# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 17:45:08*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524718.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_SRR10524718 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524718.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 17:45:07 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524718.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 747,453 |
| Mapped reads | 689,249 / 92.21% |
| Unmapped reads | 58,204 / 7.79% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 2,418 / 0.32% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 17,886 / 2.39% |
| Duplication rate | 1.91% |
| Clipped reads | 690,890 / 92.43% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 10,285,055 / 25.29% |
| Number/percentage of C's | 7,280,237 / 17.9% |
| Number/percentage of T's | 12,711,885 / 31.25% |
| Number/percentage of G's | 10,390,019 / 25.55% |
| Number/percentage of N's | 5,271 / 0.01% |
| GC Percentage | 43.45% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0131 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1547 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.89 |

## 2.5. Mismatches and indels

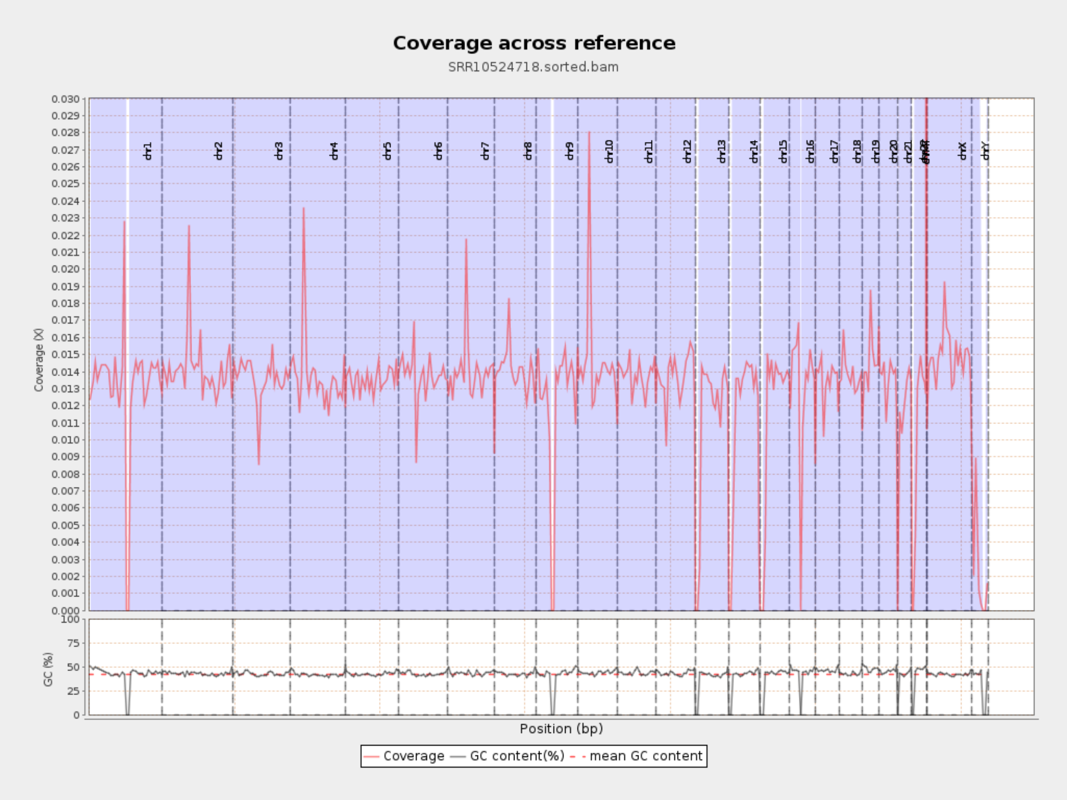
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 204,486 |
| Insertions | 2,579 |
| Mapped reads with at least one insertion | 0.37% |
| Deletions | 7,700 |
| Mapped reads with at least one deletion | 1.11% |
| Homopolymer indels | 44.59% |

## 2.6. Chromosome stats

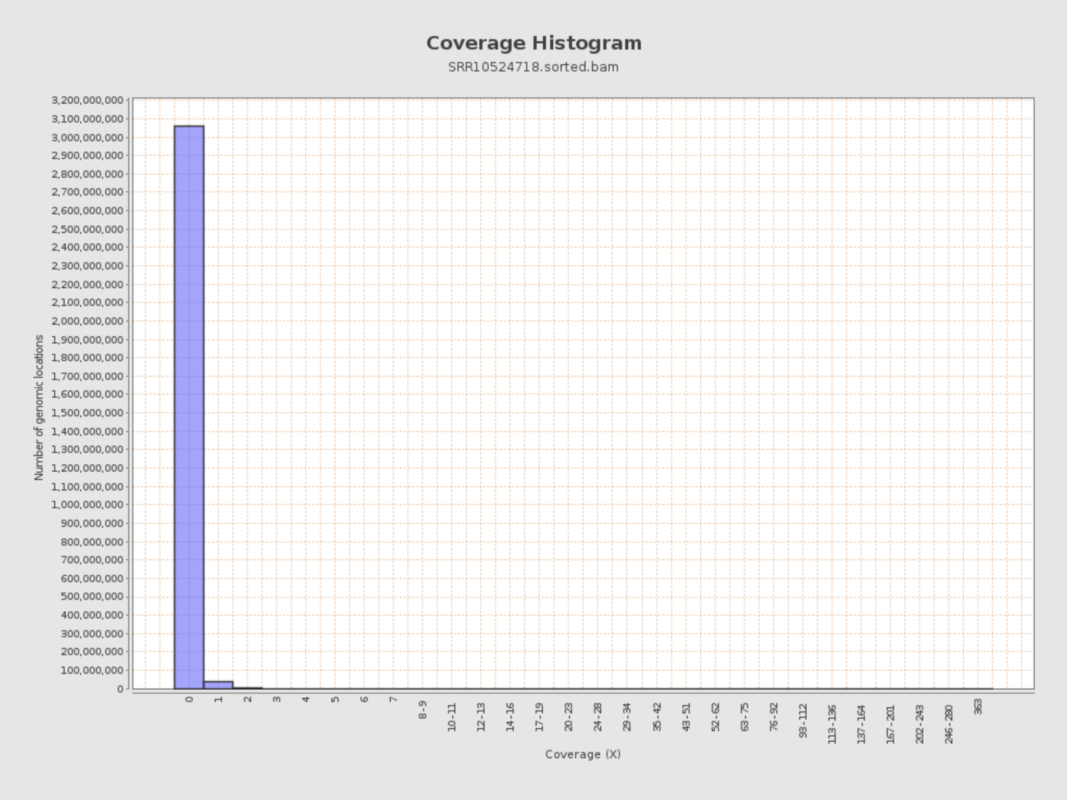
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3266505 | 0.0131 | 0.244 |
| chr2 | 243199373 | 3452839 | 0.0142 | 0.1996 |
| chr3 | 198022430 | 2688402 | 0.0136 | 0.1215 |
| chr4 | 191154276 | 2622270 | 0.0137 | 0.1326 |
| chr5 | 180915260 | 2444958 | 0.0135 | 0.122 |
| chr6 | 171115067 | 2354427 | 0.0138 | 0.1341 |
| chr7 | 159138663 | 2241141 | 0.0141 | 0.1722 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2059249 | 0.0141 | 0.1598 |
| chr9 | 141213431 | 1689410 | 0.012 | 0.1328 |
| chr10 | 135534747 | 1979403 | 0.0146 | 0.1669 |
| chr11 | 135006516 | 1856725 | 0.0138 | 0.139 |
| chr12 | 133851895 | 1839879 | 0.0137 | 0.1232 |
| chr13 | 115169878 | 1266153 | 0.011 | 0.1093 |
| chr14 | 107349540 | 1205587 | 0.0112 | 0.1114 |
| chr15 | 102531392 | 1152510 | 0.0112 | 0.1109 |
| chr16 | 90354753 | 1180128 | 0.0131 | 0.1245 |
| chr17 | 81195210 | 1091918 | 0.0134 | 0.1248 |
| chr18 | 78077248 | 1082515 | 0.0139 | 0.2078 |
| chr19 | 59128983 | 866064 | 0.0146 | 0.2069 |
| chr20 | 63025520 | 854753 | 0.0136 | 0.123 |
| chr21 | 48129895 | 541780 | 0.0113 | 0.1201 |
| chr22 | 51304566 | 485122 | 0.0095 | 0.1024 |
| chrMT | 16571 | 14907 | 0.8996 | 1.077 |
| chrX | 155270560 | 2307441 | 0.0149 | 0.1343 |
| chrY | 59373566 | 140652 | 0.0024 | 0.0953 |

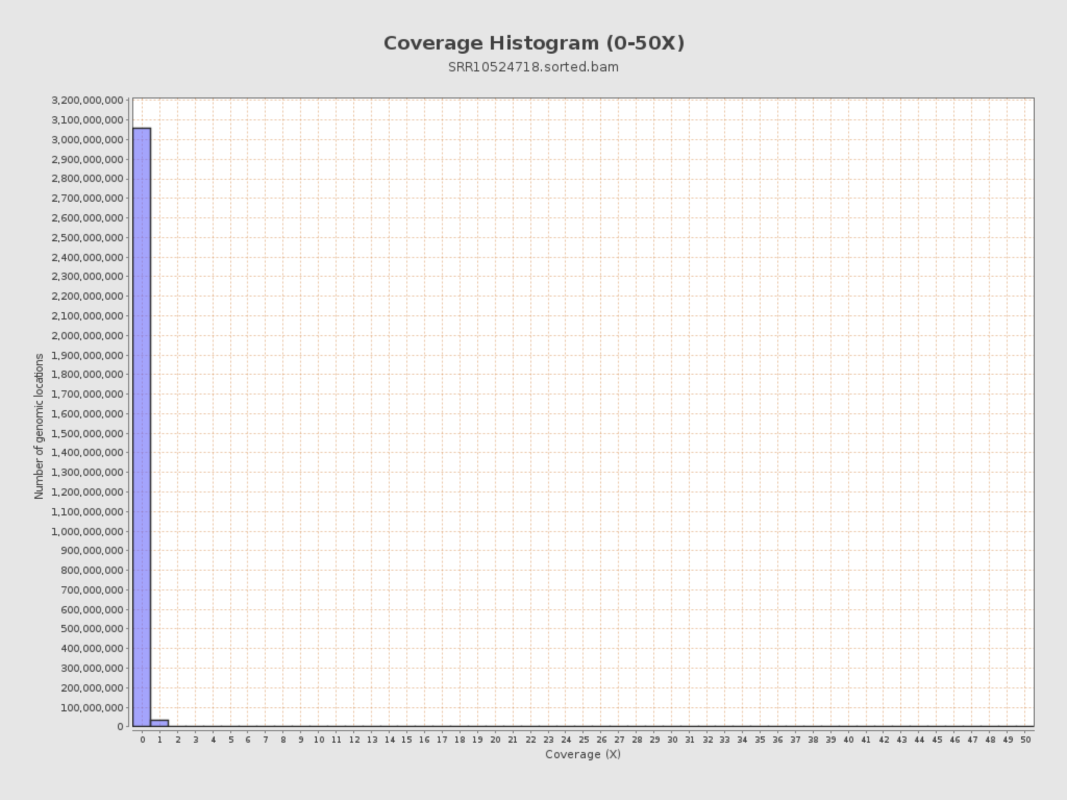
# 3. Results : Coverage across reference



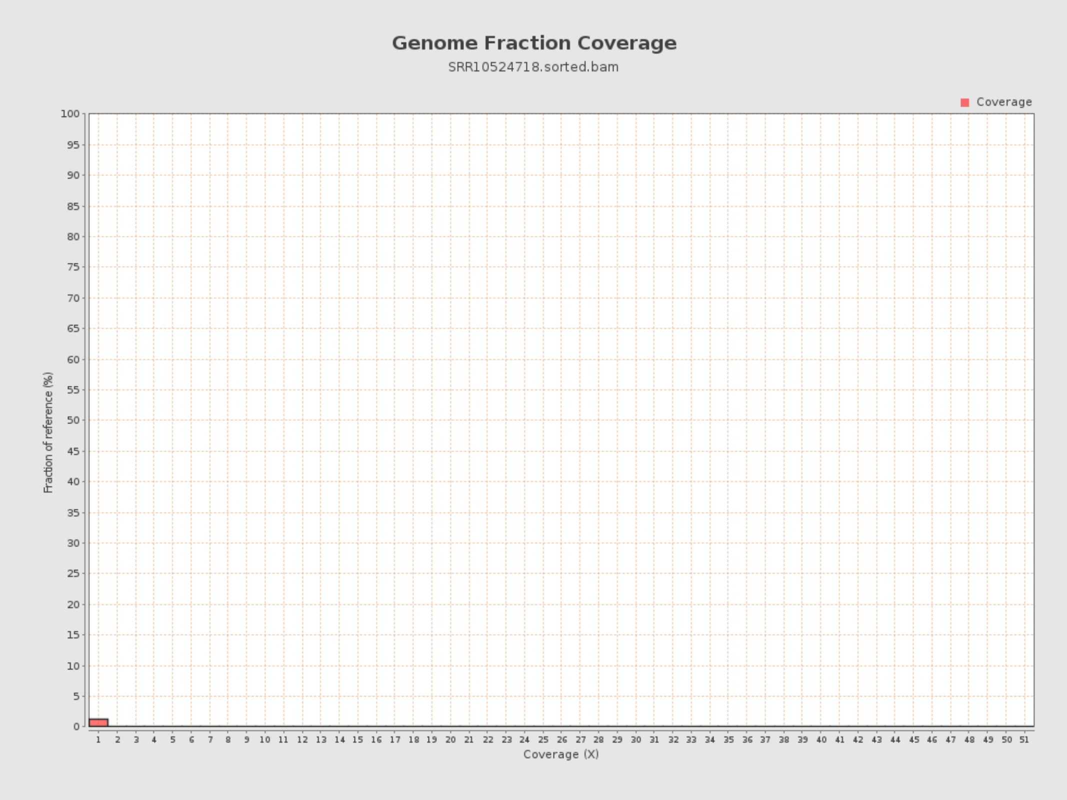
# 4. Results : Coverage Histogram



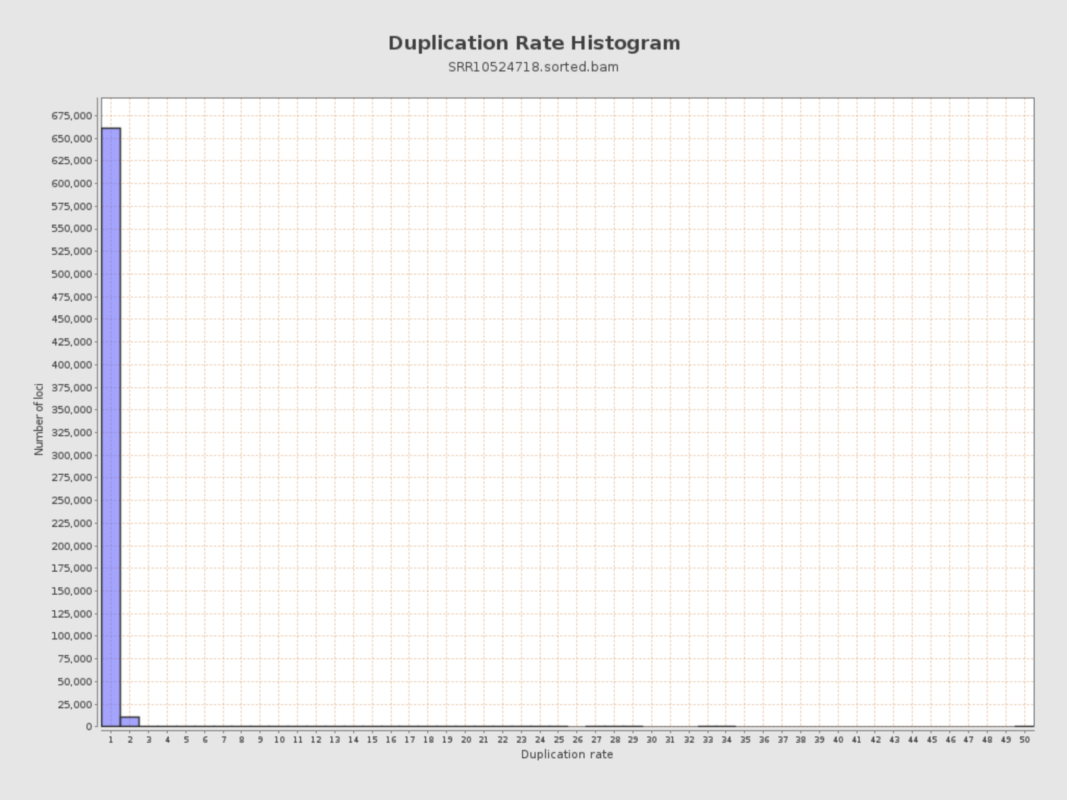
# 5. Results : Coverage Histogram (0-50X)



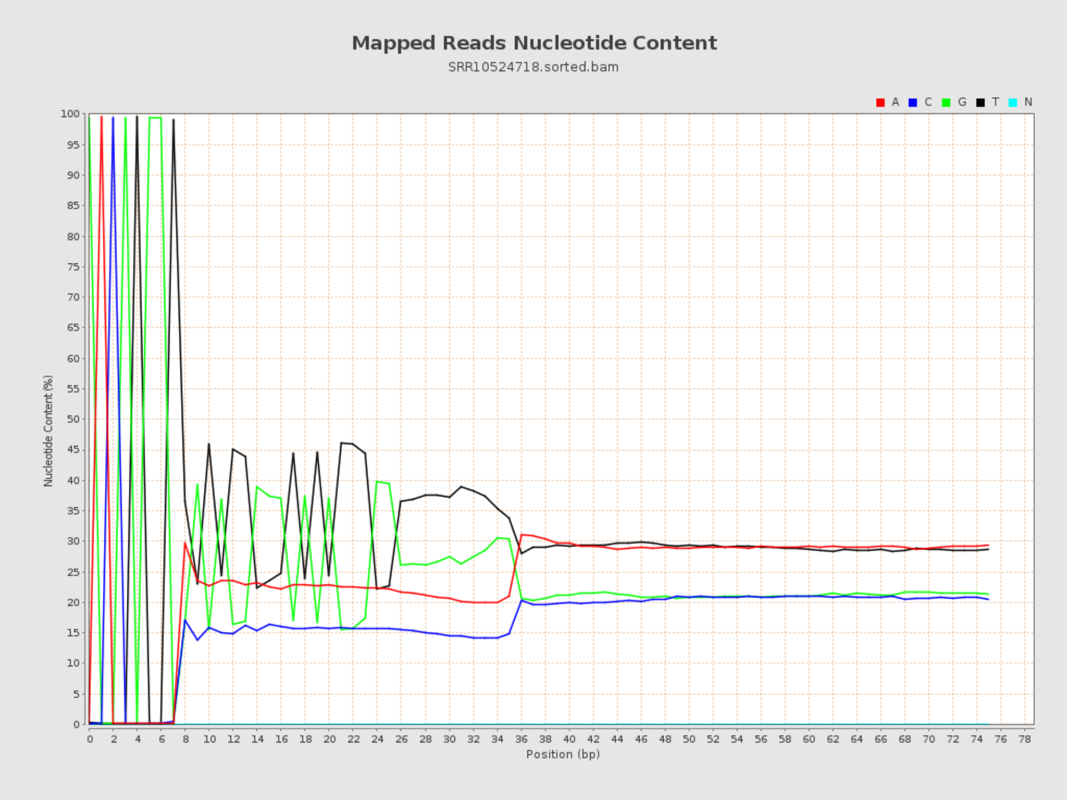
# 6. Results : Genome Fraction Coverage



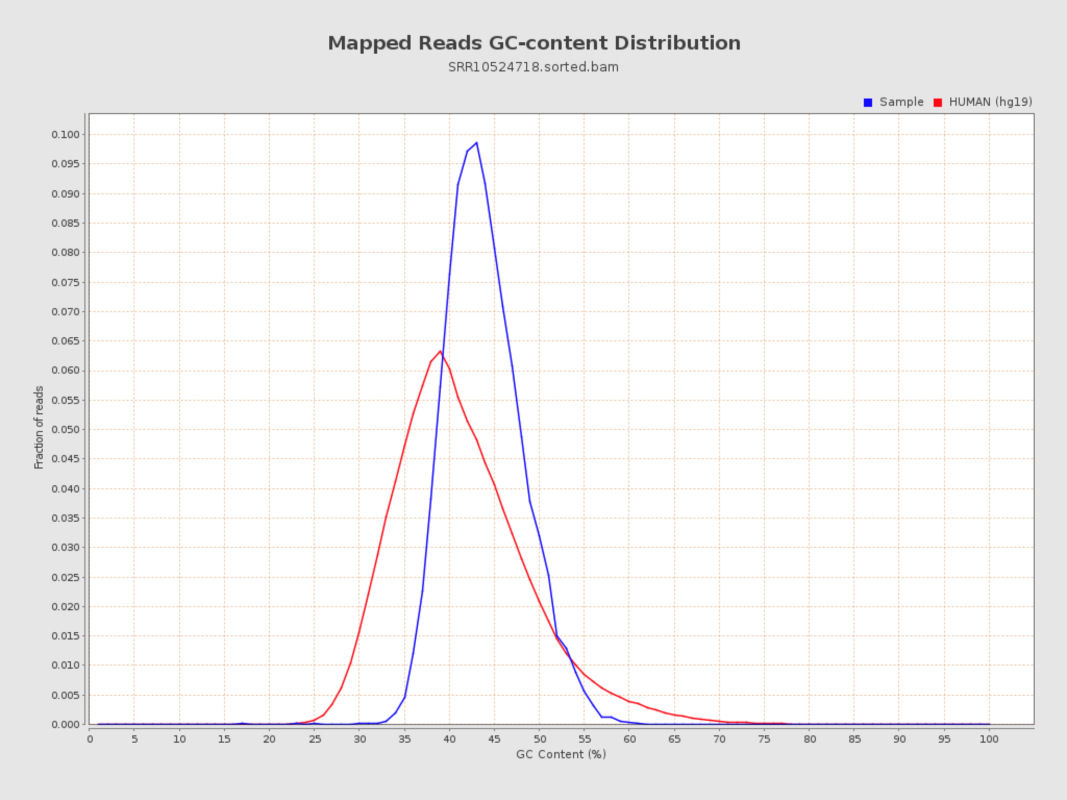
# 7. Results : Duplication Rate Histogram



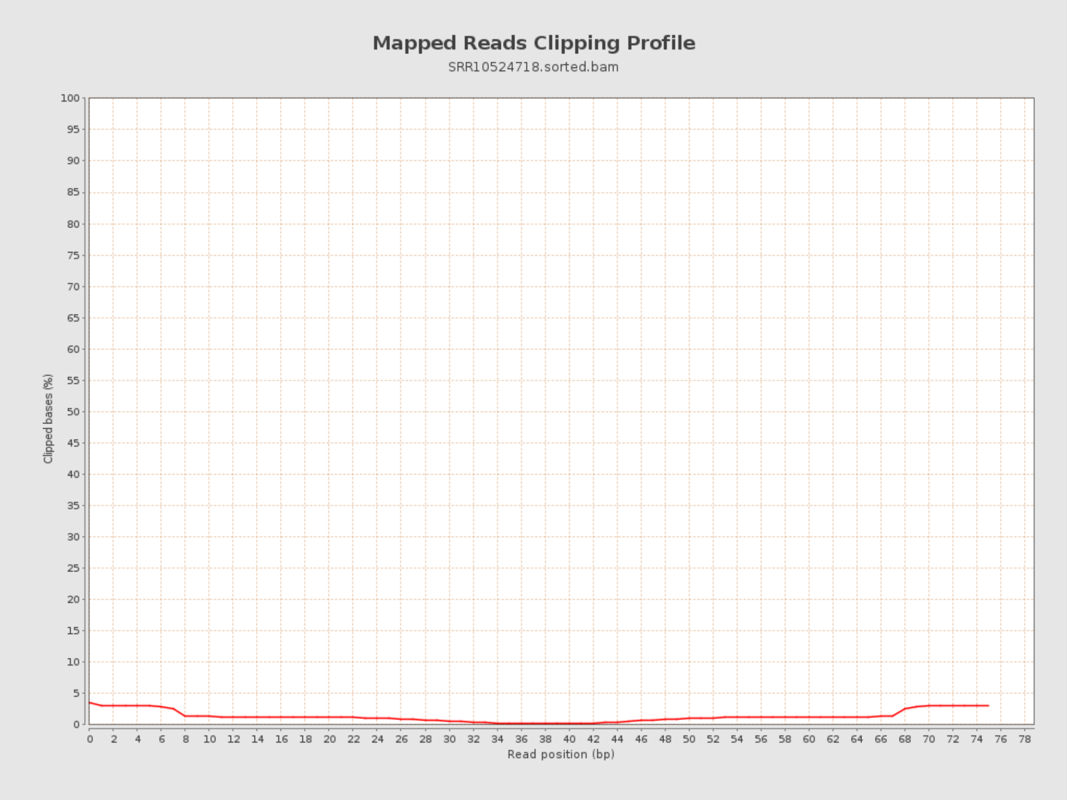
# 8. Results : Mapped Reads Nucleotide Content



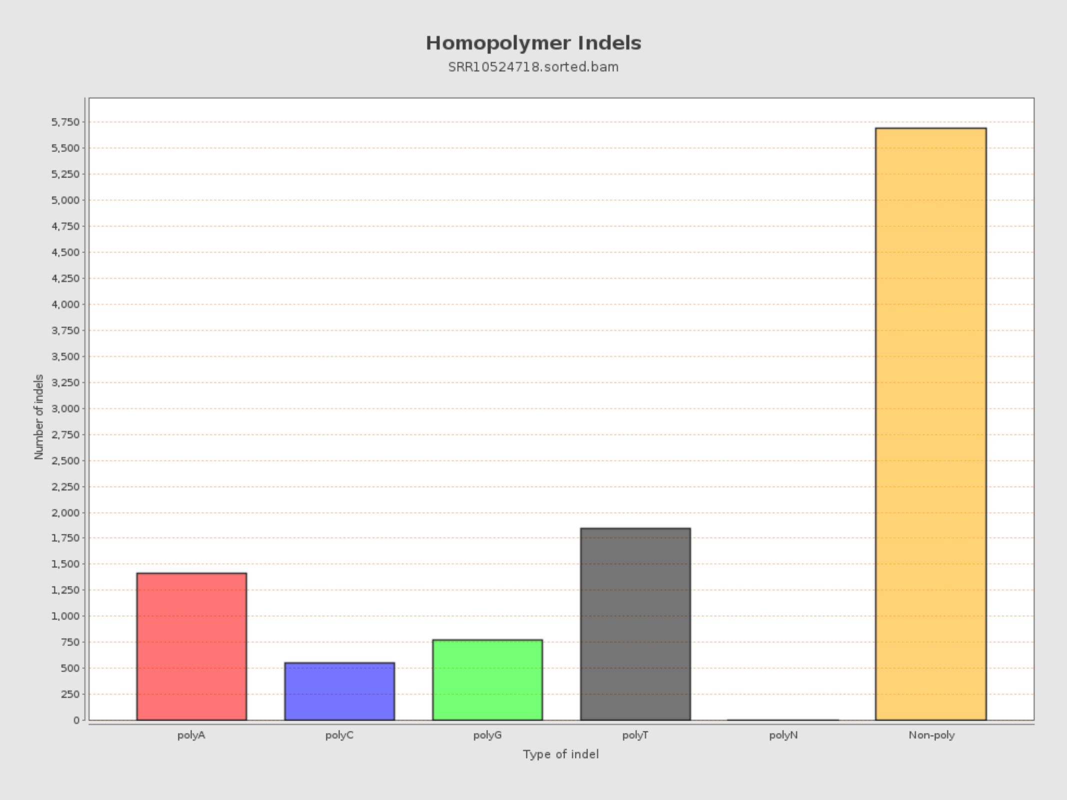
# 9. Results : Mapped Reads GC-content Distribution



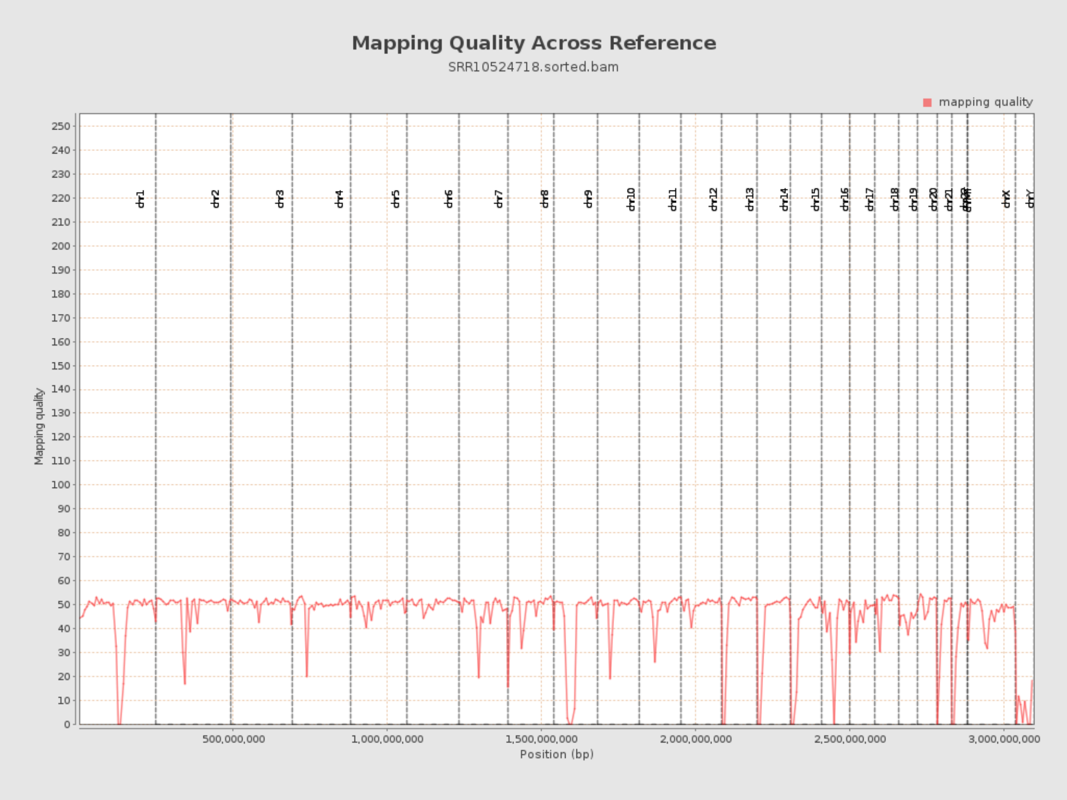
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram