# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 00:56:36*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819118.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_SRR1819118 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819118.fastq.gz` |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 00:56:36 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1819118.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,083,117 |
| Mapped reads | 993,995 / 91.77% |
| Unmapped reads | 89,122 / 8.23% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,936 / 0.36% |
| Read min/max/mean length | 30 / 76 / 76.12 |
| Duplicated reads (estimated) | 28,353 / 2.62% |
| Duplication rate | 2.14% |
| Clipped reads | 996,693 / 92.02% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 13,764,509 / 23.79% |
| Number/percentage of C's | 10,888,999 / 18.82% |
| Number/percentage of T's | 18,540,884 / 32.05% |
| Number/percentage of G's | 14,651,707 / 25.33% |
| Number/percentage of N's | 782 / 0% |
| GC Percentage | 44.15% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0187 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1879 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.86 |

## 2.5. Mismatches and indels

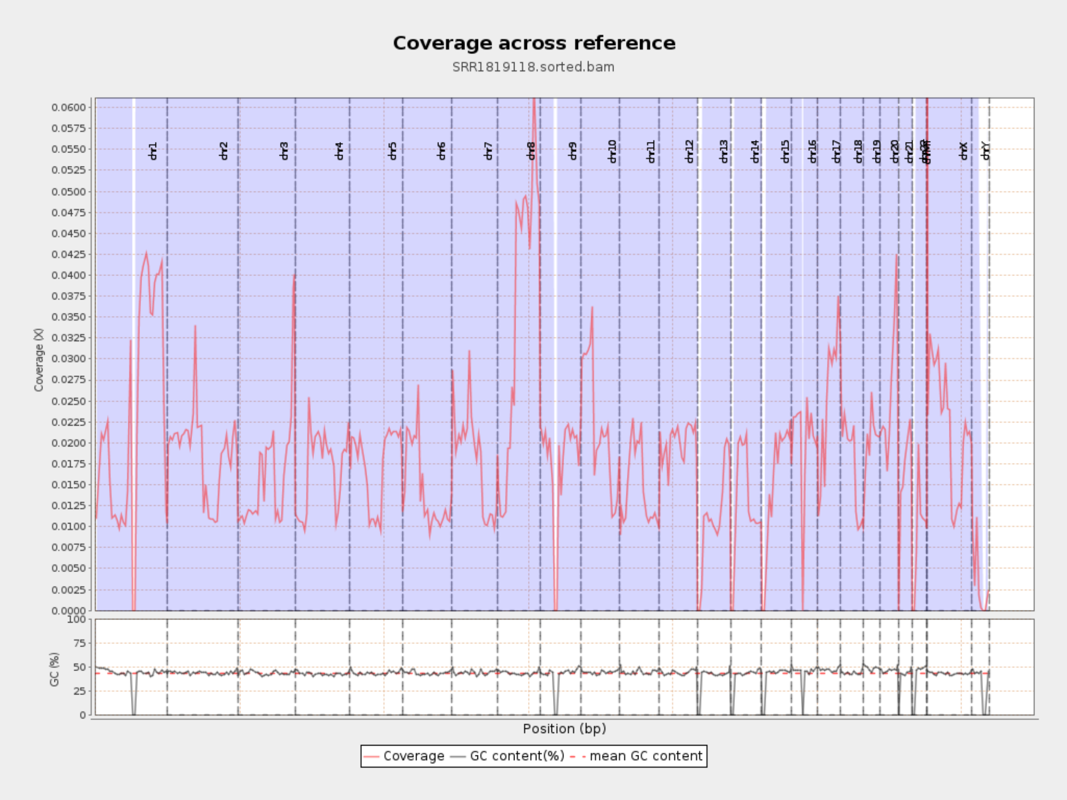
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 293,854 |
| Insertions | 3,157 |
| Mapped reads with at least one insertion | 0.32% |
| Deletions | 10,823 |
| Mapped reads with at least one deletion | 1.08% |
| Homopolymer indels | 43.81% |

## 2.6. Chromosome stats

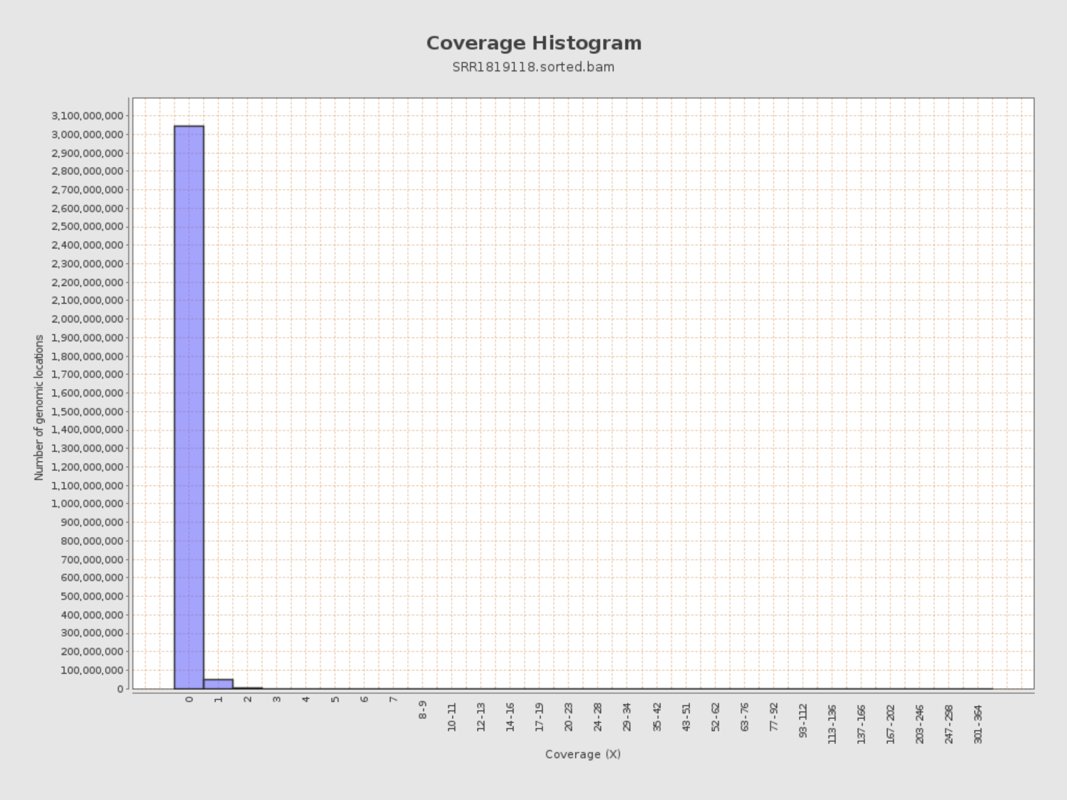
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5730648 | 0.023 | 0.3058 |
| chr2 | 243199373 | 4588691 | 0.0189 | 0.2107 |
| chr3 | 198022430 | 3154493 | 0.0159 | 0.1347 |
| chr4 | 191154276 | 3243418 | 0.017 | 0.1495 |
| chr5 | 180915260 | 3166107 | 0.0175 | 0.1407 |
| chr6 | 171115067 | 2477493 | 0.0145 | 0.1513 |
| chr7 | 159138663 | 2903397 | 0.0182 | 0.2306 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5245629 | 0.0358 | 0.2251 |
| chr9 | 141213431 | 2465830 | 0.0175 | 0.1703 |
| chr10 | 135534747 | 3024159 | 0.0223 | 0.1978 |
| chr11 | 135006516 | 2002149 | 0.0148 | 0.1701 |
| chr12 | 133851895 | 2697644 | 0.0202 | 0.1505 |
| chr13 | 115169878 | 1271348 | 0.011 | 0.1116 |
| chr14 | 107349540 | 1359148 | 0.0127 | 0.1213 |
| chr15 | 102531392 | 1534303 | 0.015 | 0.1321 |
| chr16 | 90354753 | 1794333 | 0.0199 | 0.157 |
| chr17 | 81195210 | 2045641 | 0.0252 | 0.1746 |
| chr18 | 78077248 | 1369011 | 0.0175 | 0.275 |
| chr19 | 59128983 | 1201669 | 0.0203 | 0.2429 |
| chr20 | 63025520 | 1662066 | 0.0264 | 0.1746 |
| chr21 | 48129895 | 793540 | 0.0165 | 0.1442 |
| chr22 | 51304566 | 482513 | 0.0094 | 0.1025 |
| chrMT | 16571 | 4674 | 0.2821 | 0.5635 |
| chrX | 155270560 | 3454064 | 0.0222 | 0.1716 |
| chrY | 59373566 | 193080 | 0.0033 | 0.0983 |

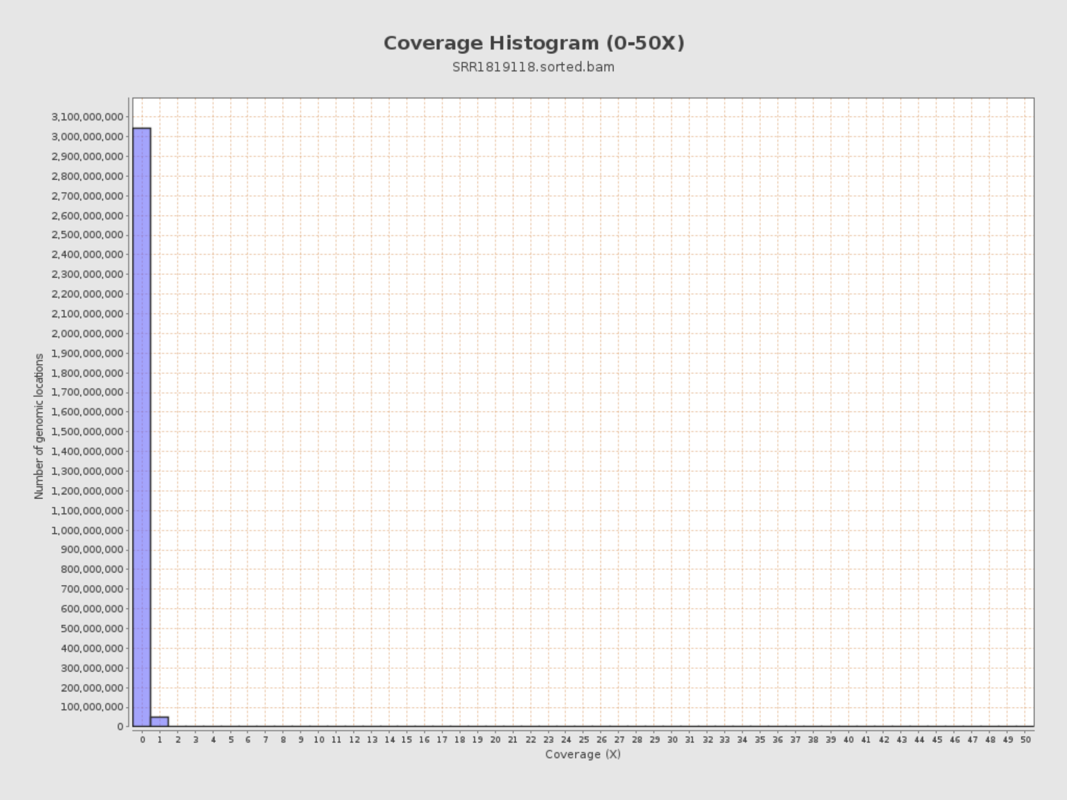
# 3. Results : Coverage across reference



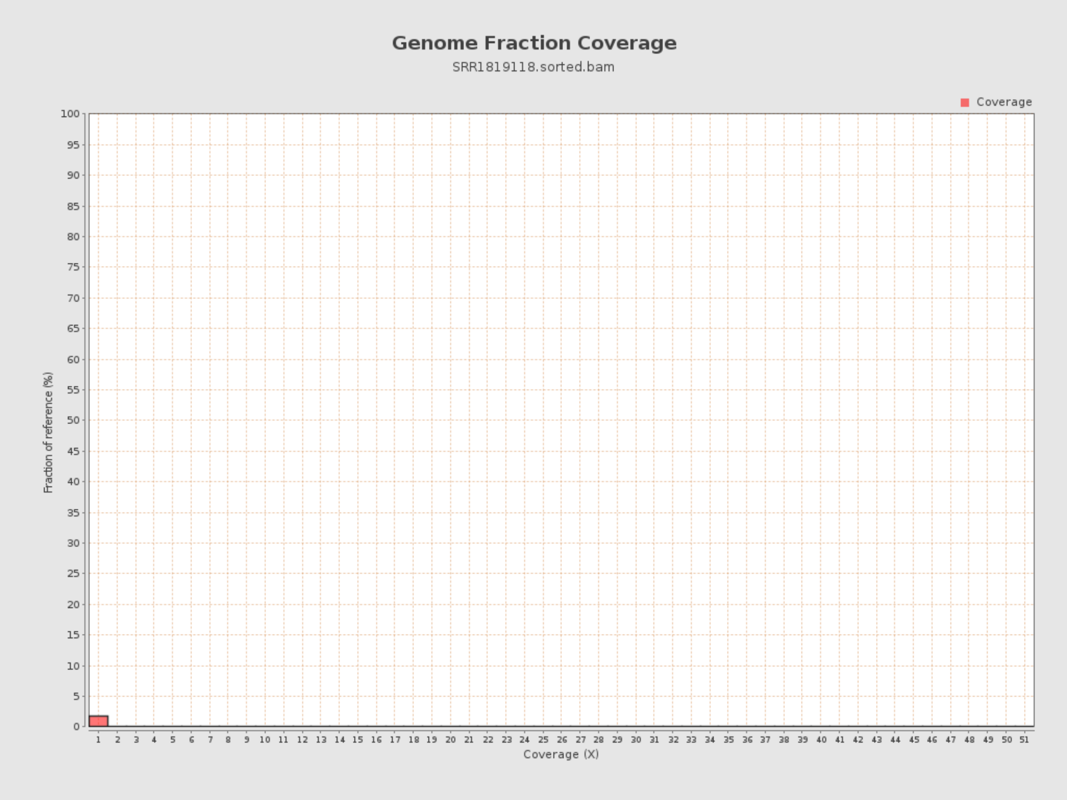
# 4. Results : Coverage Histogram



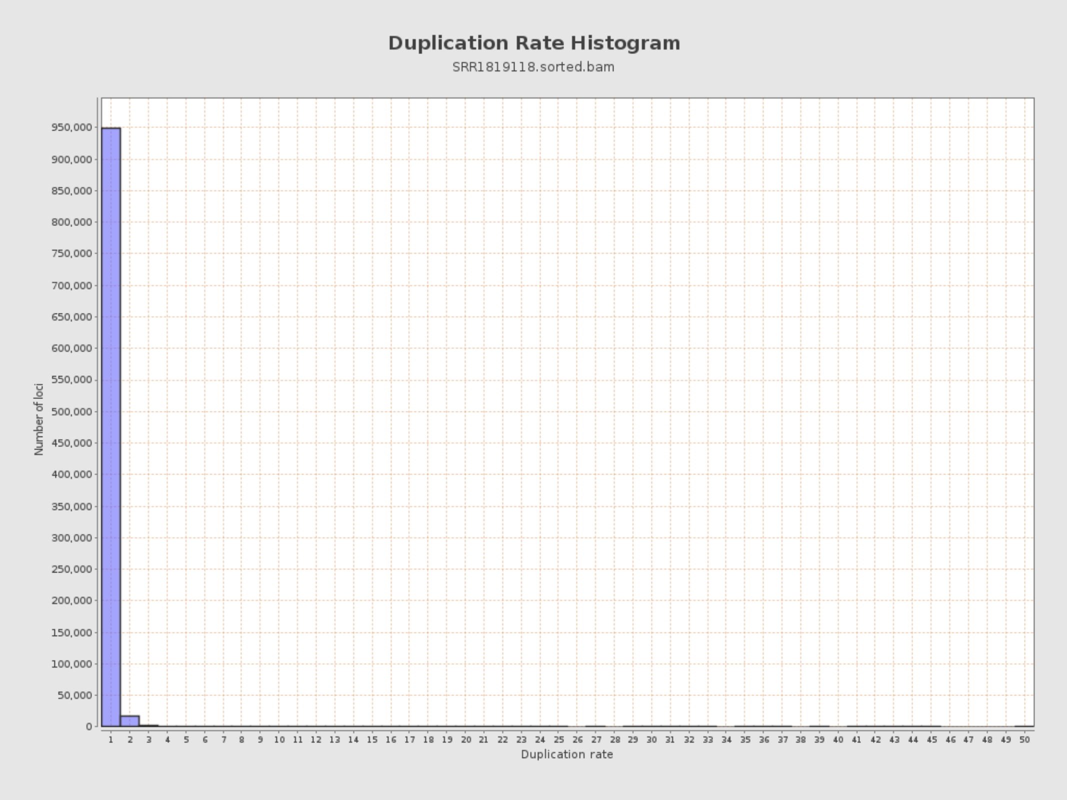
# 5. Results : Coverage Histogram (0-50X)



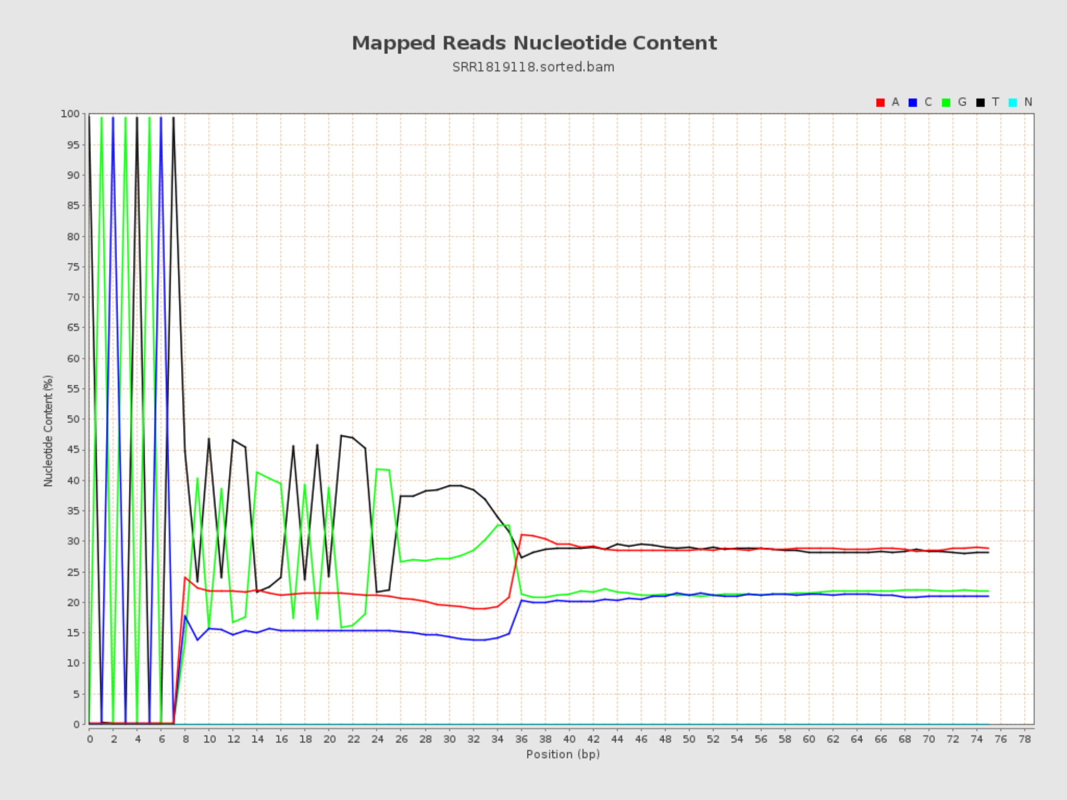
# 6. Results : Genome Fraction Coverage



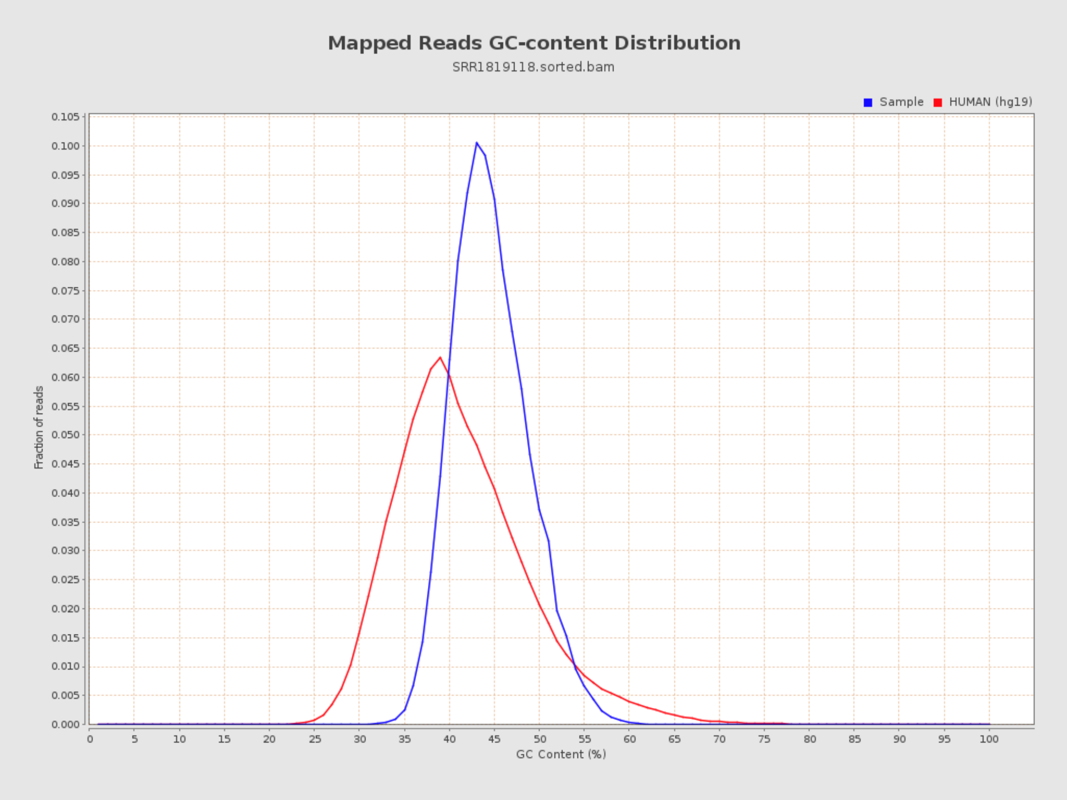
# 7. Results : Duplication Rate Histogram



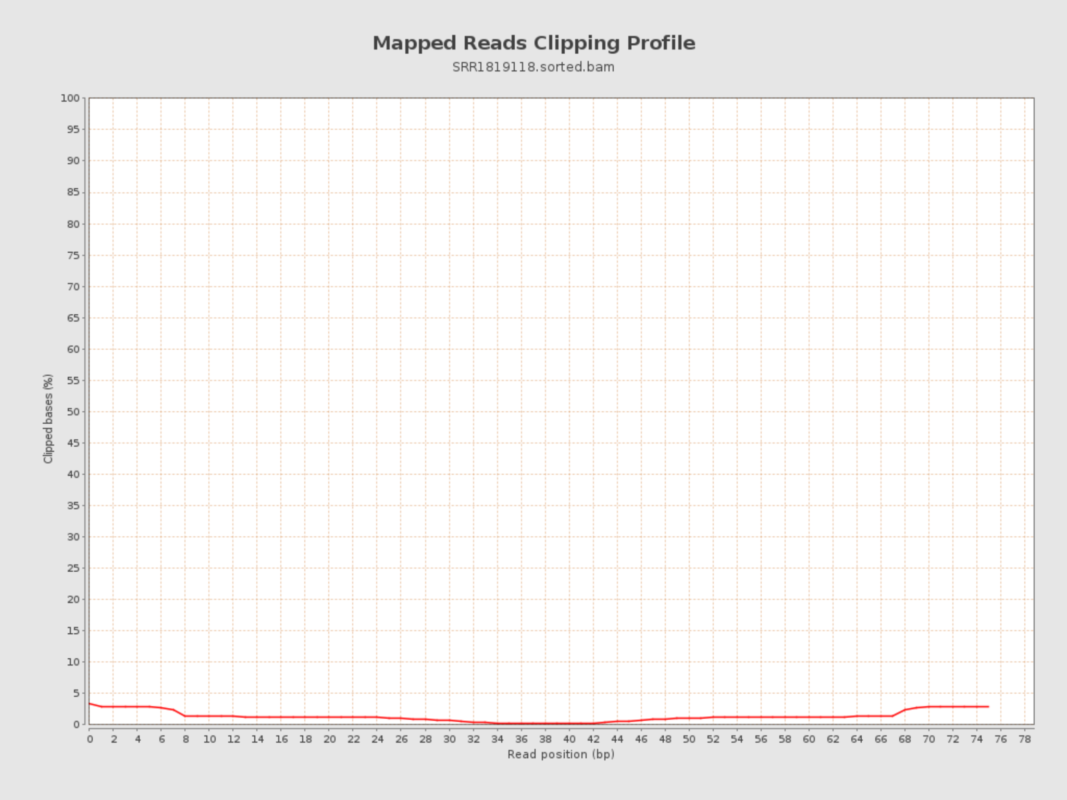
# 8. Results : Mapped Reads Nucleotide Content



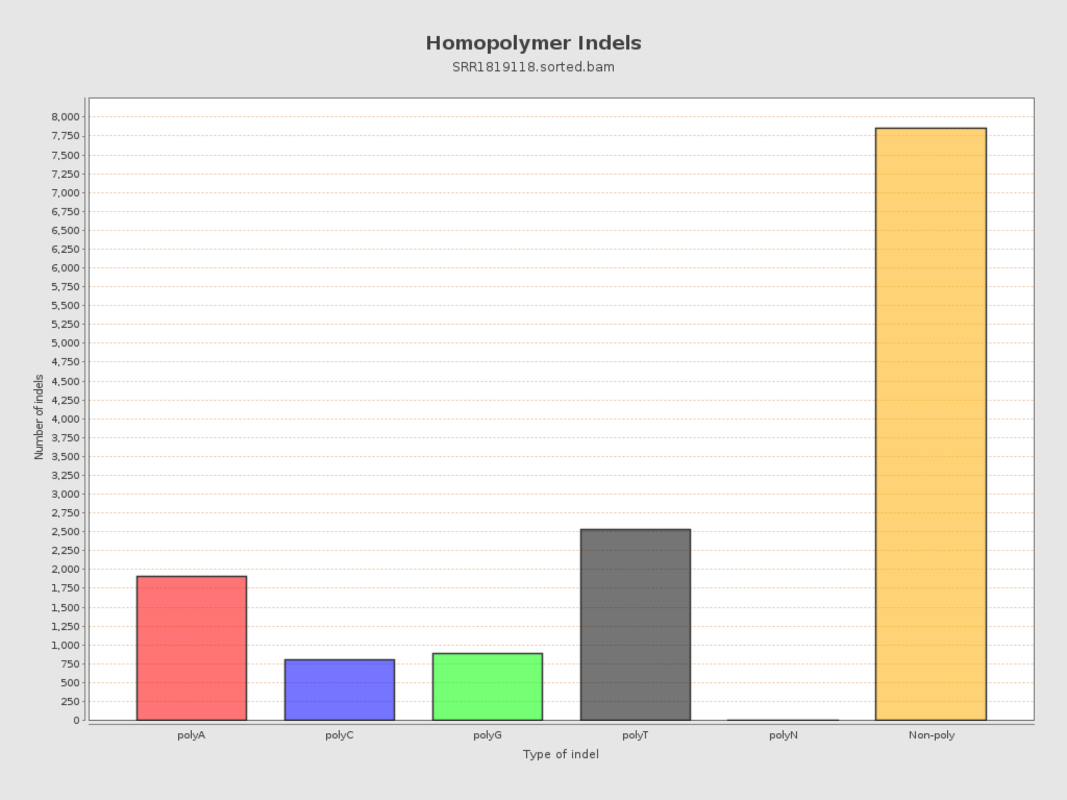
# 9. Results : Mapped Reads GC-content Distribution



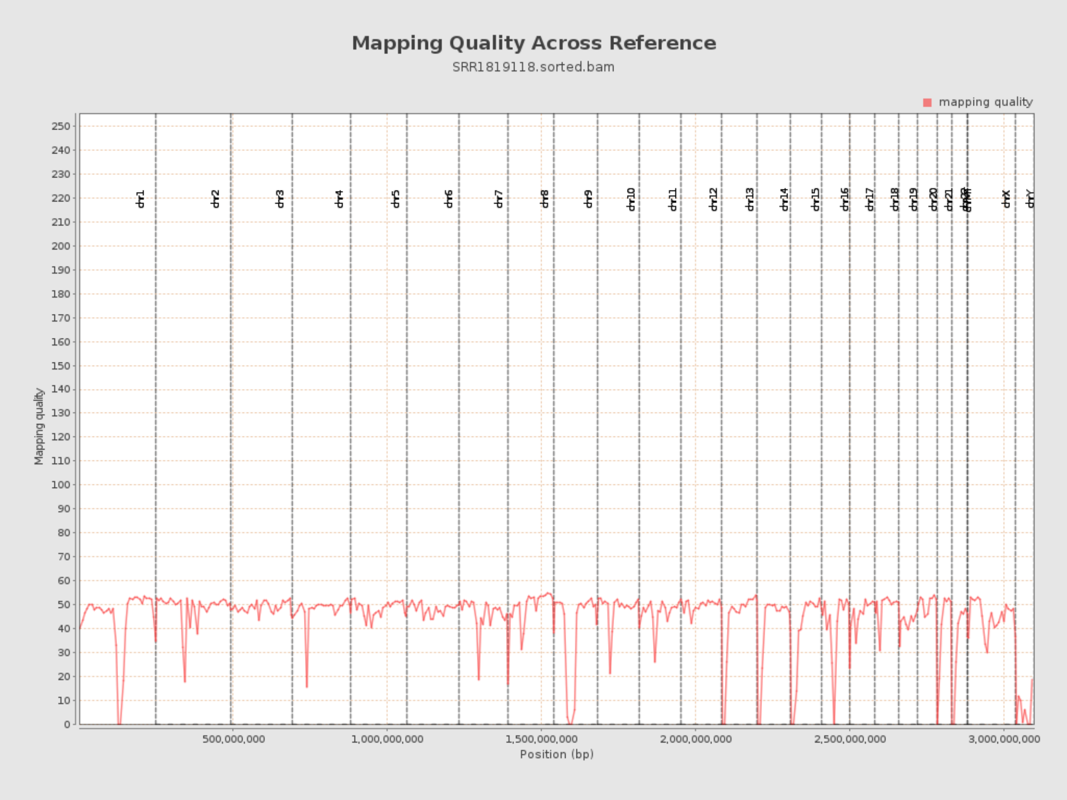
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram