# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 21:47:31*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524816.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_SRR10524816 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524816.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 21:47:30 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524816.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 836,346 |
| Mapped reads | 764,532 / 91.41% |
| Unmapped reads | 71,814 / 8.59% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 2,582 / 0.31% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 17,425 / 2.08% |
| Duplication rate | 1.73% |
| Clipped reads | 765,235 / 91.5% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 10,862,217 / 24.82% |
| Number/percentage of C's | 8,444,270 / 19.3% |
| Number/percentage of T's | 13,809,771 / 31.56% |
| Number/percentage of G's | 10,634,451 / 24.3% |
| Number/percentage of N's | 5,213 / 0.01% |
| GC Percentage | 43.6% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0141 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1497 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.67 |

## 2.5. Mismatches and indels

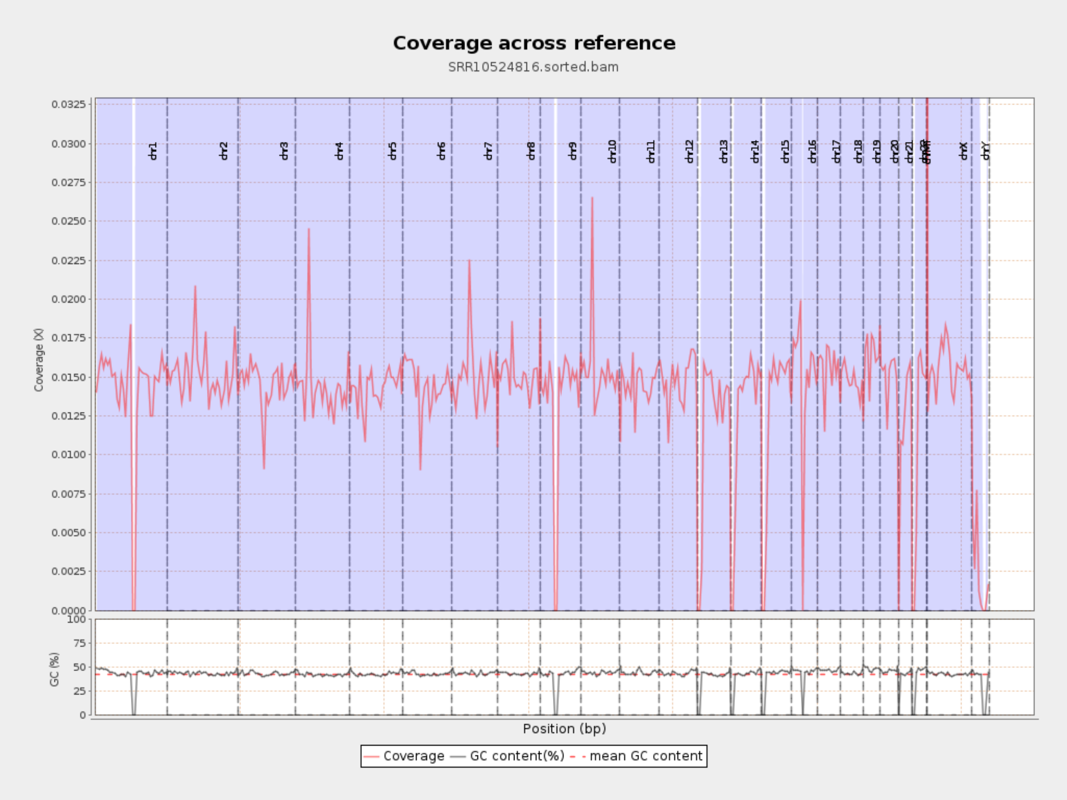
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 220,818 |
| Insertions | 3,150 |
| Mapped reads with at least one insertion | 0.41% |
| Deletions | 8,779 |
| Mapped reads with at least one deletion | 1.14% |
| Homopolymer indels | 43.04% |

## 2.6. Chromosome stats

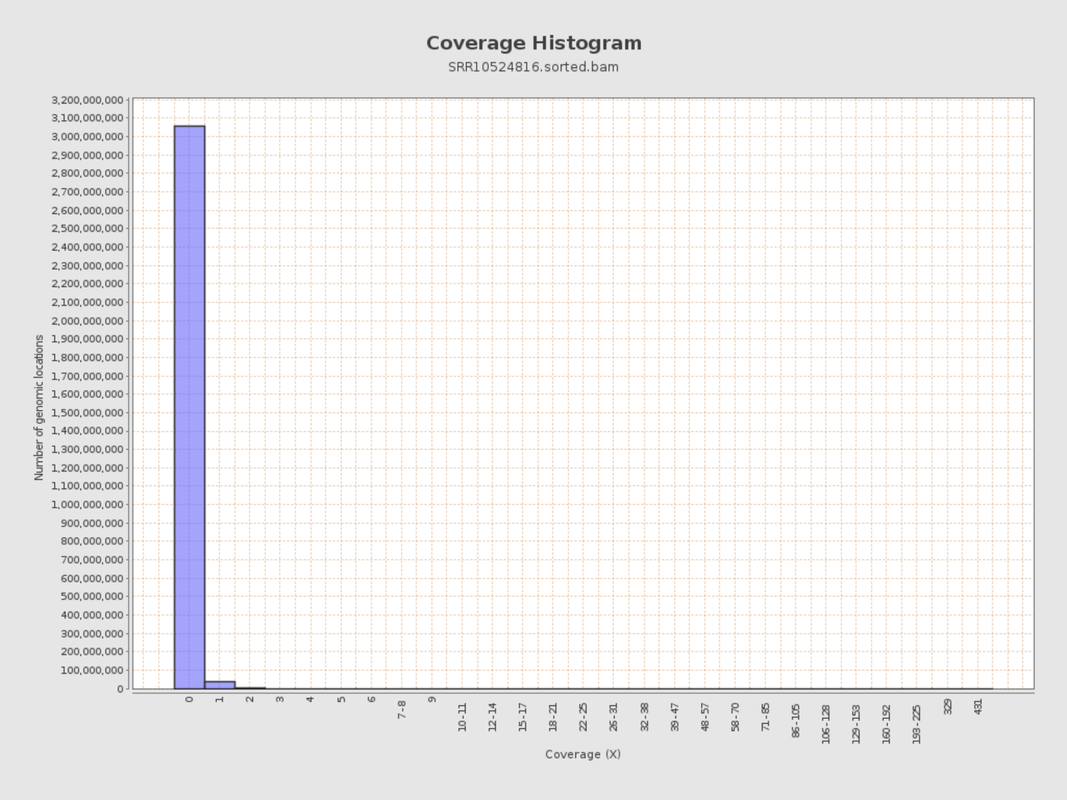
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3496545 | 0.014 | 0.1852 |
| chr2 | 243199373 | 3701986 | 0.0152 | 0.2217 |
| chr3 | 198022430 | 2882267 | 0.0146 | 0.1277 |
| chr4 | 191154276 | 2770052 | 0.0145 | 0.1347 |
| chr5 | 180915260 | 2596831 | 0.0144 | 0.126 |
| chr6 | 171115067 | 2470784 | 0.0144 | 0.134 |
| chr7 | 159138663 | 2420455 | 0.0152 | 0.1753 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2192470 | 0.015 | 0.1424 |
| chr9 | 141213431 | 1865596 | 0.0132 | 0.1354 |
| chr10 | 135534747 | 2103074 | 0.0155 | 0.1608 |
| chr11 | 135006516 | 1958955 | 0.0145 | 0.1398 |
| chr12 | 133851895 | 1978390 | 0.0148 | 0.1288 |
| chr13 | 115169878 | 1363482 | 0.0118 | 0.1143 |
| chr14 | 107349540 | 1325585 | 0.0123 | 0.1177 |
| chr15 | 102531392 | 1277114 | 0.0125 | 0.1182 |
| chr16 | 90354753 | 1323258 | 0.0146 | 0.1334 |
| chr17 | 81195210 | 1262557 | 0.0155 | 0.134 |
| chr18 | 78077248 | 1157416 | 0.0148 | 0.1874 |
| chr19 | 59128983 | 966889 | 0.0164 | 0.1628 |
| chr20 | 63025520 | 943814 | 0.015 | 0.13 |
| chr21 | 48129895 | 578902 | 0.012 | 0.1215 |
| chr22 | 51304566 | 559396 | 0.0109 | 0.1102 |
| chrMT | 16571 | 25827 | 1.5586 | 1.5376 |
| chrX | 155270560 | 2412066 | 0.0155 | 0.136 |
| chrY | 59373566 | 136417 | 0.0023 | 0.0701 |

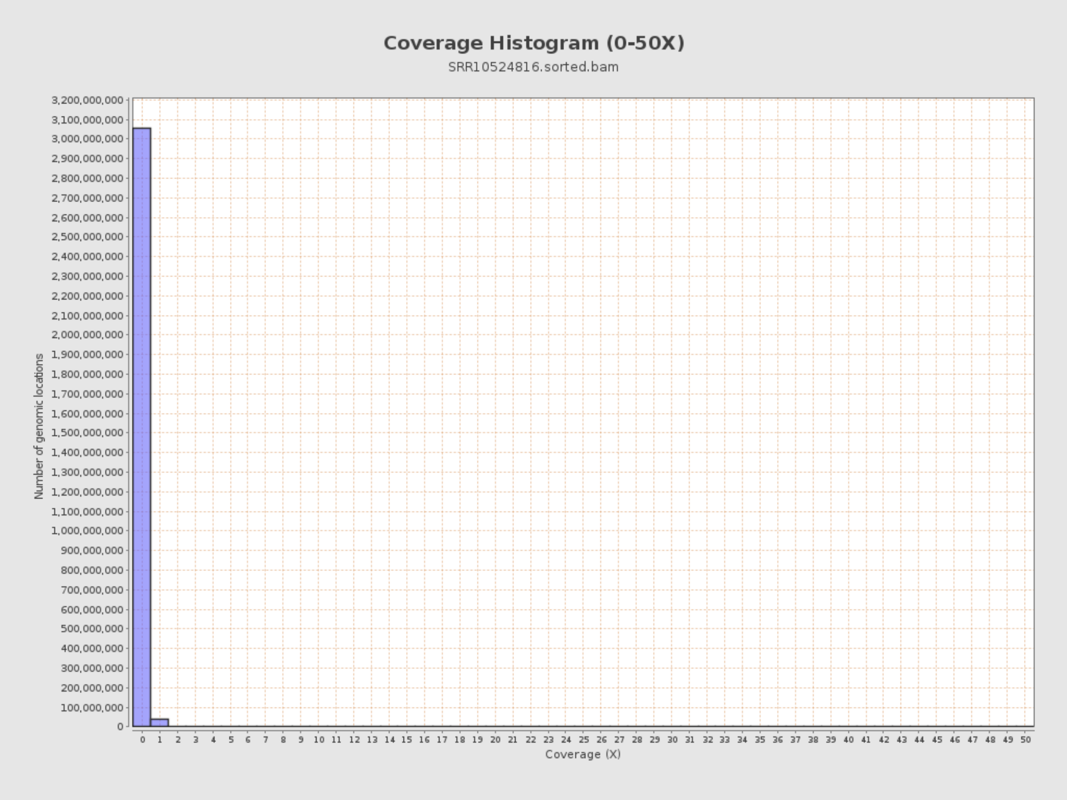
# 3. Results : Coverage across reference



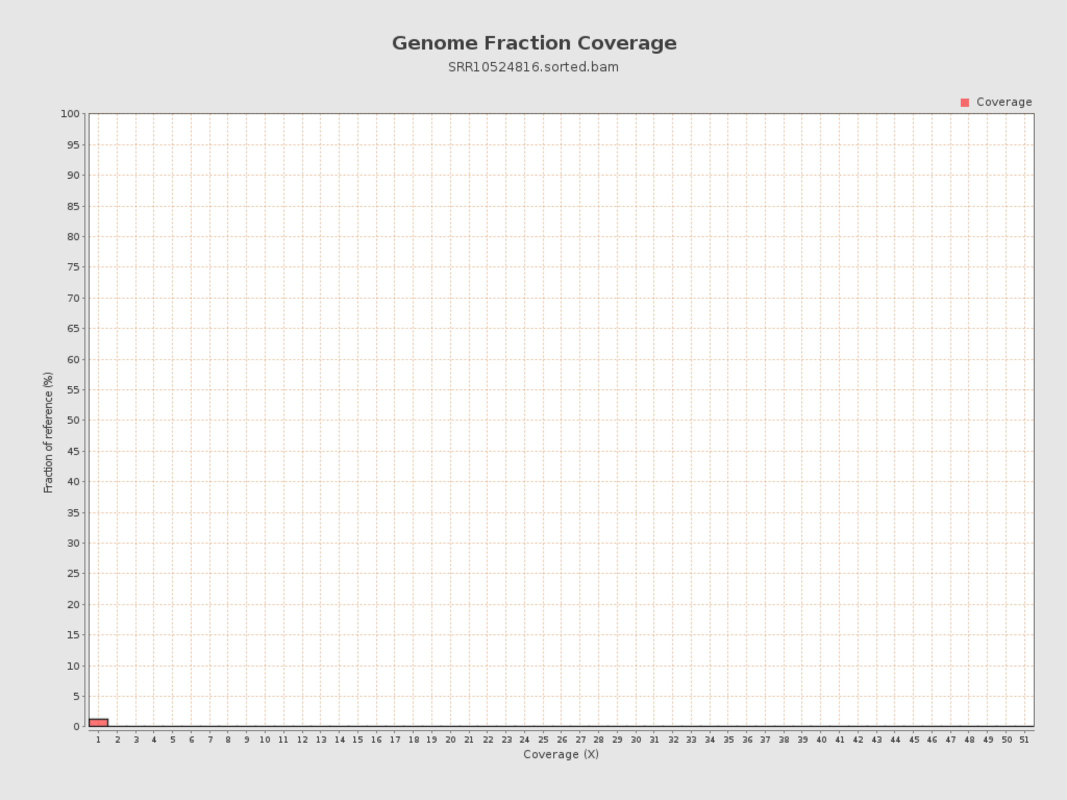
# 4. Results : Coverage Histogram



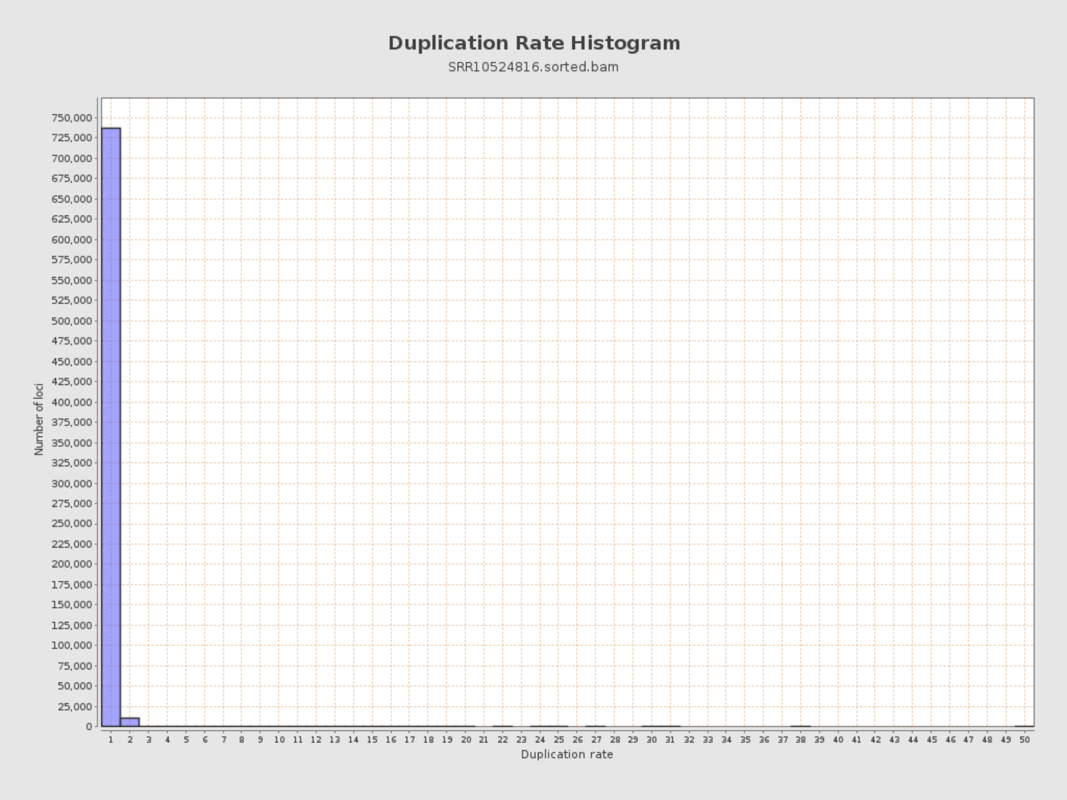
# 5. Results : Coverage Histogram (0-50X)



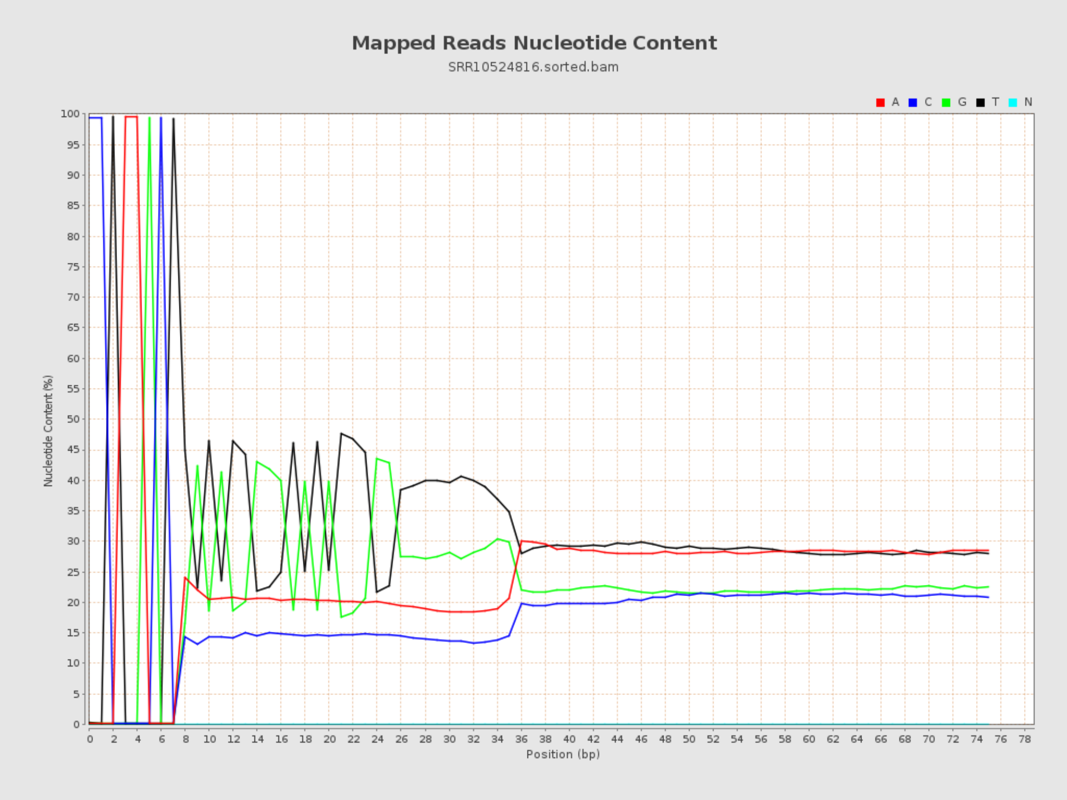
# 6. Results : Genome Fraction Coverage



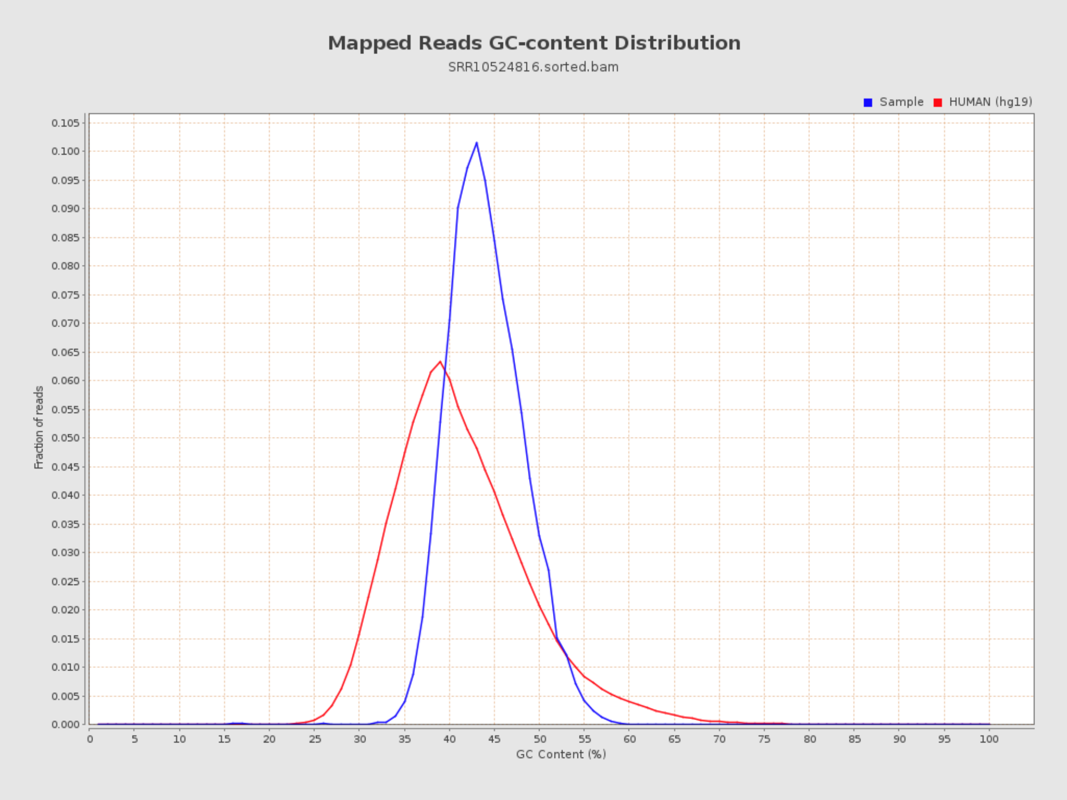
# 7. Results : Duplication Rate Histogram



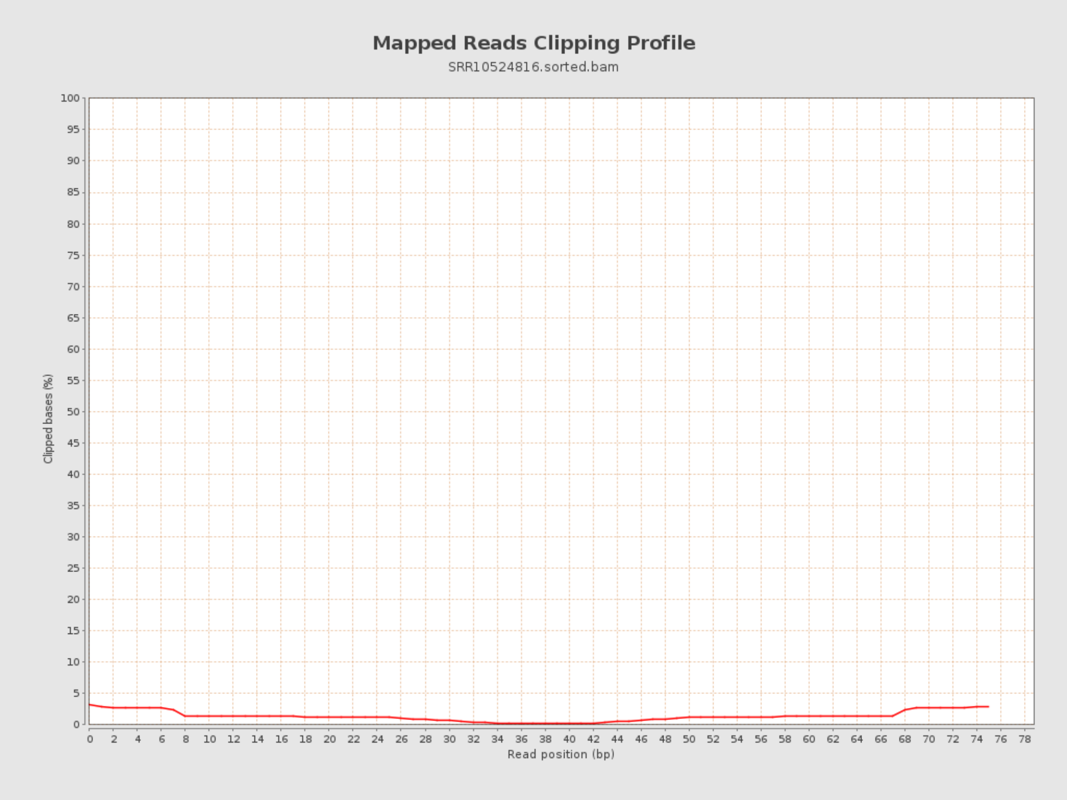
# 8. Results : Mapped Reads Nucleotide Content



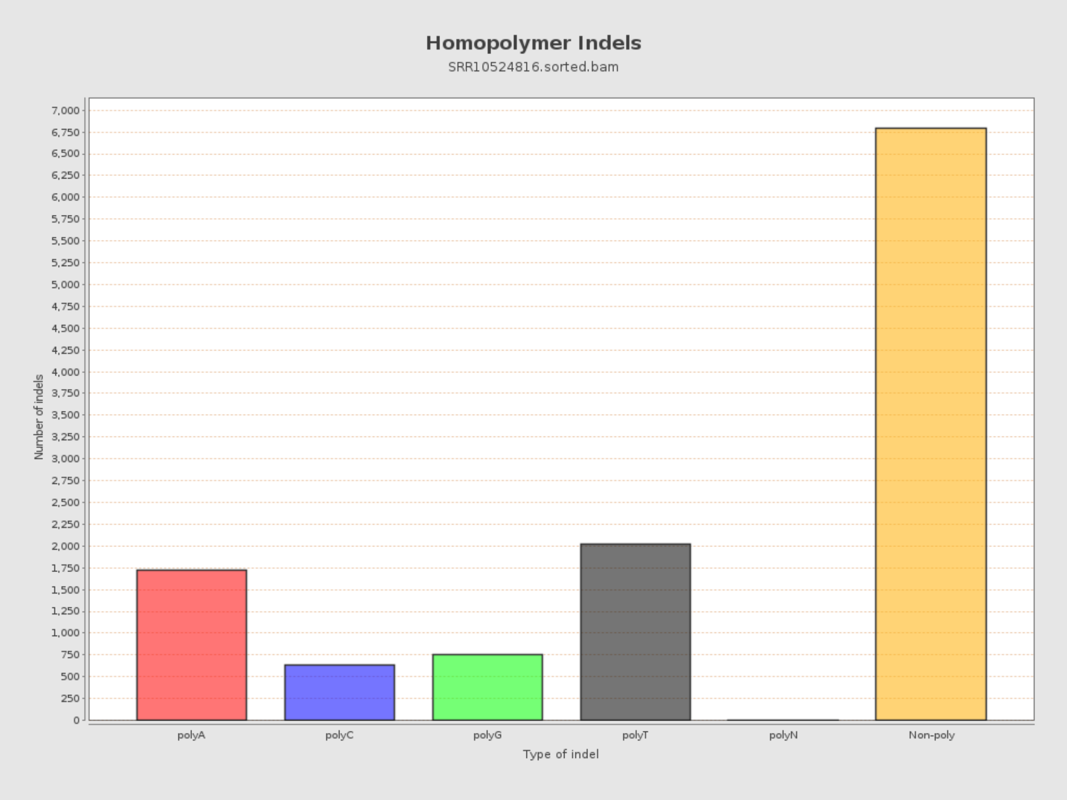
# 9. Results : Mapped Reads GC-content Distribution



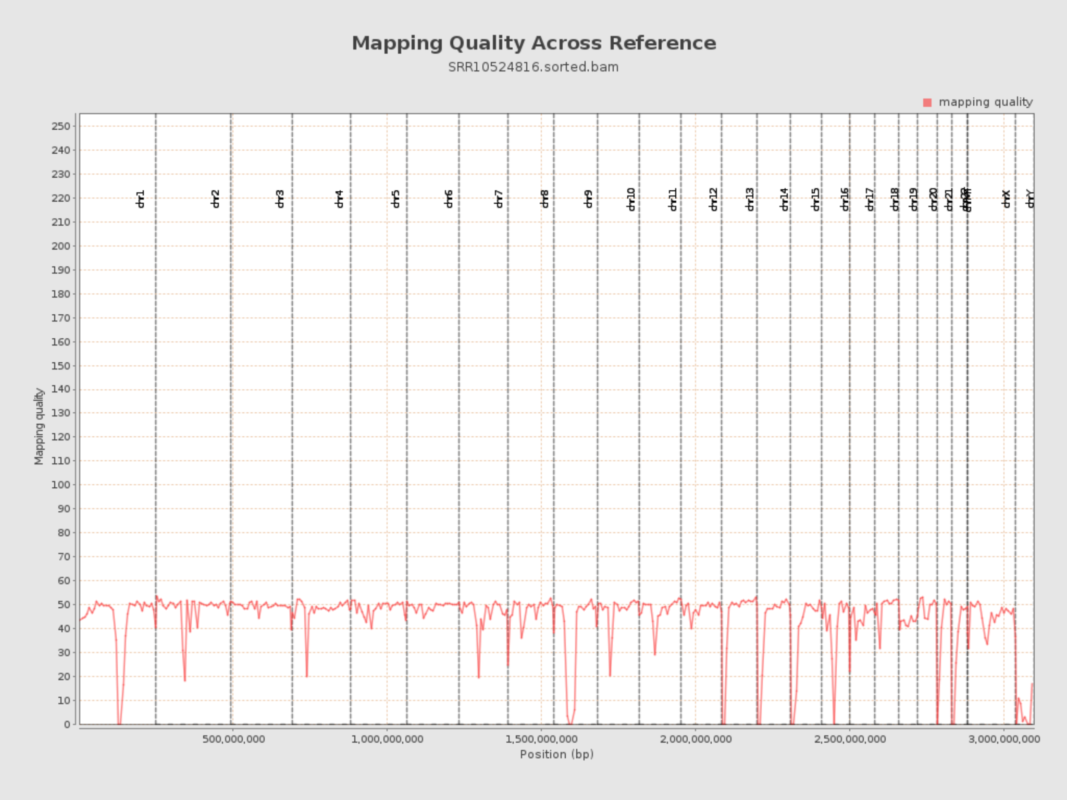
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram