# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 01:28:14*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524387.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_SRR10524387 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524387.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 01:28:14 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524387.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 831,104 |
| Mapped reads | 761,672 / 91.65% |
| Unmapped reads | 69,432 / 8.35% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 2,784 / 0.33% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 19,964 / 2.4% |
| Duplication rate | 1.92% |
| Clipped reads | 762,015 / 91.69% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 11,480,898 / 25.8% |
| Number/percentage of C's | 7,479,944 / 16.81% |
| Number/percentage of T's | 14,331,348 / 32.2% |
| Number/percentage of G's | 11,209,203 / 25.19% |
| Number/percentage of N's | 5,620 / 0.01% |
| GC Percentage | 41.99% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0144 |
| | |

| | |
|---|---|
| Standard Deviation | 0.169 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.03 |

## 2.5. Mismatches and indels

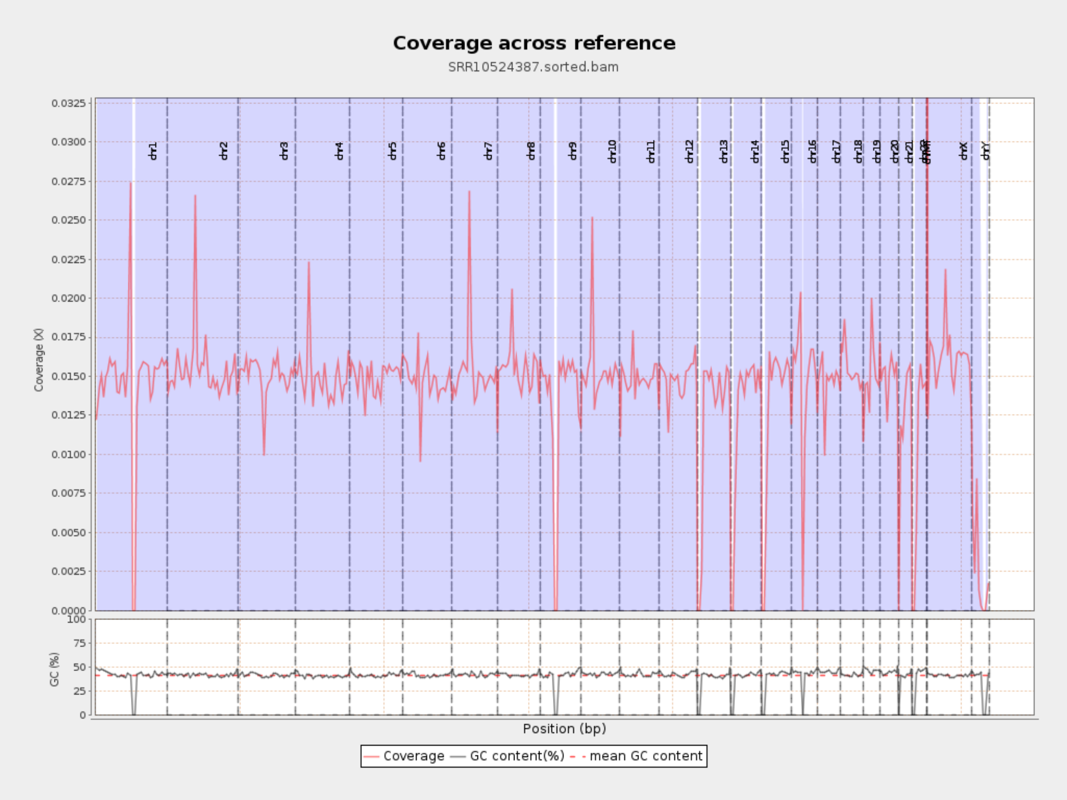
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 218,005 |
| Insertions | 3,376 |
| Mapped reads with at least one insertion | 0.44% |
| Deletions | 8,153 |
| Mapped reads with at least one deletion | 1.06% |
| Homopolymer indels | 42.73% |

## 2.6. Chromosome stats

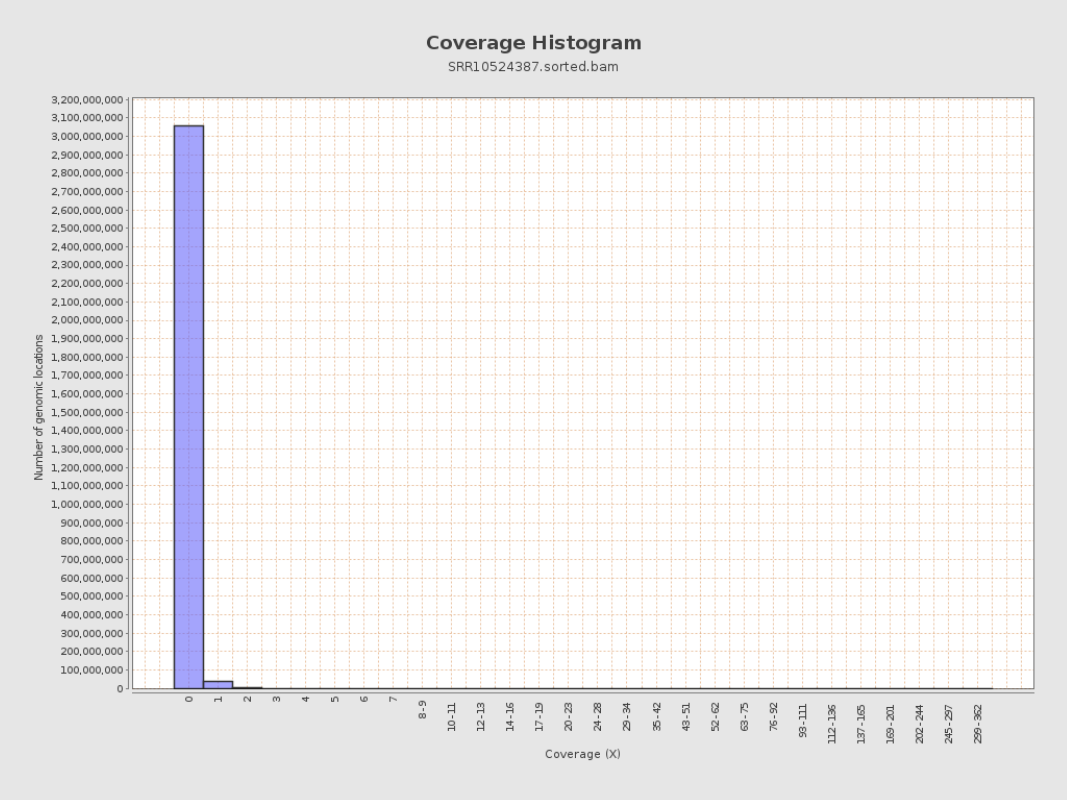
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3597803 | 0.0144 | 0.3057 |
| chr2 | 243199373 | 3766317 | 0.0155 | 0.1911 |
| chr3 | 198022430 | 2978825 | 0.015 | 0.1277 |
| chr4 | 191154276 | 2866729 | 0.015 | 0.1355 |
| chr5 | 180915260 | 2712584 | 0.015 | 0.1284 |
| chr6 | 171115067 | 2520956 | 0.0147 | 0.1344 |
| chr7 | 159138663 | 2464552 | 0.0155 | 0.2168 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2279283 | 0.0156 | 0.161 |
| chr9 | 141213431 | 1870583 | 0.0132 | 0.1418 |
| chr10 | 135534747 | 2100799 | 0.0155 | 0.1559 |
| chr11 | 135006516 | 2014267 | 0.0149 | 0.1521 |
| chr12 | 133851895 | 1992467 | 0.0149 | 0.1296 |
| chr13 | 115169878 | 1401877 | 0.0122 | 0.1149 |
| chr14 | 107349540 | 1331329 | 0.0124 | 0.12 |
| chr15 | 102531392 | 1303855 | 0.0127 | 0.1179 |
| chr16 | 90354753 | 1296798 | 0.0144 | 0.1293 |
| chr17 | 81195210 | 1188057 | 0.0146 | 0.1324 |
| chr18 | 78077248 | 1213530 | 0.0155 | 0.2413 |
| chr19 | 59128983 | 900189 | 0.0152 | 0.2173 |
| chr20 | 63025520 | 944064 | 0.015 | 0.1282 |
| chr21 | 48129895 | 589876 | 0.0123 | 0.1227 |
| chr22 | 51304566 | 519633 | 0.0101 | 0.1053 |
| chrMT | 16571 | 2938 | 0.1773 | 0.4768 |
| chrX | 155270560 | 2520689 | 0.0162 | 0.1446 |
| chrY | 59373566 | 141779 | 0.0024 | 0.0743 |

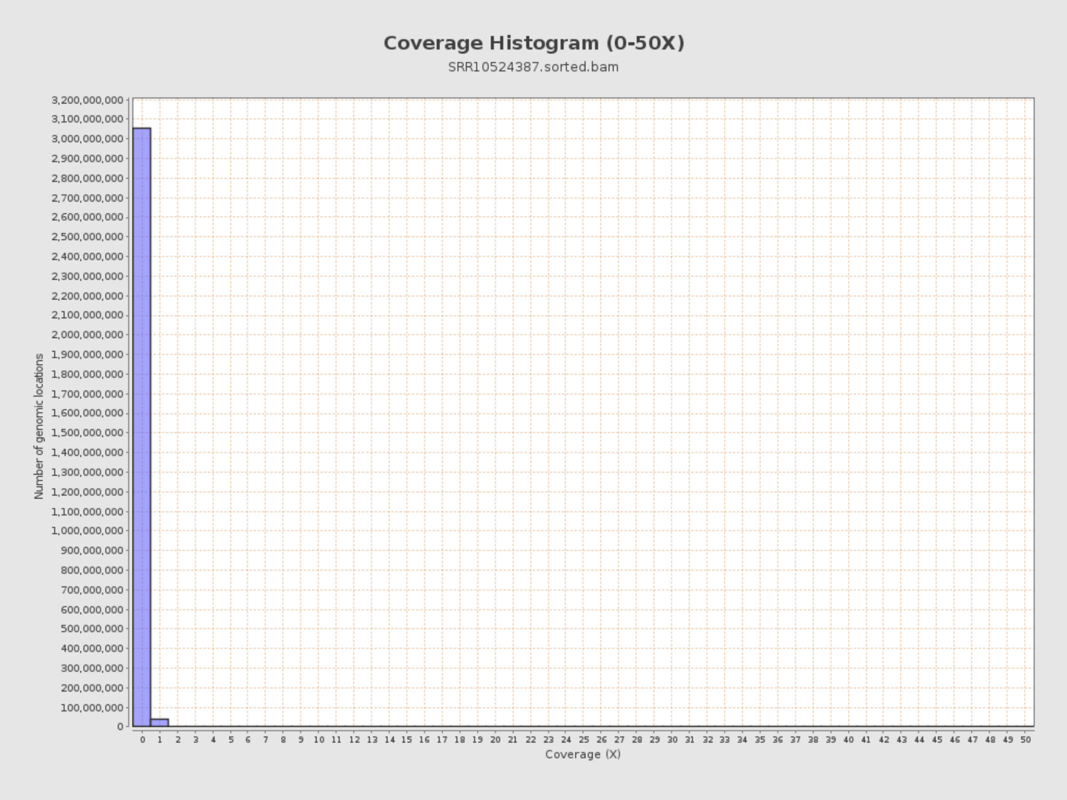
# 3. Results : Coverage across reference



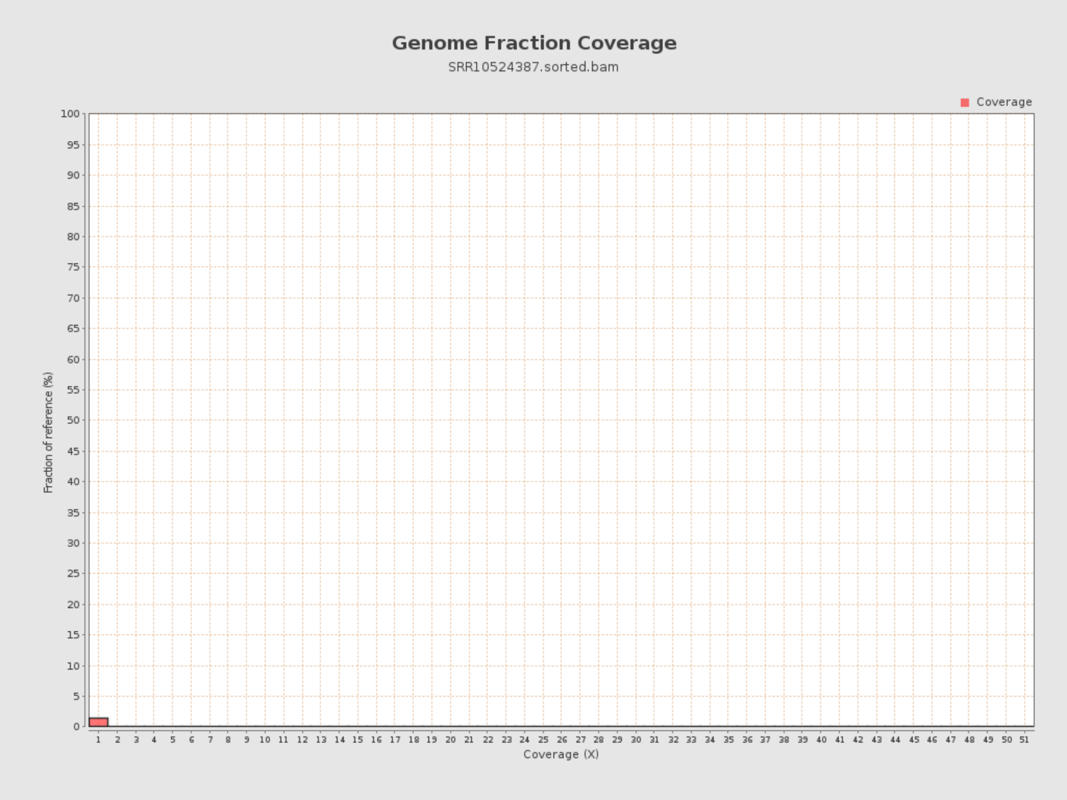
# 4. Results : Coverage Histogram



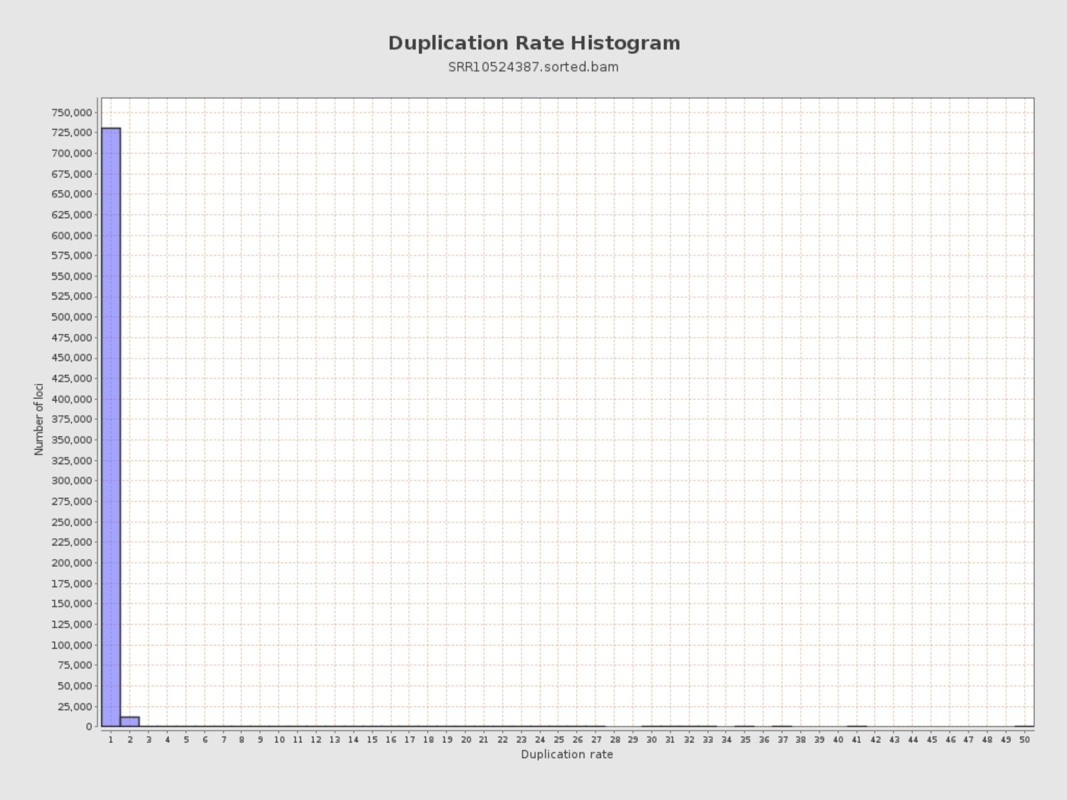
# 5. Results : Coverage Histogram (0-50X)



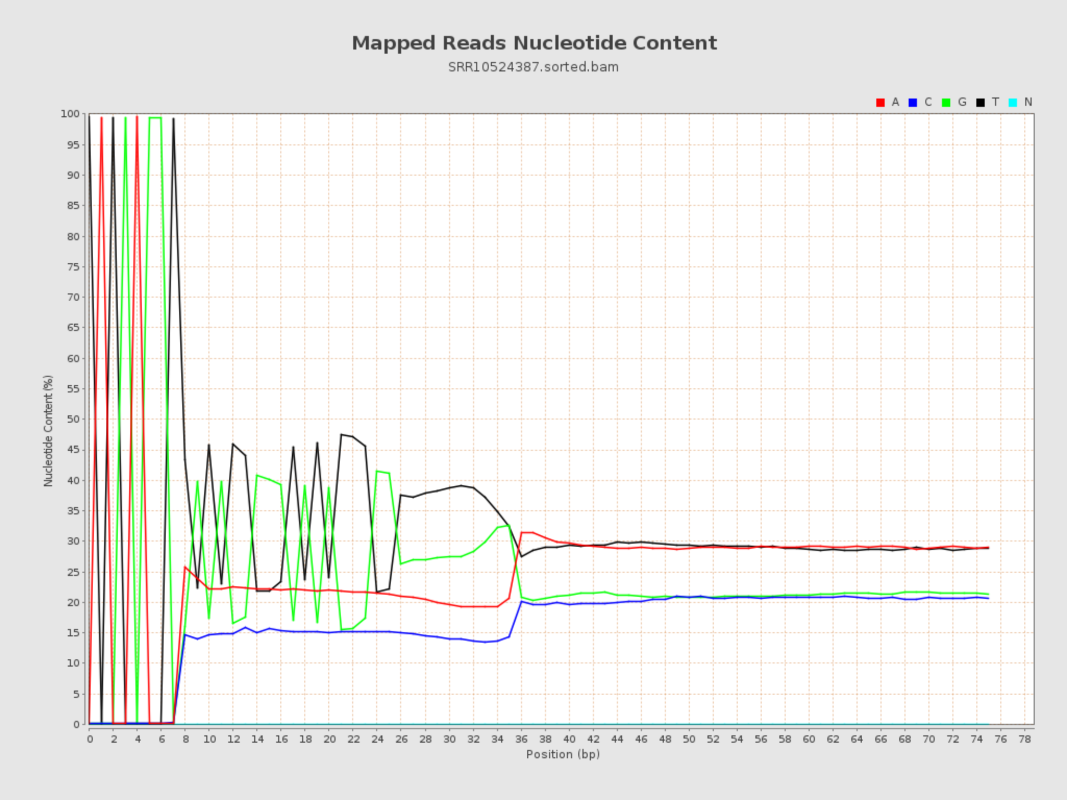
# 6. Results : Genome Fraction Coverage



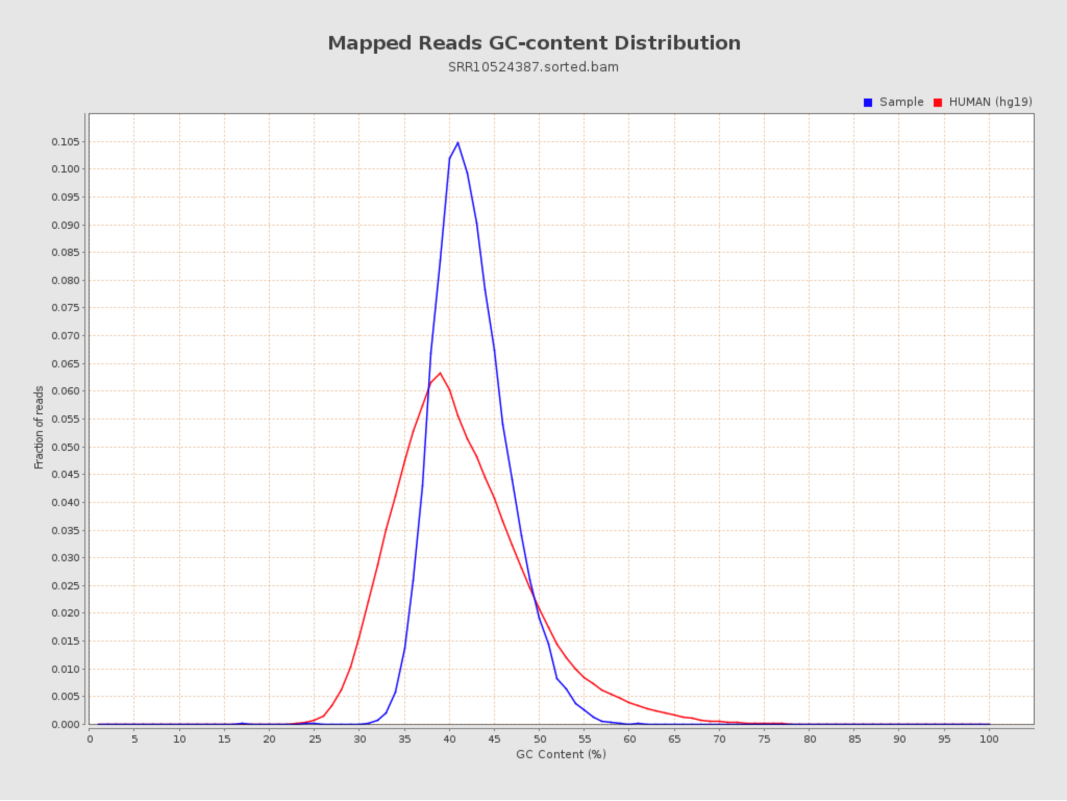
# 7. Results : Duplication Rate Histogram



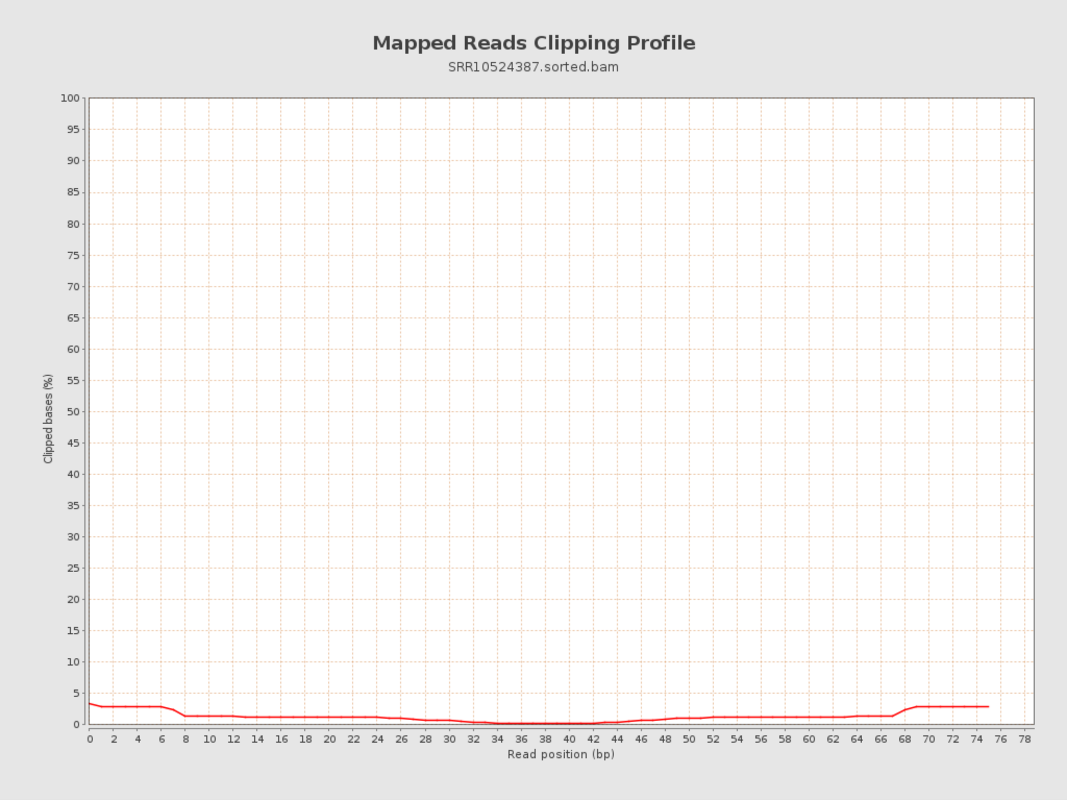
# 8. Results : Mapped Reads Nucleotide Content



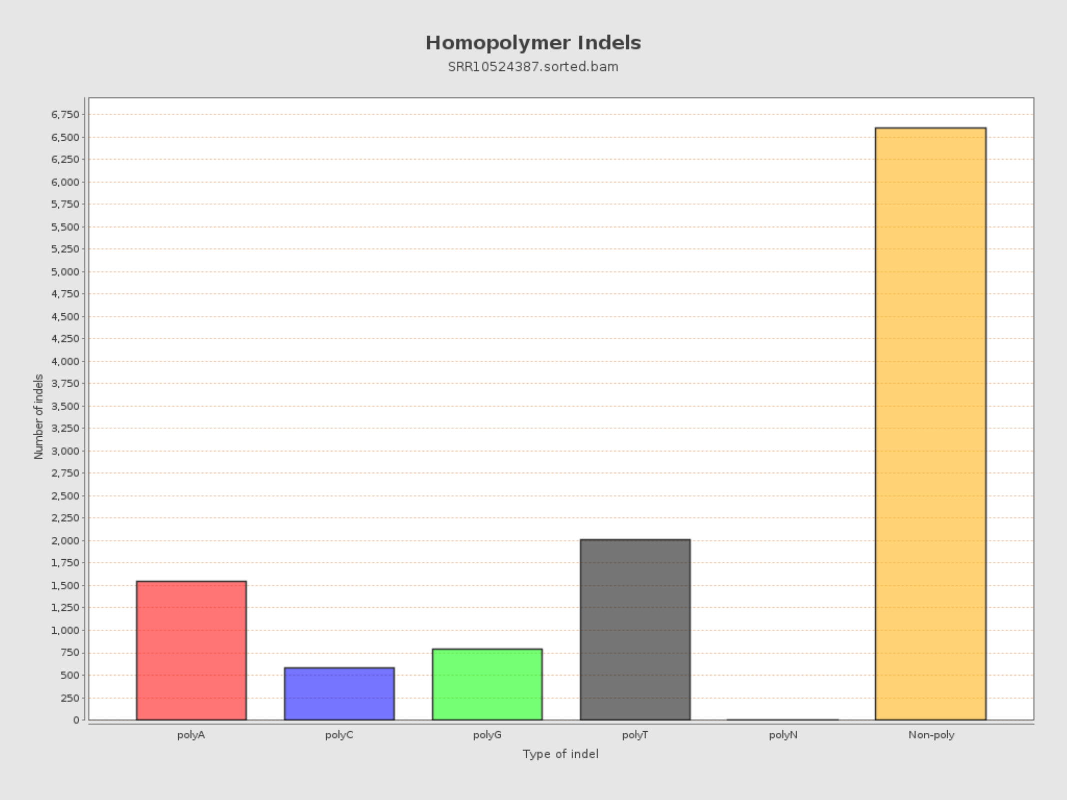
# 9. Results : Mapped Reads GC-content Distribution



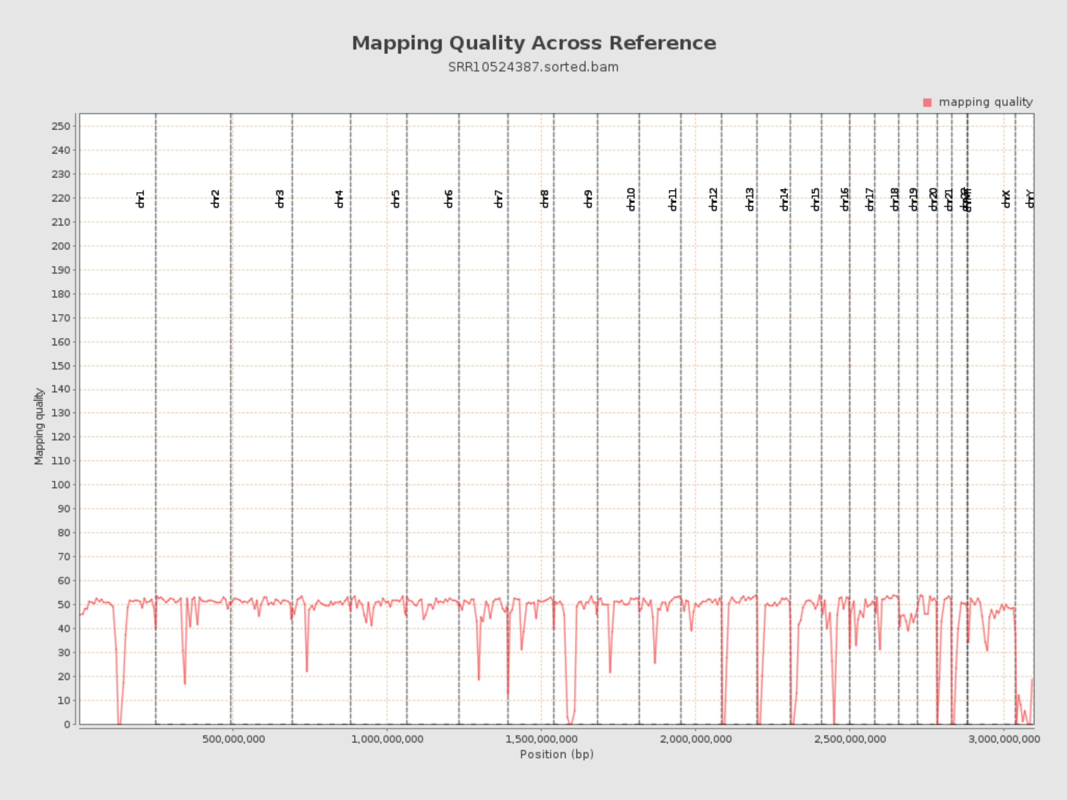
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram