# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 09:45:32*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008750.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_SRR6008750 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008750.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 14 09:45:32 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6008750.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 922,612 |
| Mapped reads | 521,133 / 56.48% |
| Unmapped reads | 401,479 / 43.52% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 2,811 / 0.3% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 14,351 / 1.56% |
| Duplication rate | 2.35% |
| Clipped reads | 358,257 / 38.83% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 8,717,590 / 27.75% |
| Number/percentage of C's | 5,280,725 / 16.81% |
| Number/percentage of T's | 9,872,865 / 31.42% |
| Number/percentage of G's | 7,546,801 / 24.02% |
| Number/percentage of N's | 1,909 / 0.01% |
| GC Percentage | 40.83% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0102 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1168 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.99 |

## 2.5. Mismatches and indels

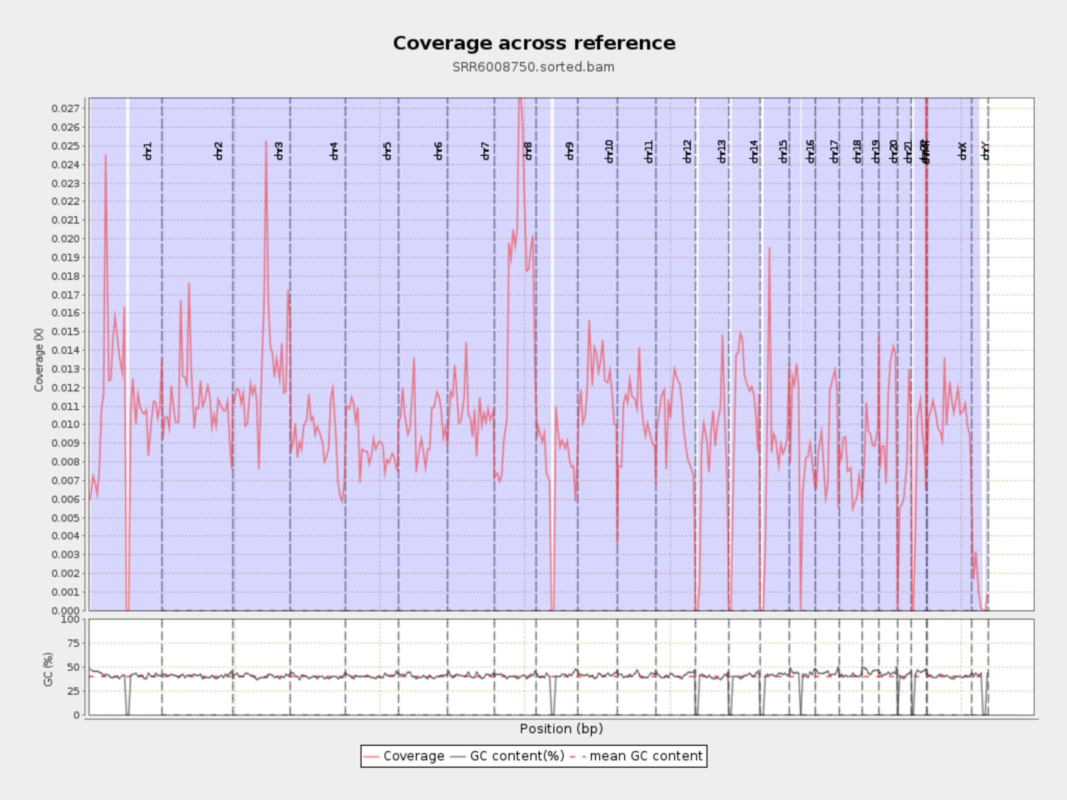
| | |
|---|---|
| General error rate | 1.09% |
| Mismatches | 338,802 |
| Insertions | 2,387 |
| Mapped reads with at least one insertion | 0.46% |
| Deletions | 11,426 |
| Mapped reads with at least one deletion | 2.17% |
| Homopolymer indels | 48.41% |

## 2.6. Chromosome stats

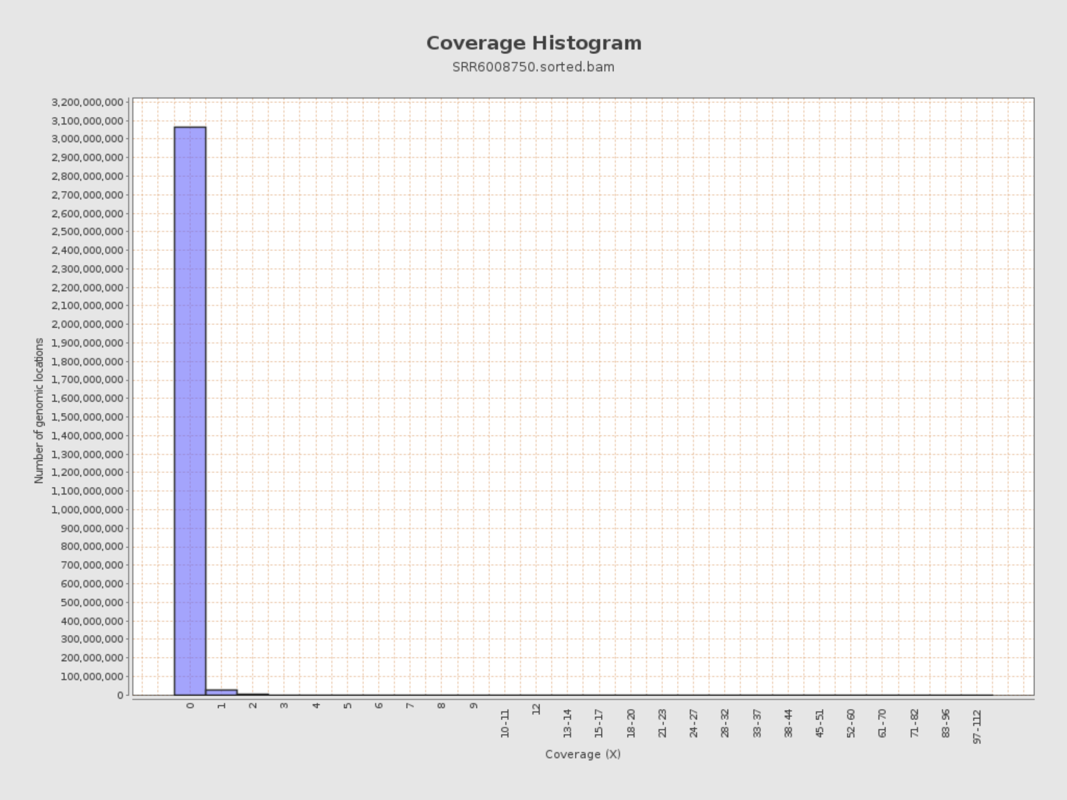
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 2686482 | 0.0108 | 0.1423 |
| chr2 | 243199373 | 2749984 | 0.0113 | 0.1277 |
| chr3 | 198022430 | 2573288 | 0.013 | 0.1213 |
| chr4 | 191154276 | 1745413 | 0.0091 | 0.1025 |
| chr5 | 180915260 | 1627140 | 0.009 | 0.1014 |
| chr6 | 171115067 | 1715933 | 0.01 | 0.1124 |
| chr7 | 159138663 | 1730245 | 0.0109 | 0.1288 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2421066 | 0.0165 | 0.1545 |
| chr9 | 141213431 | 1088947 | 0.0077 | 0.1026 |
| chr10 | 135534747 | 1668629 | 0.0123 | 0.1276 |
| chr11 | 135006516 | 1389870 | 0.0103 | 0.1223 |
| chr12 | 133851895 | 1364953 | 0.0102 | 0.107 |
| chr13 | 115169878 | 941345 | 0.0082 | 0.0961 |
| chr14 | 107349540 | 1116941 | 0.0104 | 0.1079 |
| chr15 | 102531392 | 840729 | 0.0082 | 0.0964 |
| chr16 | 90354753 | 792158 | 0.0088 | 0.1032 |
| chr17 | 81195210 | 750958 | 0.0092 | 0.1072 |
| chr18 | 78077248 | 577193 | 0.0074 | 0.1294 |
| chr19 | 59128983 | 558456 | 0.0094 | 0.1166 |
| chr20 | 63025520 | 668493 | 0.0106 | 0.1102 |
| chr21 | 48129895 | 346418 | 0.0072 | 0.0926 |
| chr22 | 51304566 | 348678 | 0.0068 | 0.0869 |
| chrMT | 16571 | 13736 | 0.8289 | 1.0632 |
| chrX | 155270560 | 1649533 | 0.0106 | 0.1111 |
| chrY | 59373566 | 70441 | 0.0012 | 0.0378 |

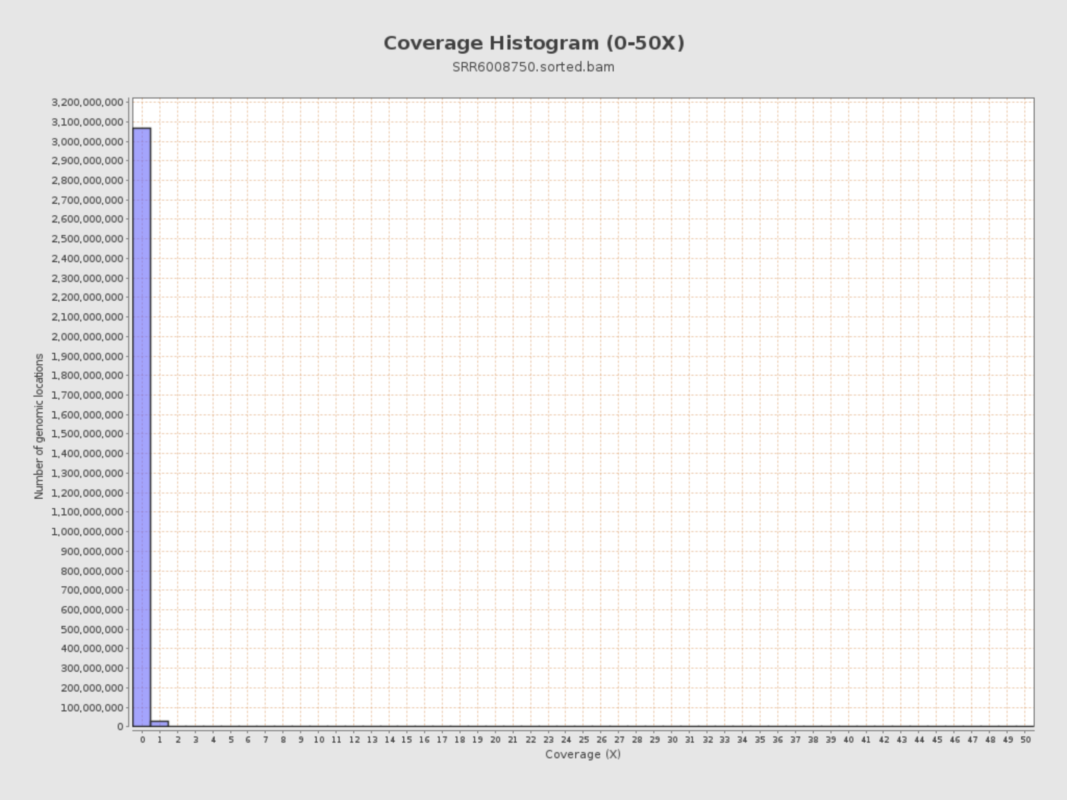
# 3. Results : Coverage across reference



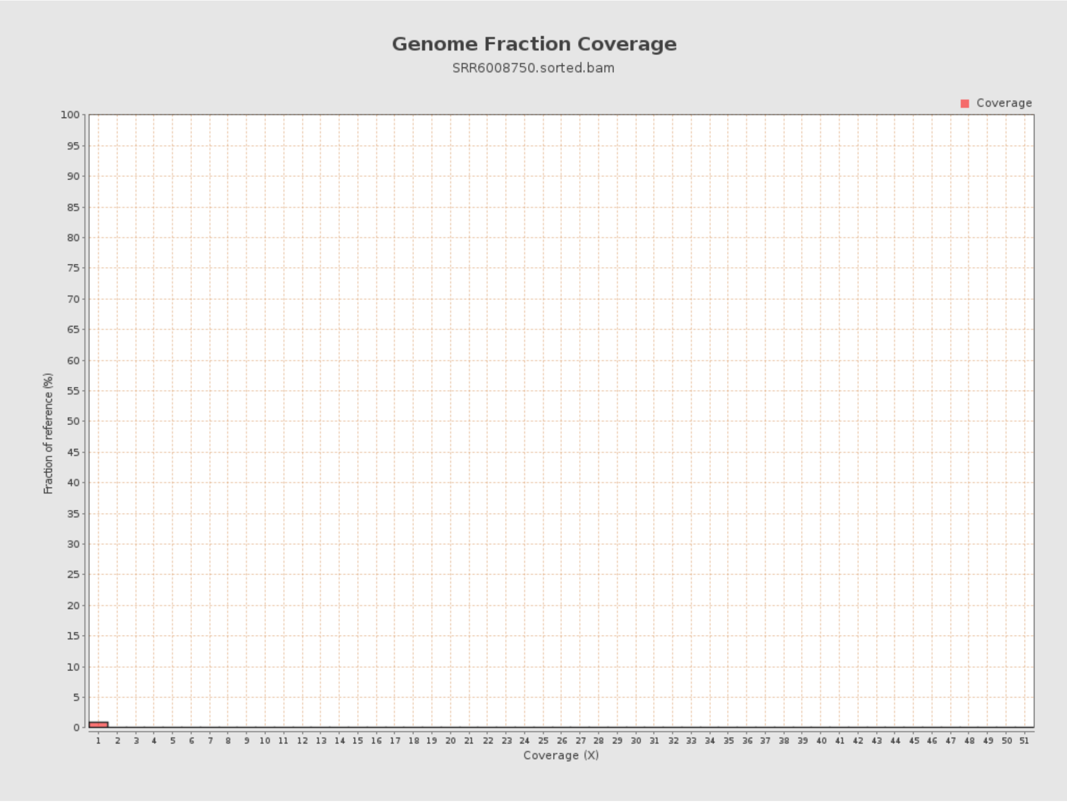
# 4. Results : Coverage Histogram



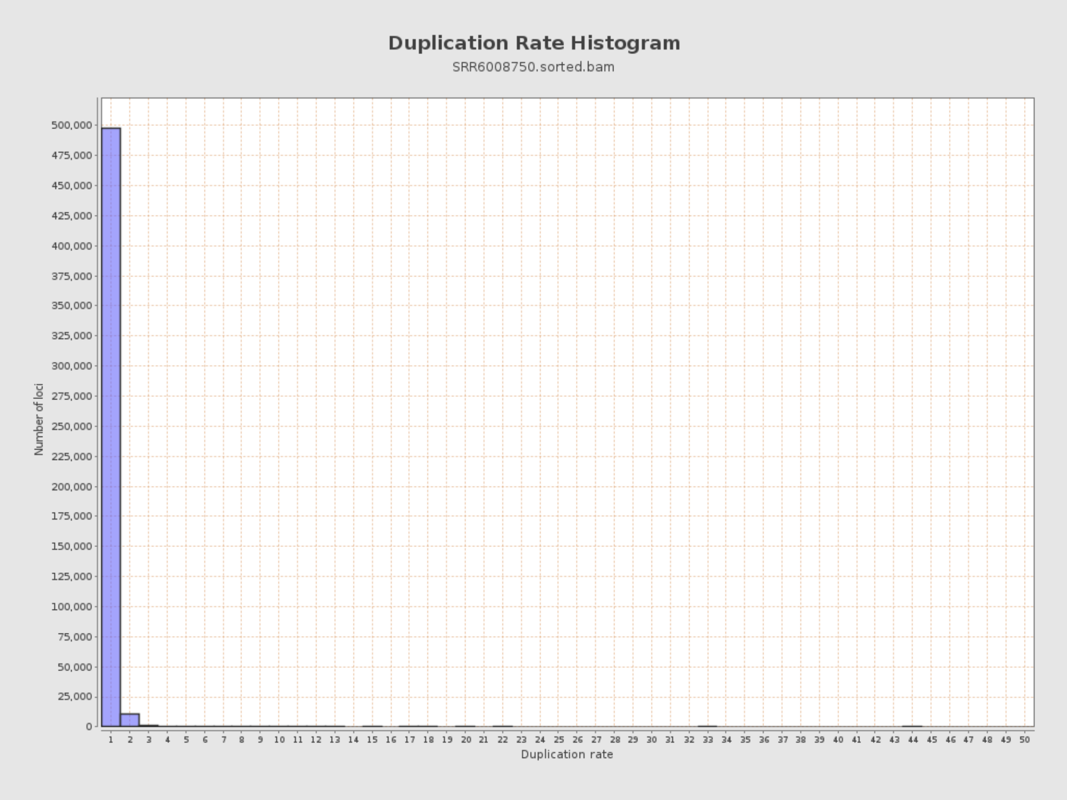
# 5. Results : Coverage Histogram (0-50X)



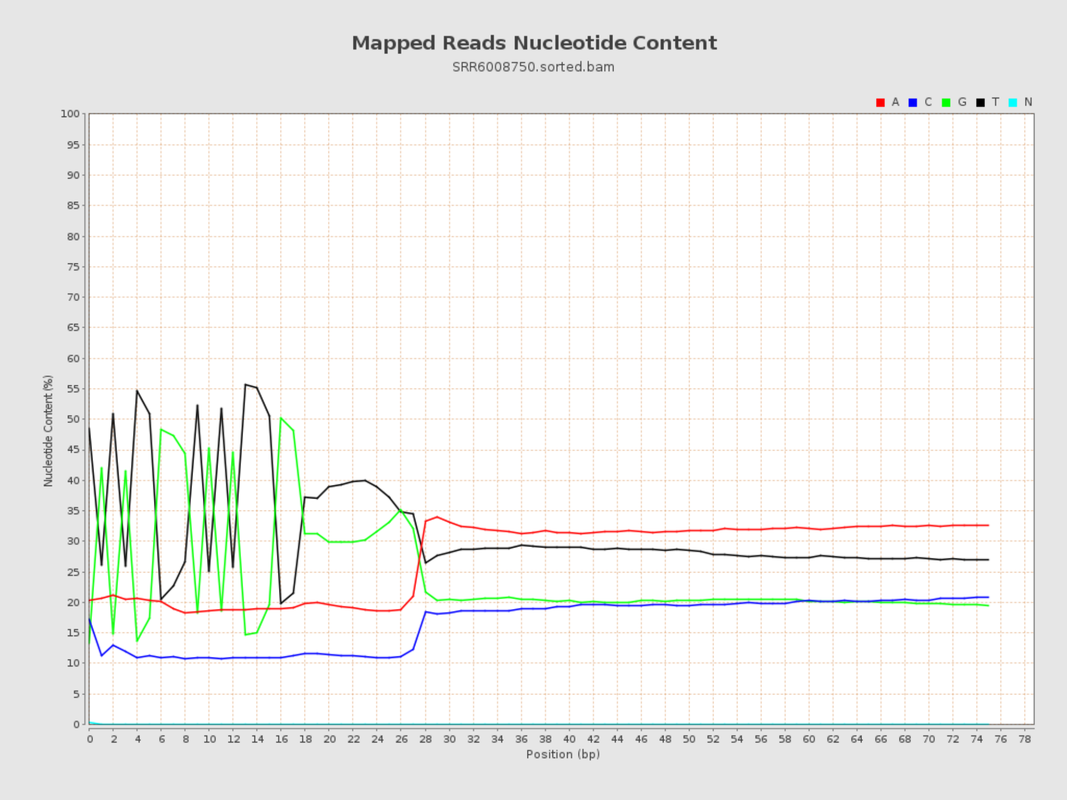
# 6. Results : Genome Fraction Coverage



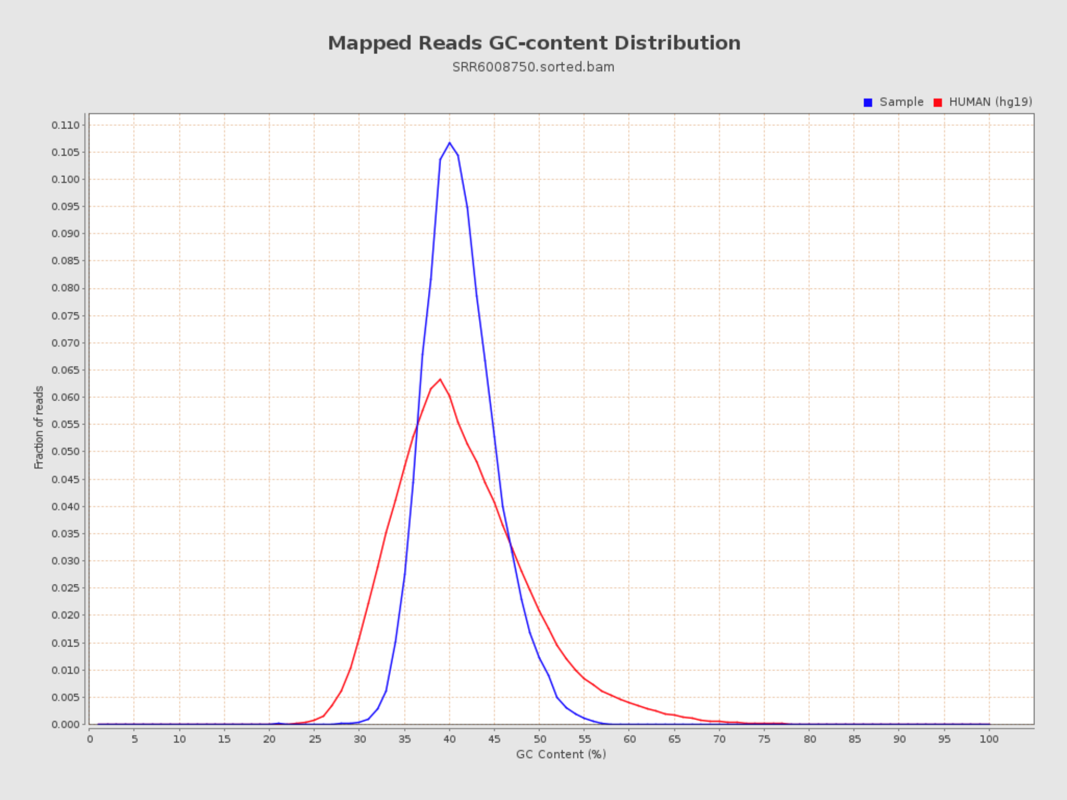
# 7. Results : Duplication Rate Histogram



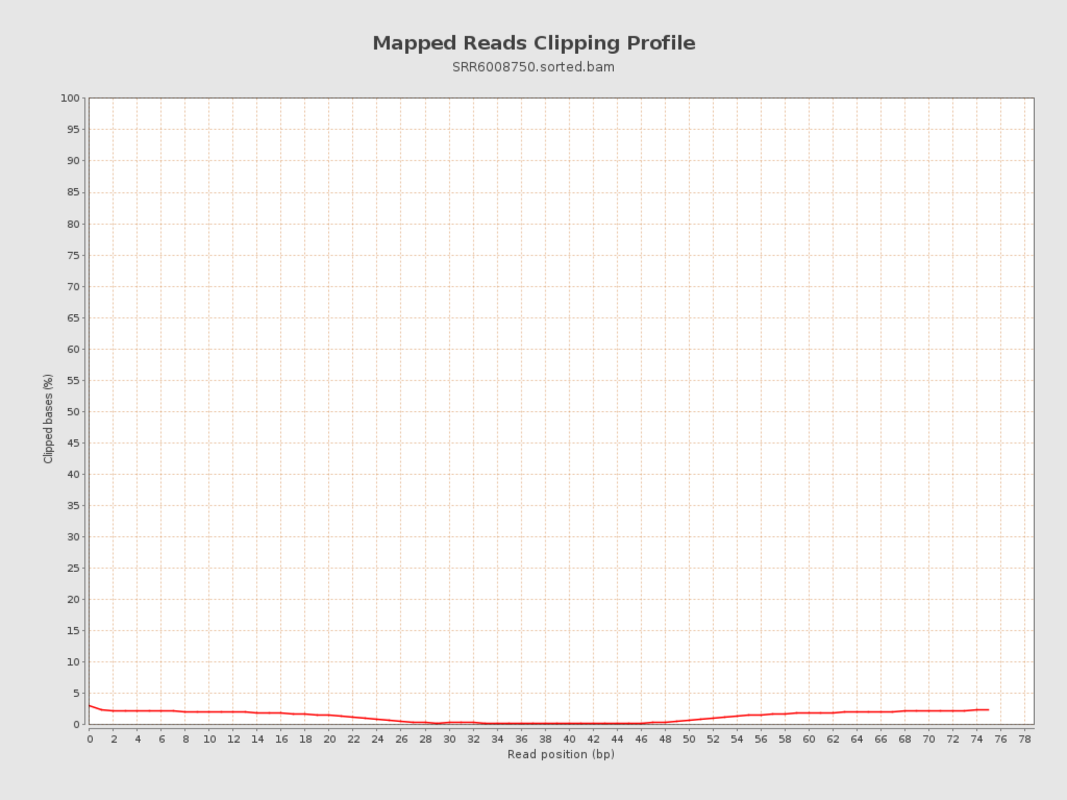
# 8. Results : Mapped Reads Nucleotide Content



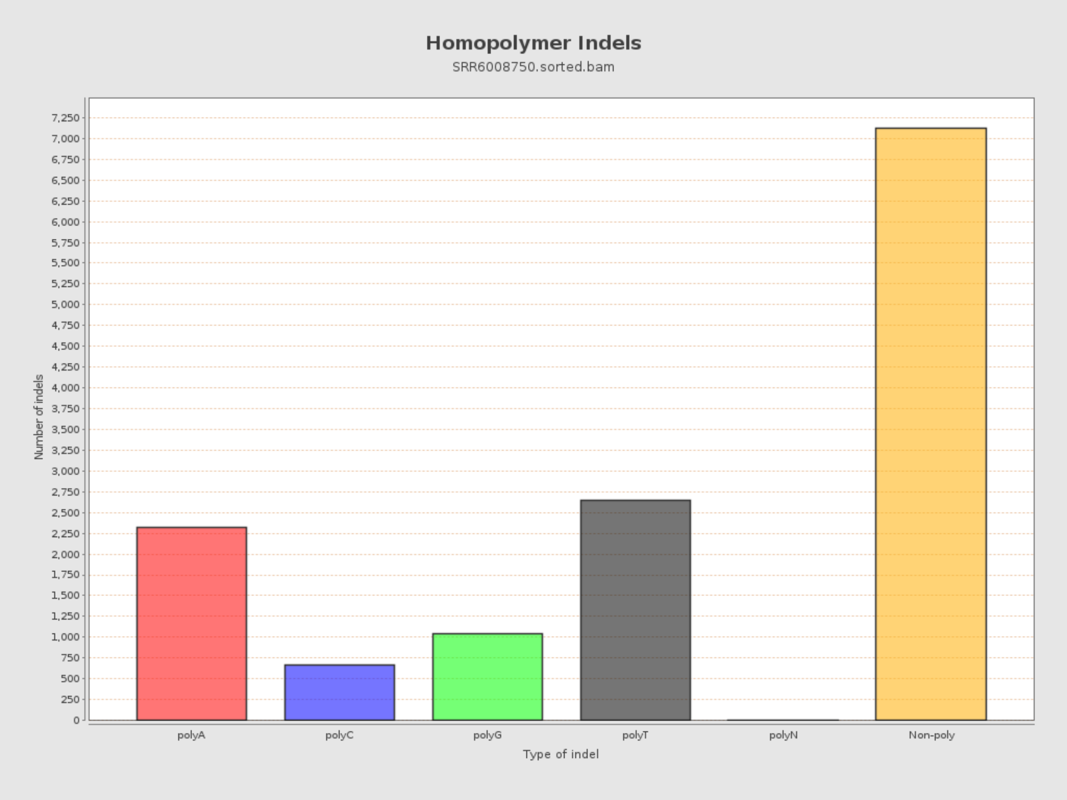
# 9. Results : Mapped Reads GC-content Distribution



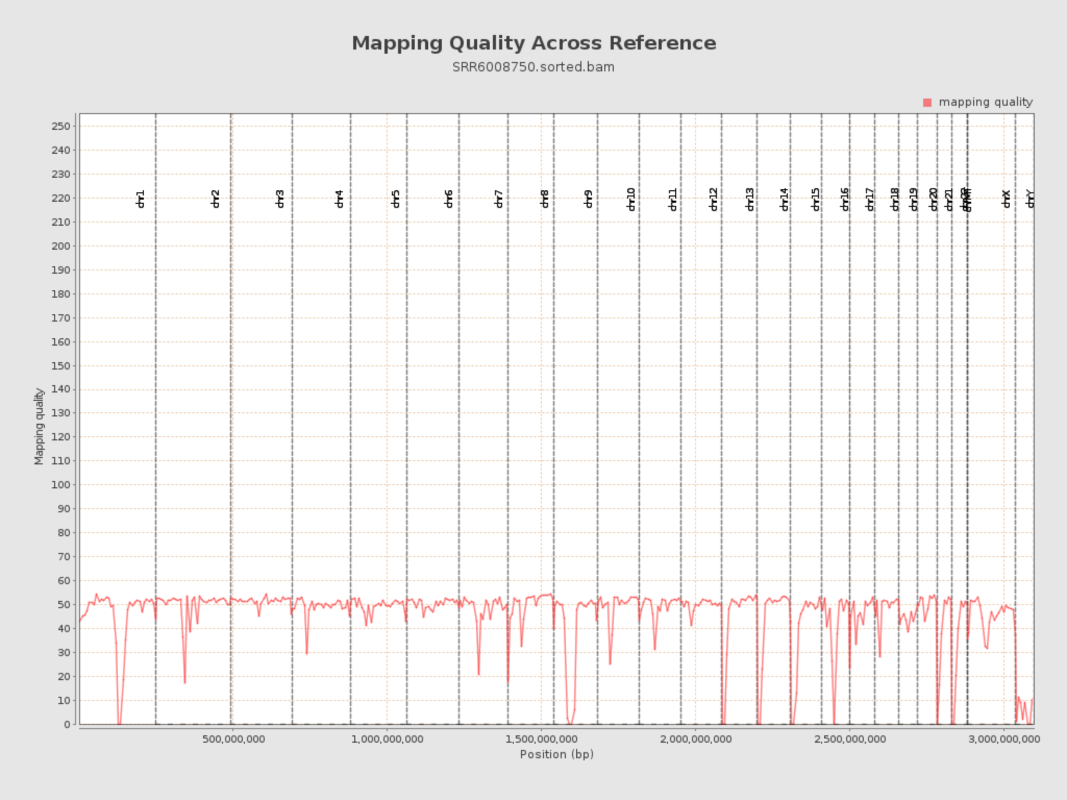
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram