# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 17:46:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524719.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_SRR10524719 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524719.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 17:46:49 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524719.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 609,017 |
| Mapped reads | 559,383 / 91.85% |
| Unmapped reads | 49,634 / 8.15% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,887 / 0.31% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 12,510 / 2.05% |
| Duplication rate | 1.62% |
| Clipped reads | 559,519 / 91.87% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 8,247,950 / 25.15% |
| Number/percentage of C's | 6,360,474 / 19.39% |
| Number/percentage of T's | 10,316,708 / 31.45% |
| Number/percentage of G's | 7,869,566 / 23.99% |
| Number/percentage of N's | 4,678 / 0.01% |
| GC Percentage | 43.39% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0106 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1336 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.63 |

## 2.5. Mismatches and indels

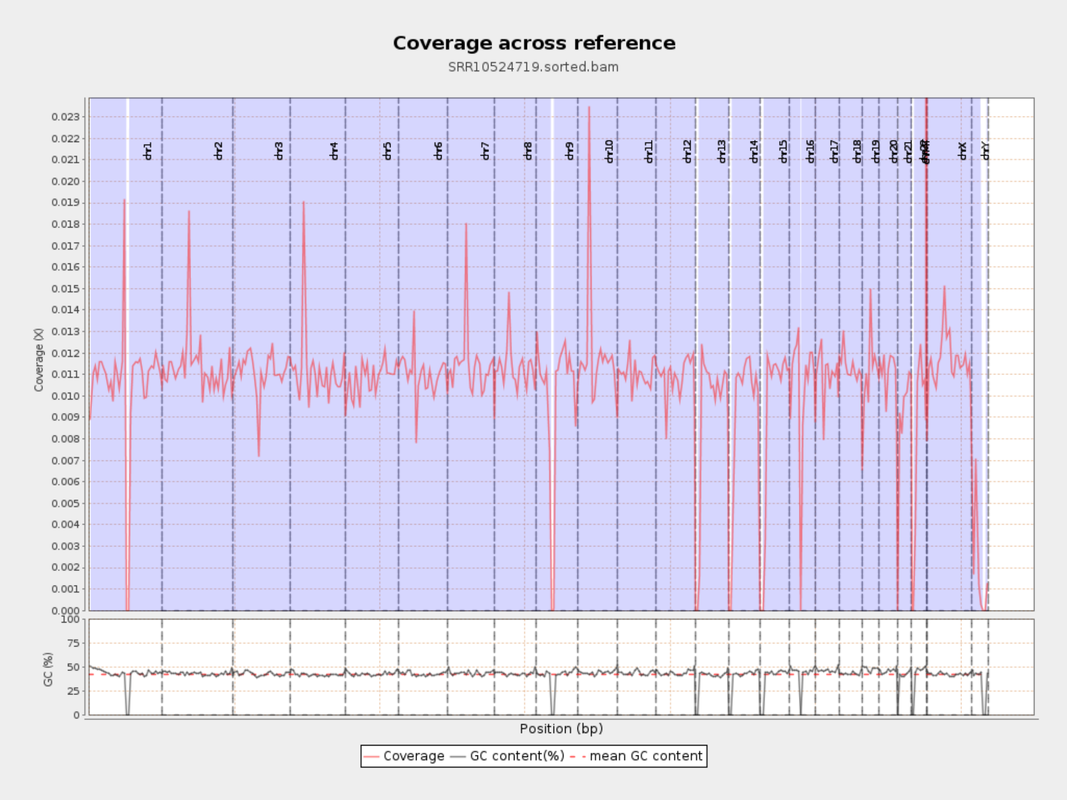
| | |
|---|---|
| General error rate | 0.53% |
| Mismatches | 167,051 |
| Insertions | 2,812 |
| Mapped reads with at least one insertion | 0.5% |
| Deletions | 6,258 |
| Mapped reads with at least one deletion | 1.11% |
| Homopolymer indels | 41.61% |

## 2.6. Chromosome stats

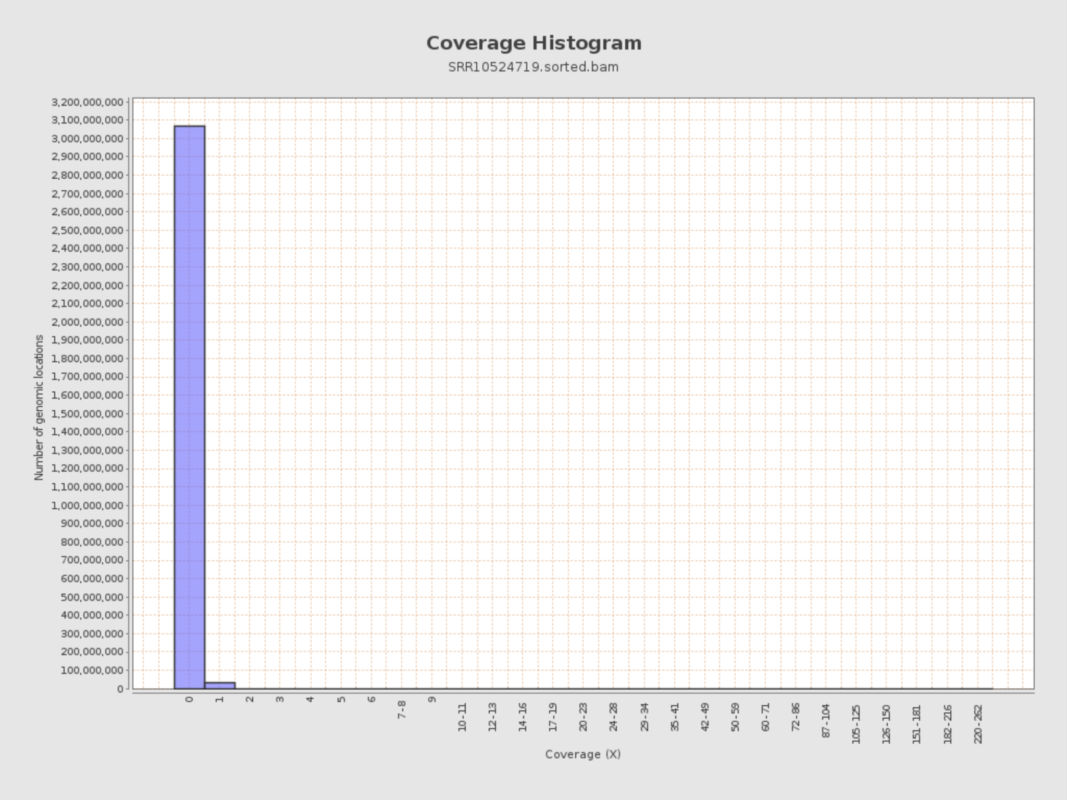
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 2626973 | 0.0105 | 0.2119 |
| chr2 | 243199373 | 2775397 | 0.0114 | 0.1632 |
| chr3 | 198022430 | 2201040 | 0.0111 | 0.109 |
| chr4 | 191154276 | 2137235 | 0.0112 | 0.1155 |
| chr5 | 180915260 | 1963133 | 0.0109 | 0.1079 |
| chr6 | 171115067 | 1885435 | 0.011 | 0.1175 |
| chr7 | 159138663 | 1829442 | 0.0115 | 0.1527 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1661028 | 0.0113 | 0.1398 |
| chr9 | 141213431 | 1380749 | 0.0098 | 0.1164 |
| chr10 | 135534747 | 1619389 | 0.0119 | 0.1397 |
| chr11 | 135006516 | 1491645 | 0.011 | 0.1209 |
| chr12 | 133851895 | 1462203 | 0.0109 | 0.1091 |
| chr13 | 115169878 | 1038795 | 0.009 | 0.0986 |
| chr14 | 107349540 | 969124 | 0.009 | 0.0993 |
| chr15 | 102531392 | 937484 | 0.0091 | 0.0993 |
| chr16 | 90354753 | 937980 | 0.0104 | 0.1096 |
| chr17 | 81195210 | 890407 | 0.011 | 0.1114 |
| chr18 | 78077248 | 890287 | 0.0114 | 0.1762 |
| chr19 | 59128983 | 661754 | 0.0112 | 0.1675 |
| chr20 | 63025520 | 699281 | 0.0111 | 0.1097 |
| chr21 | 48129895 | 430464 | 0.0089 | 0.106 |
| chr22 | 51304566 | 390172 | 0.0076 | 0.0904 |
| chrMT | 16571 | 7503 | 0.4528 | 0.7657 |
| chrX | 155270560 | 1809463 | 0.0117 | 0.1165 |
| chrY | 59373566 | 113131 | 0.0019 | 0.0763 |

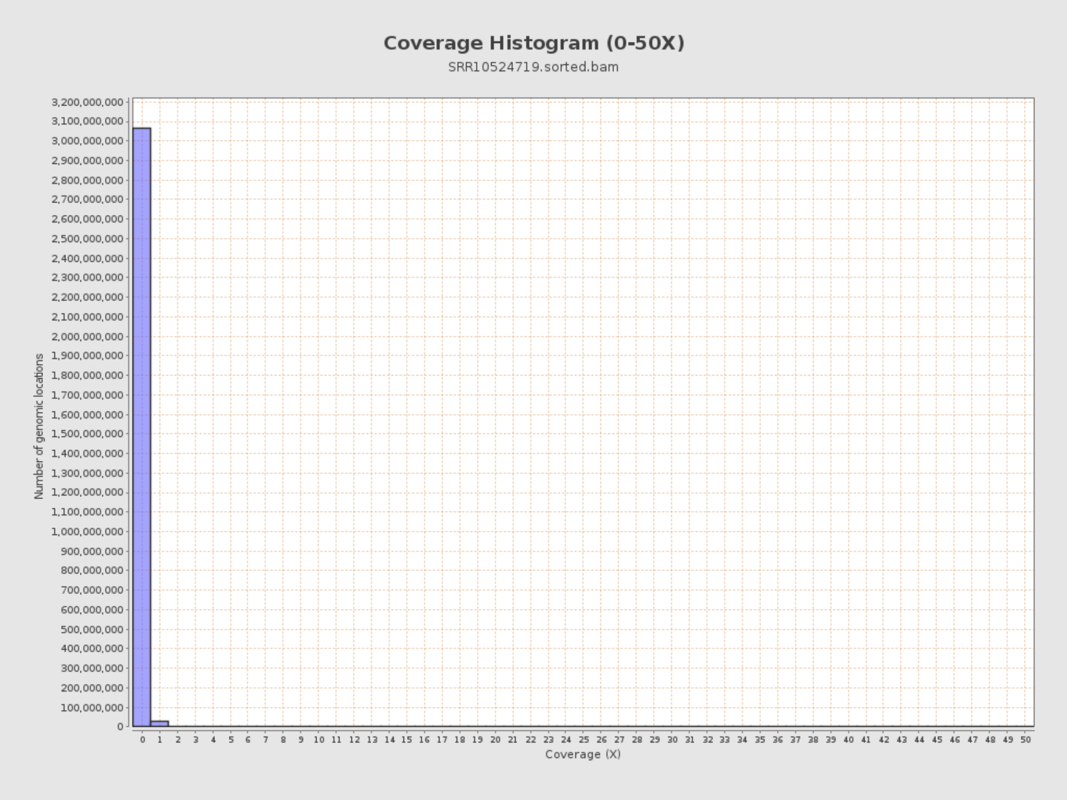
# 3. Results : Coverage across reference



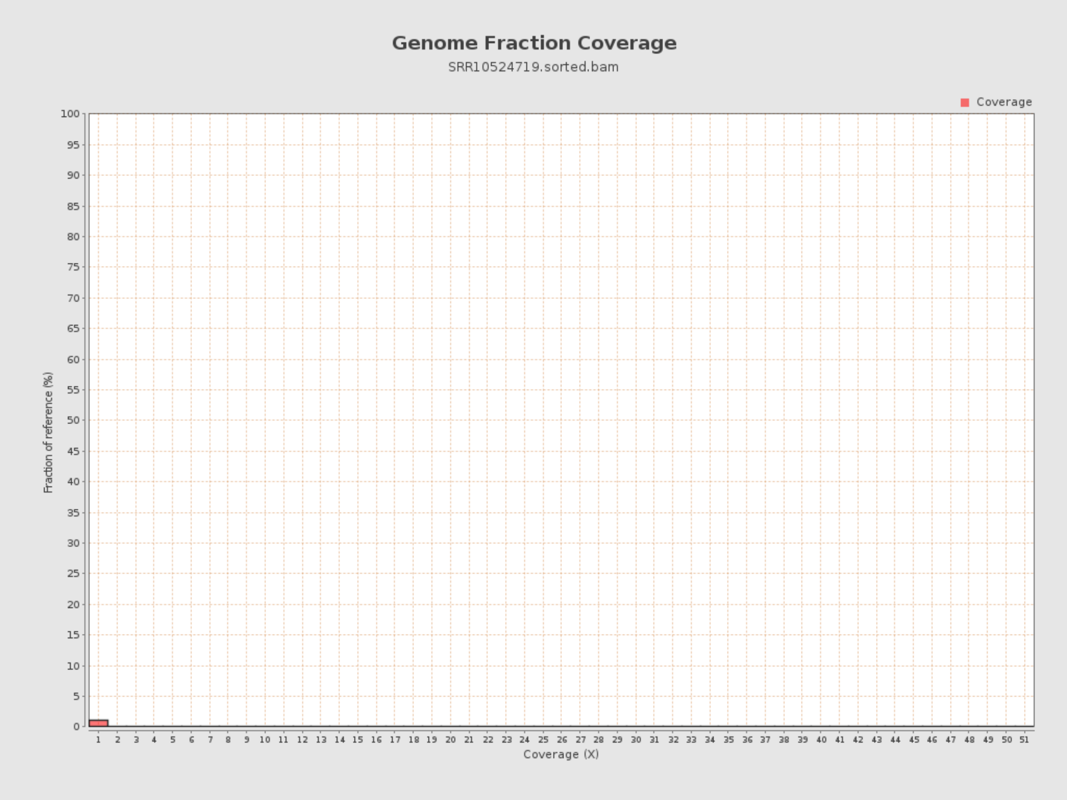
# 4. Results : Coverage Histogram



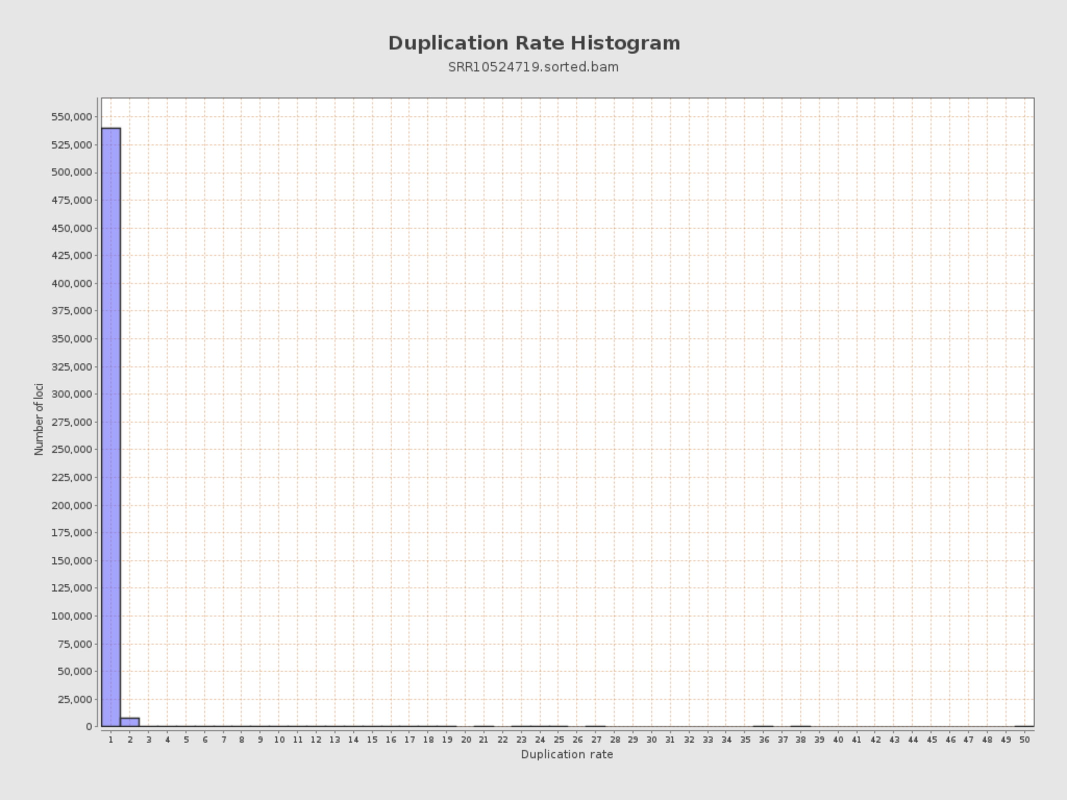
# 5. Results : Coverage Histogram (0-50X)



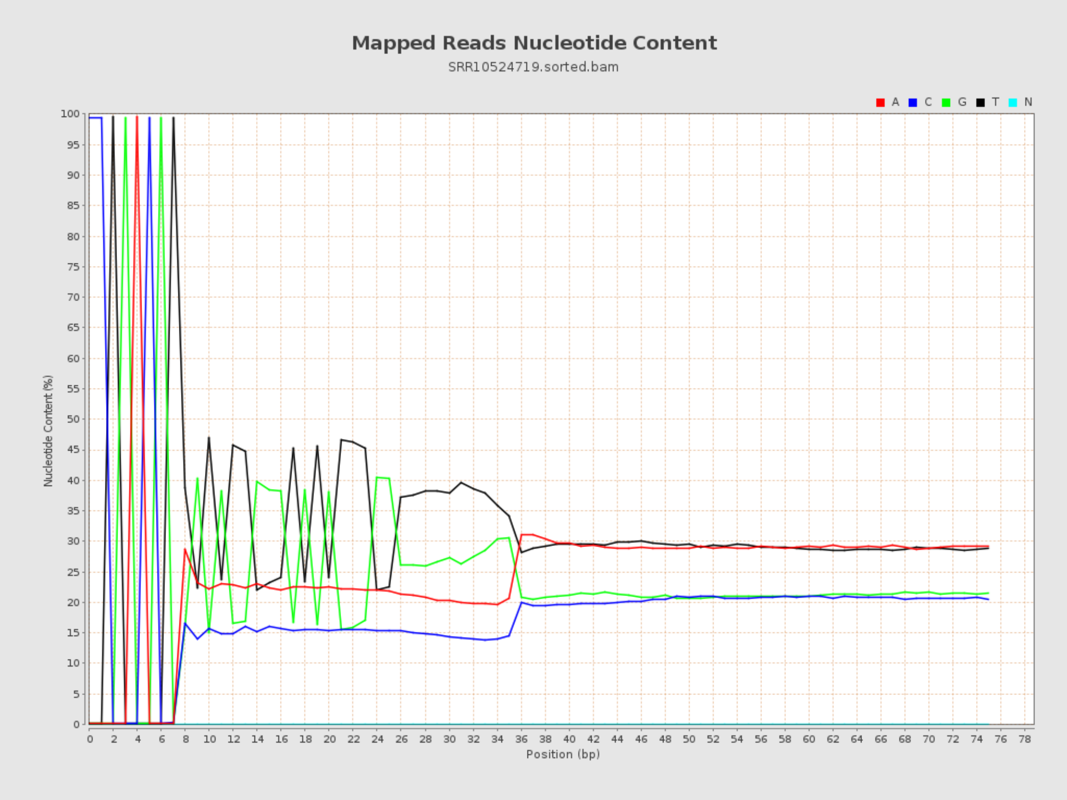
# 6. Results : Genome Fraction Coverage



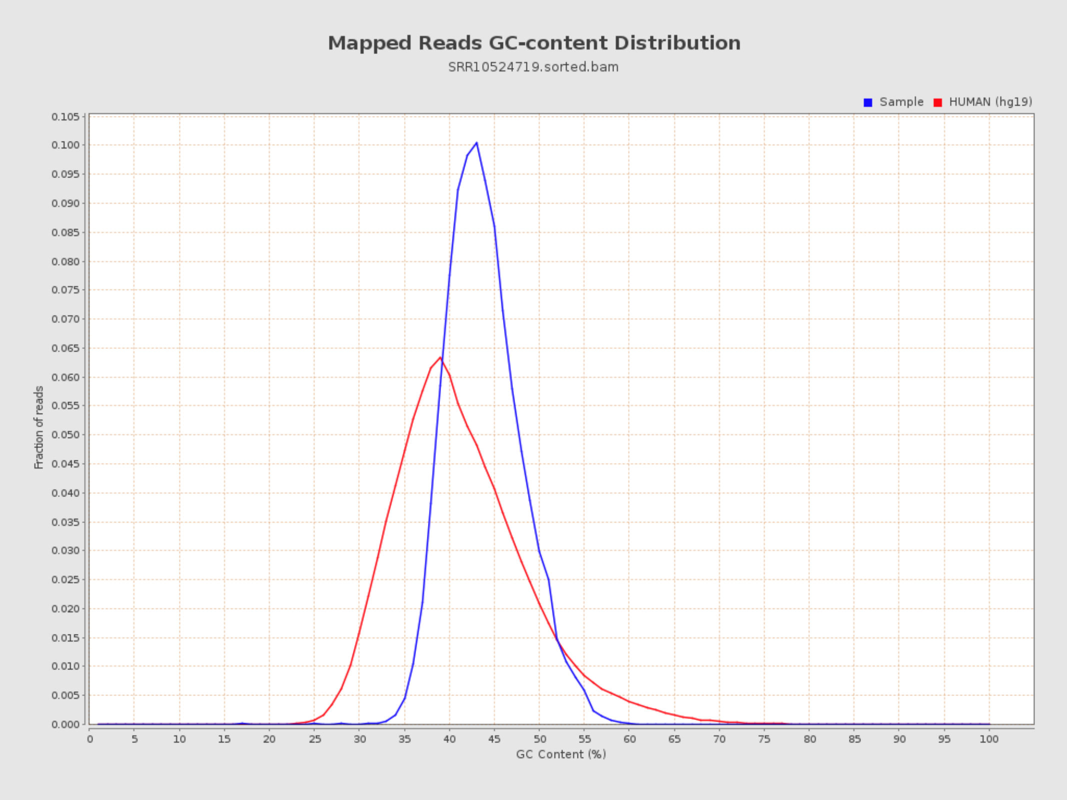
# 7. Results : Duplication Rate Histogram



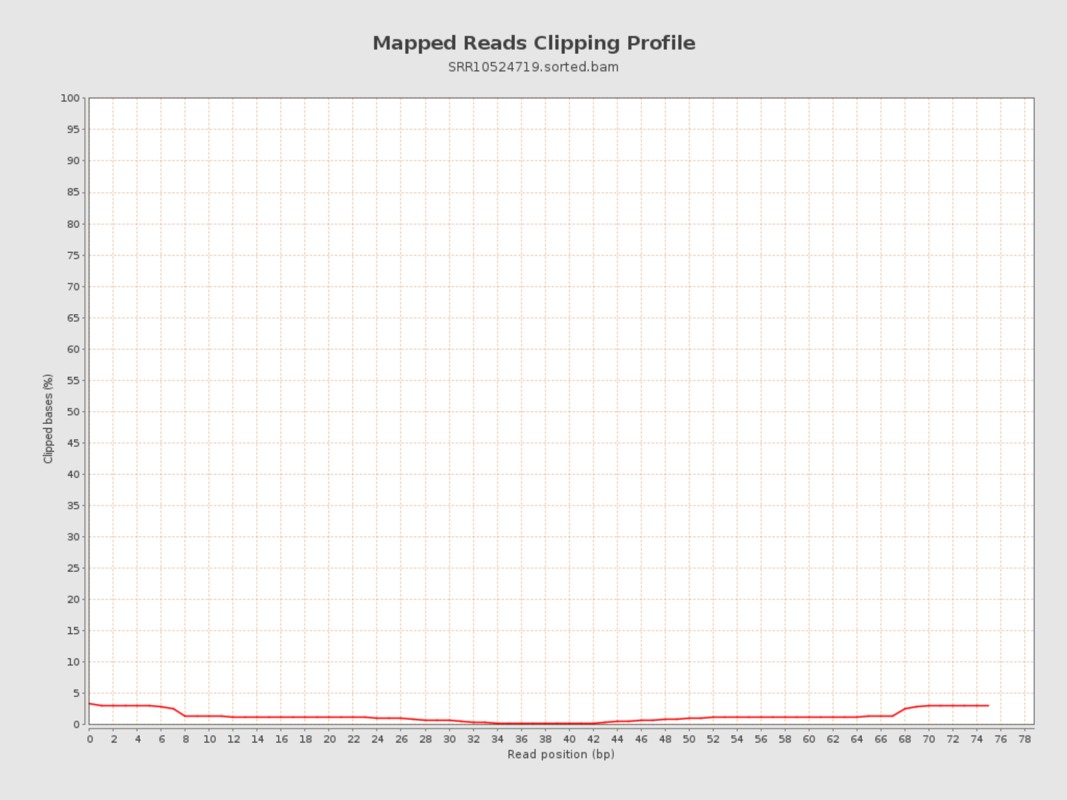
# 8. Results : Mapped Reads Nucleotide Content



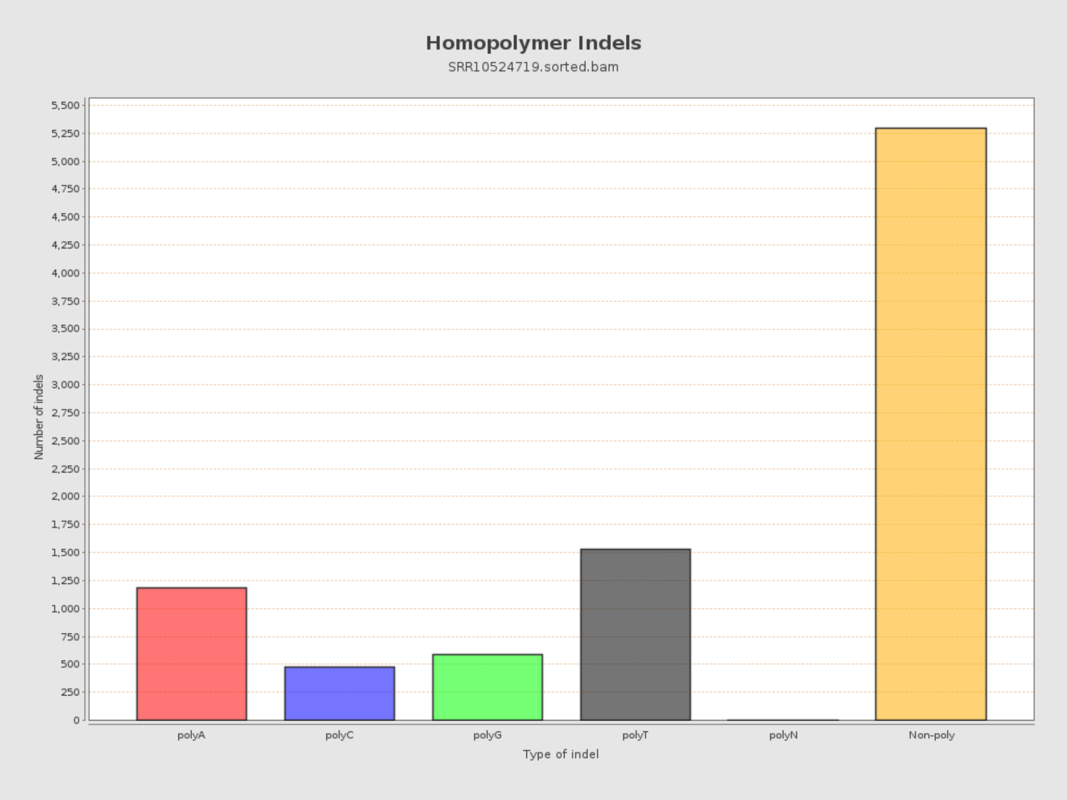
# 9. Results : Mapped Reads GC-content Distribution



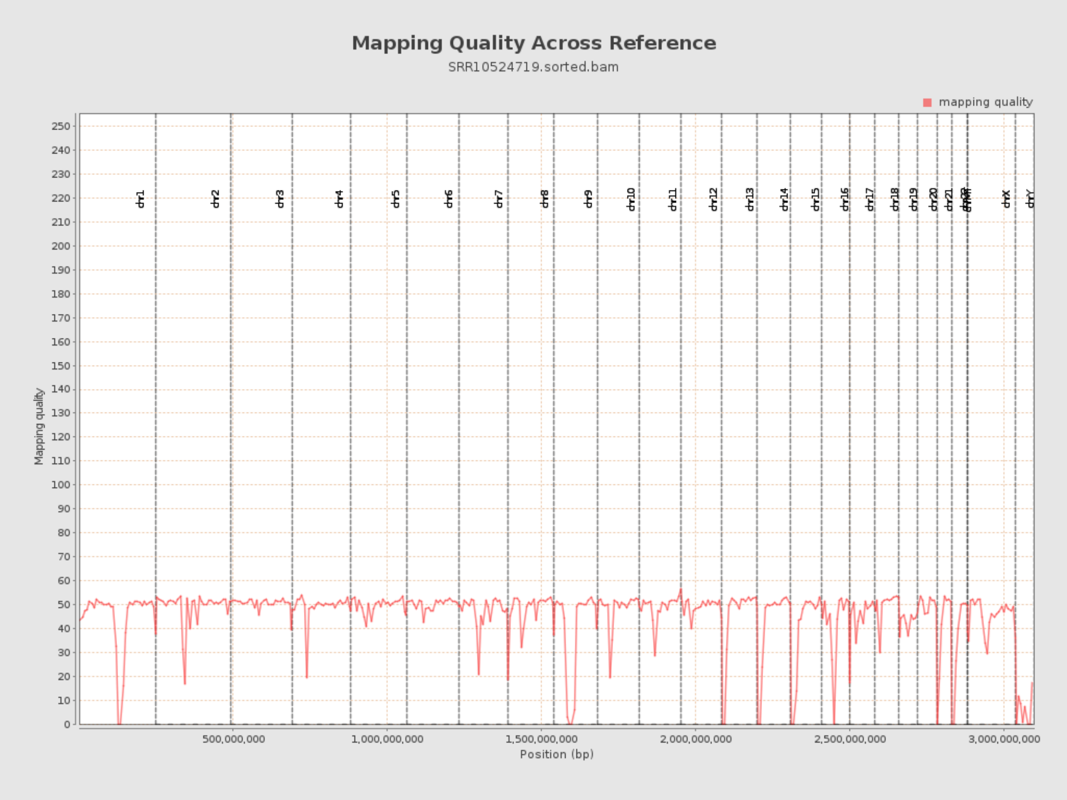
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram