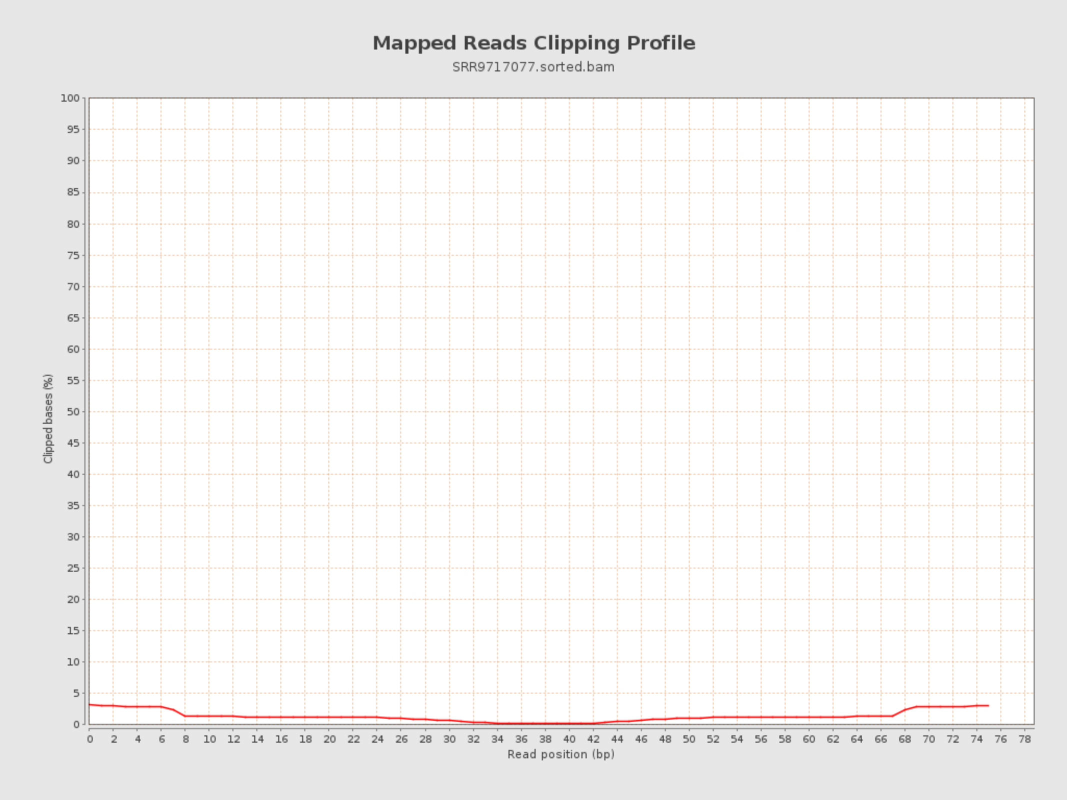
# 8. Results : Mapped Reads Nucleotide Content



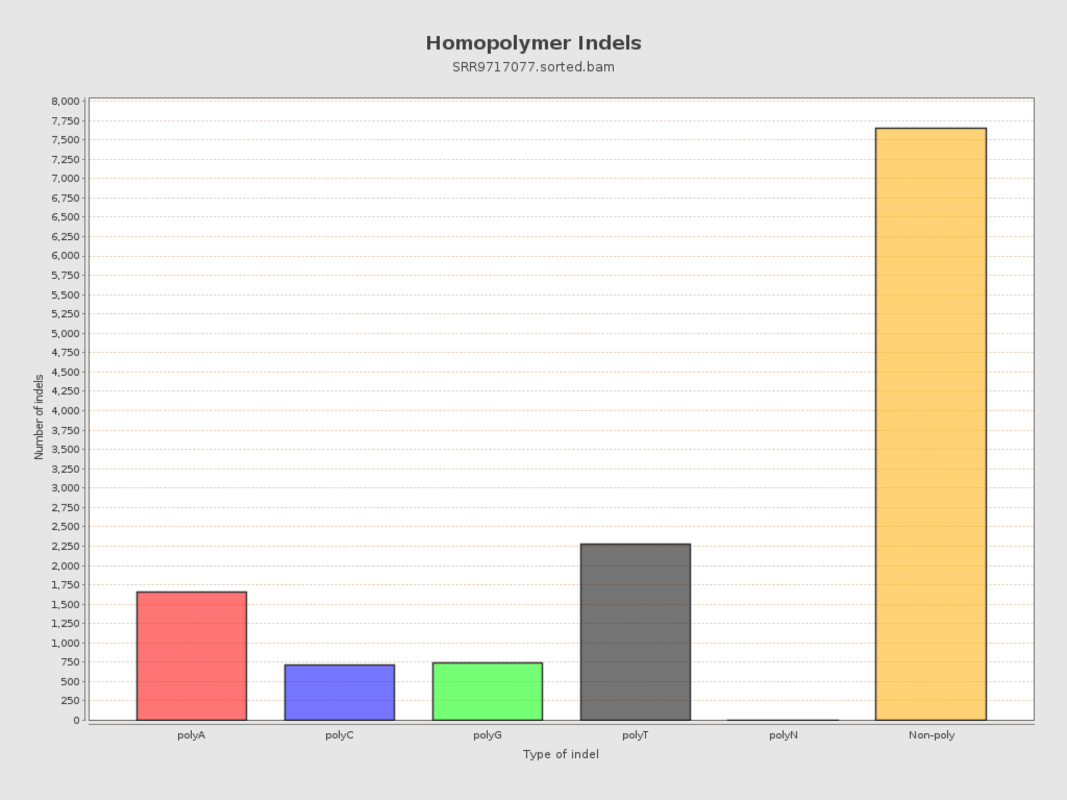
# 9. Results : Mapped Reads GC-content Distribution



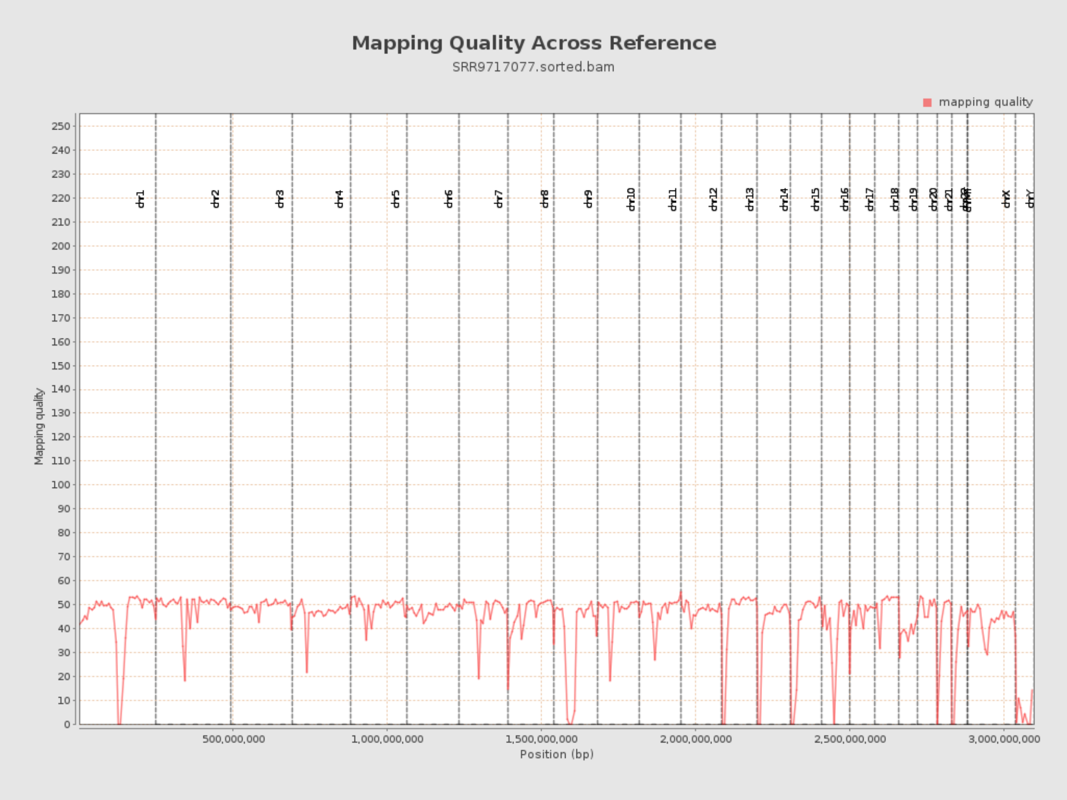
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram