# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 21:56:46*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525183.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_SRR10525183 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525183.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 21:56:46 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525183.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 741,335 |
| Mapped reads | 699,684 / 94.38% |
| Unmapped reads | 41,651 / 5.62% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 2,263 / 0.31% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 12,398 / 1.67% |
| Duplication rate | 1.24% |
| Clipped reads | 699,875 / 94.41% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 11,112,351 / 25.99% |
| Number/percentage of C's | 9,065,500 / 21.2% |
| Number/percentage of T's | 12,539,272 / 29.33% |
| Number/percentage of G's | 10,034,549 / 23.47% |
| Number/percentage of N's | 991 / 0% |
| GC Percentage | 44.68% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0138 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1588 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.85 |

## 2.5. Mismatches and indels

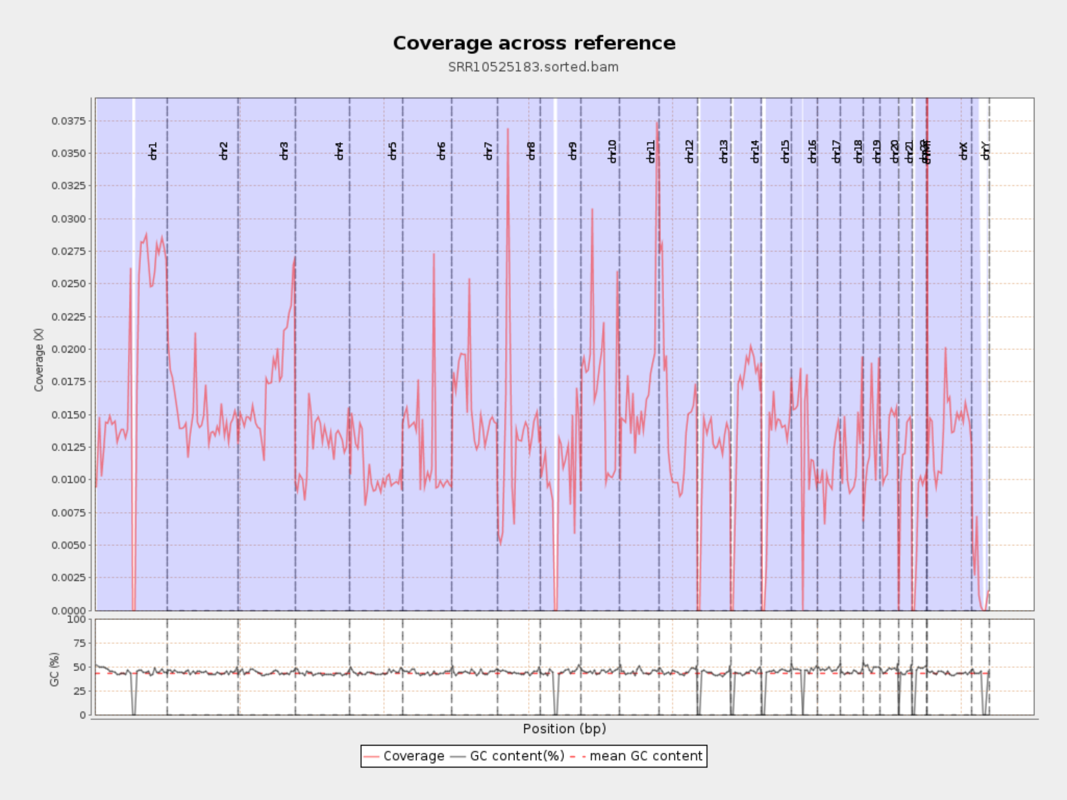
| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 207,235 |
| Insertions | 3,144 |
| Mapped reads with at least one insertion | 0.45% |
| Deletions | 8,803 |
| Mapped reads with at least one deletion | 1.25% |
| Homopolymer indels | 43.22% |

## 2.6. Chromosome stats

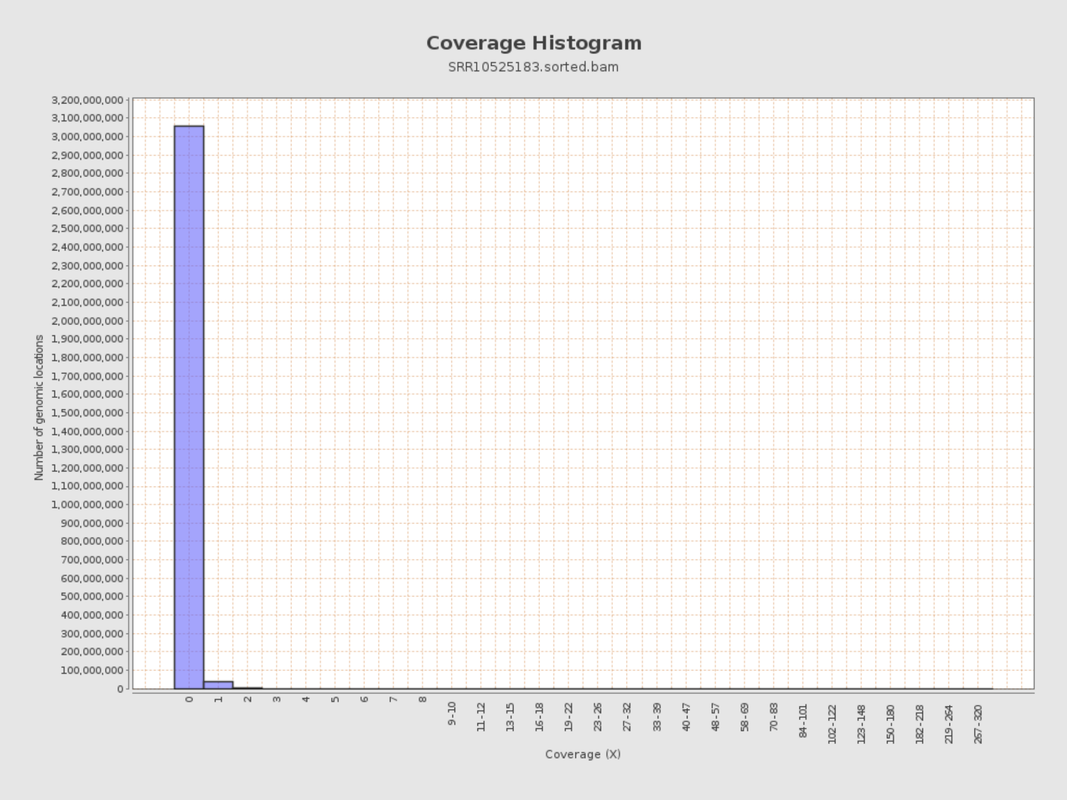
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 4642327 | 0.0186 | 0.2855 |
| chr2 | 243199373 | 3624654 | 0.0149 | 0.1717 |
| chr3 | 198022430 | 3425900 | 0.0173 | 0.1379 |
| chr4 | 191154276 | 2432498 | 0.0127 | 0.1205 |
| chr5 | 180915260 | 1945643 | 0.0108 | 0.1073 |
| chr6 | 171115067 | 2154766 | 0.0126 | 0.1249 |
| chr7 | 159138663 | 2550384 | 0.016 | 0.2145 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1990090 | 0.0136 | 0.1361 |
| chr9 | 141213431 | 1437977 | 0.0102 | 0.1241 |
| chr10 | 135534747 | 2356474 | 0.0174 | 0.1794 |
| chr11 | 135006516 | 2280348 | 0.0169 | 0.1475 |
| chr12 | 133851895 | 1970450 | 0.0147 | 0.1265 |
| chr13 | 115169878 | 1341943 | 0.0117 | 0.1116 |
| chr14 | 107349540 | 1639033 | 0.0153 | 0.1296 |
| chr15 | 102531392 | 1191737 | 0.0116 | 0.1112 |
| chr16 | 90354753 | 1183457 | 0.0131 | 0.1276 |
| chr17 | 81195210 | 878054 | 0.0108 | 0.1101 |
| chr18 | 78077248 | 910673 | 0.0117 | 0.2085 |
| chr19 | 59128983 | 781927 | 0.0132 | 0.2071 |
| chr20 | 63025520 | 813409 | 0.0129 | 0.1187 |
| chr21 | 48129895 | 554031 | 0.0115 | 0.1155 |
| chr22 | 51304566 | 353871 | 0.0069 | 0.086 |
| chrMT | 16571 | 2152 | 0.1299 | 0.353 |
| chrX | 155270560 | 2179631 | 0.014 | 0.1268 |
| chrY | 59373566 | 125533 | 0.0021 | 0.0681 |

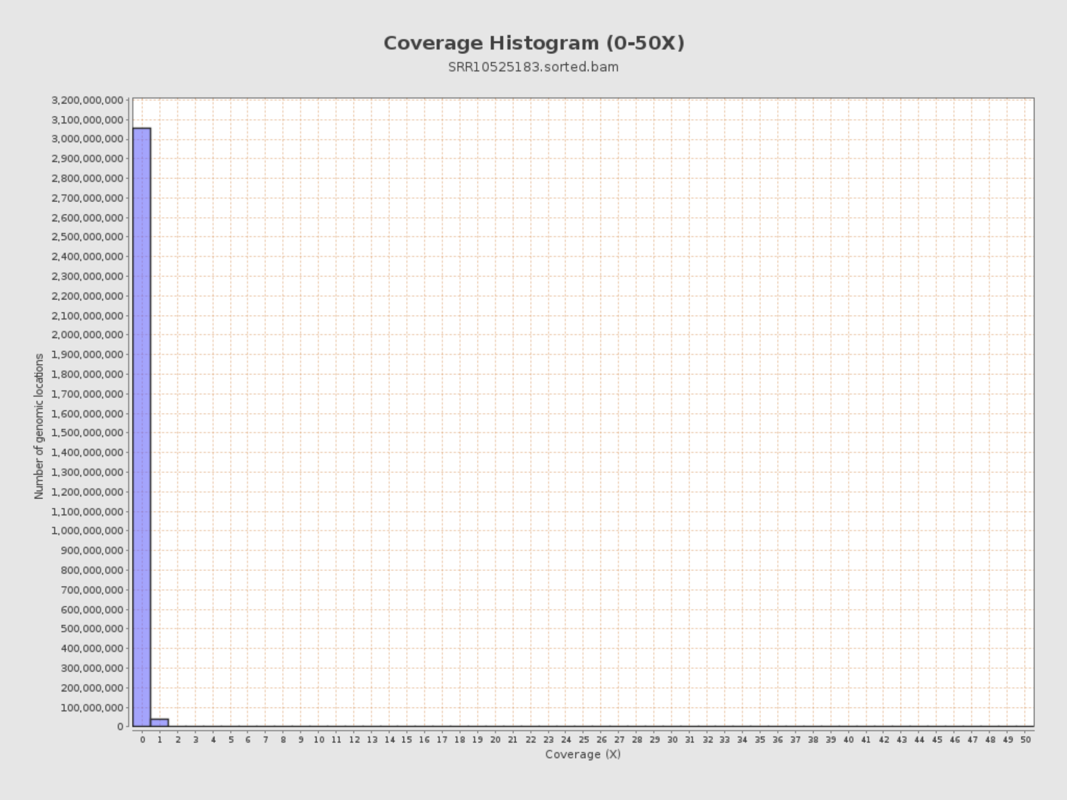
# 3. Results : Coverage across reference



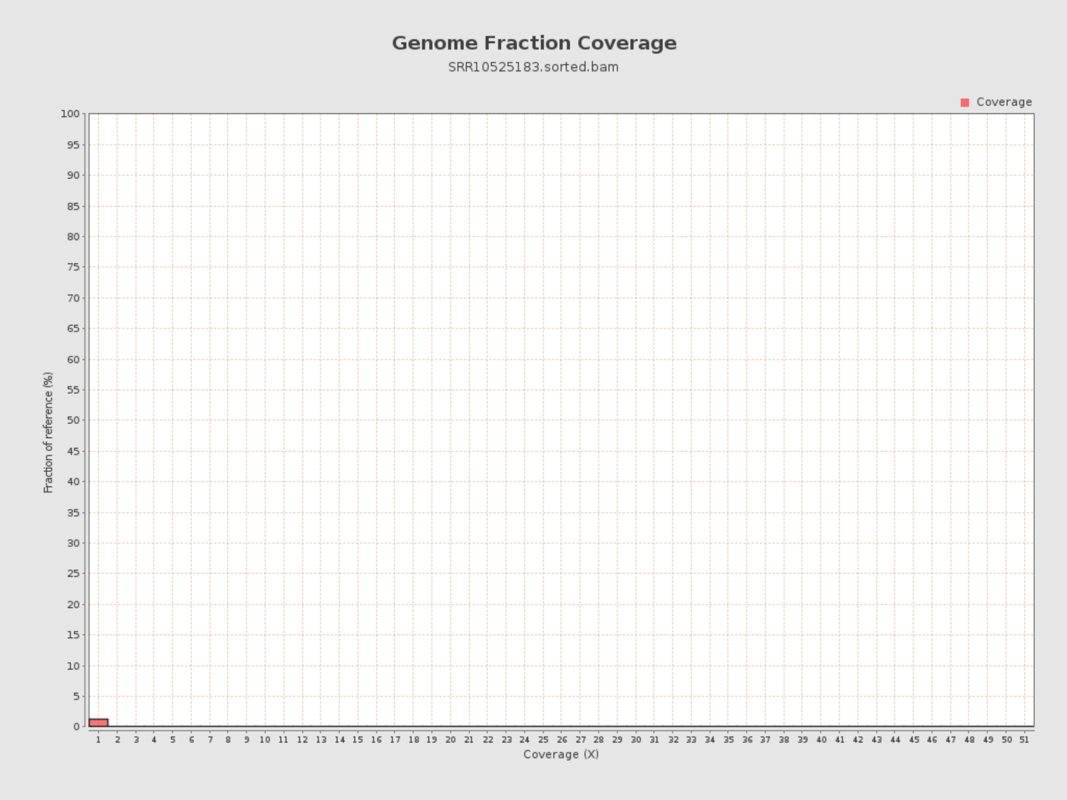
# 4. Results : Coverage Histogram



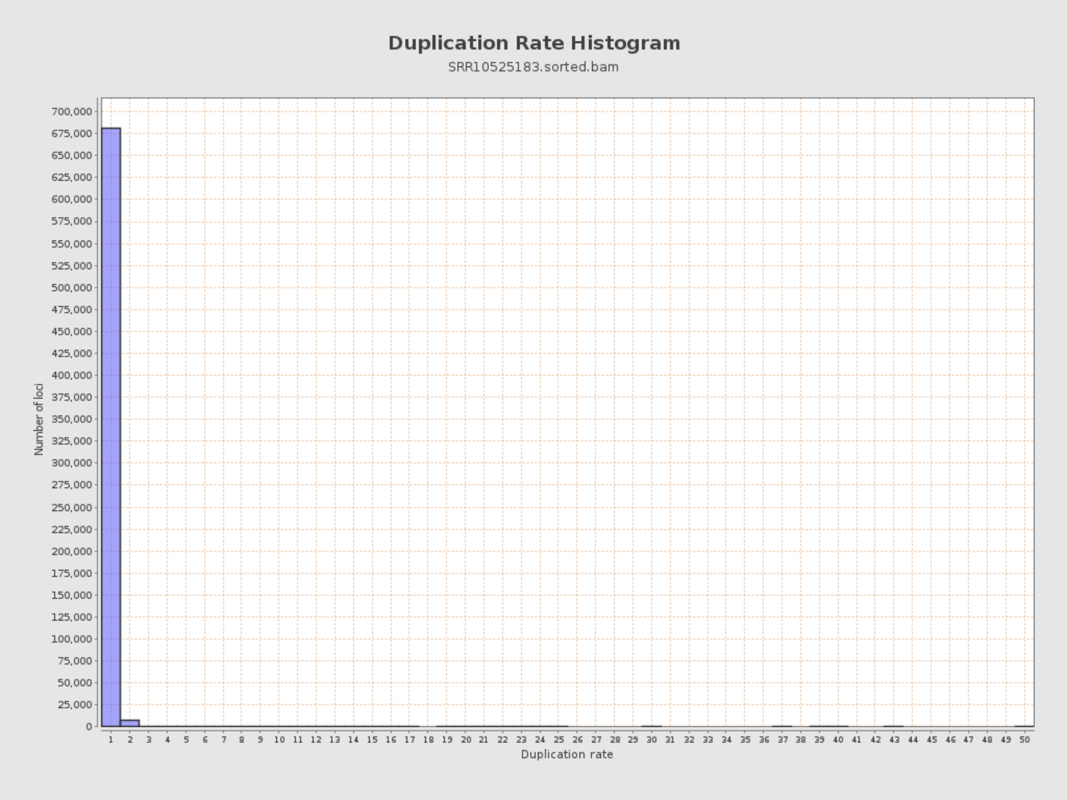
# 5. Results : Coverage Histogram (0-50X)



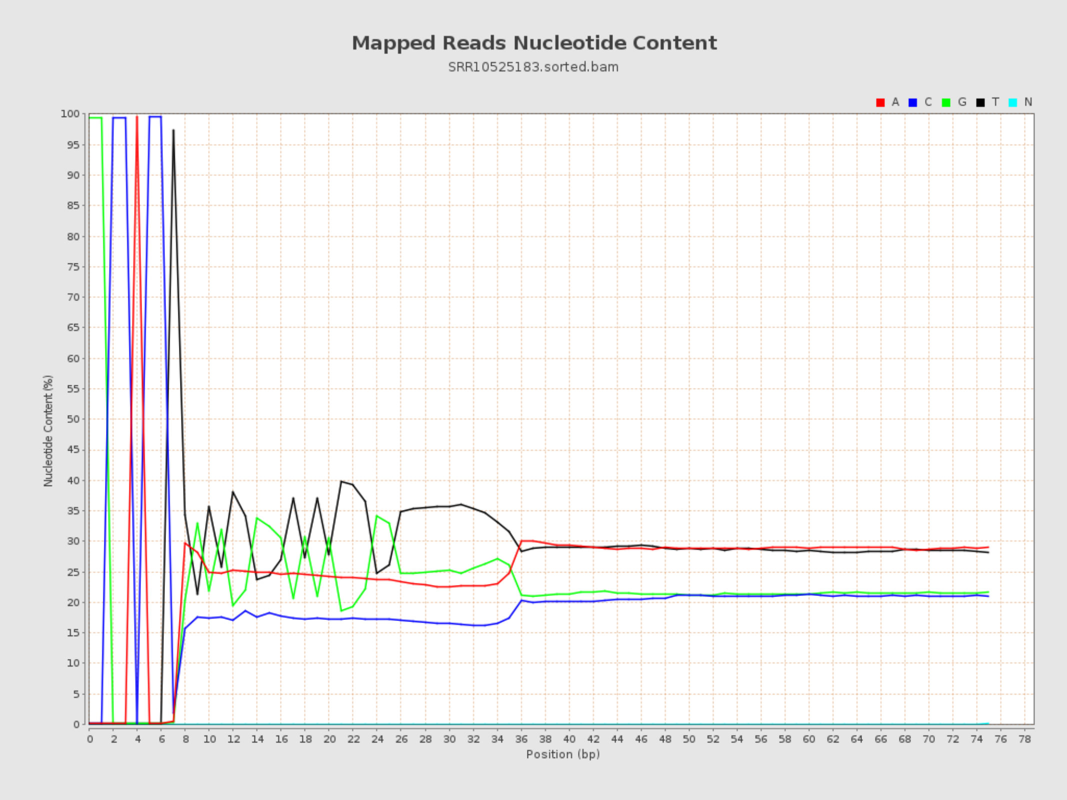
# 6. Results : Genome Fraction Coverage



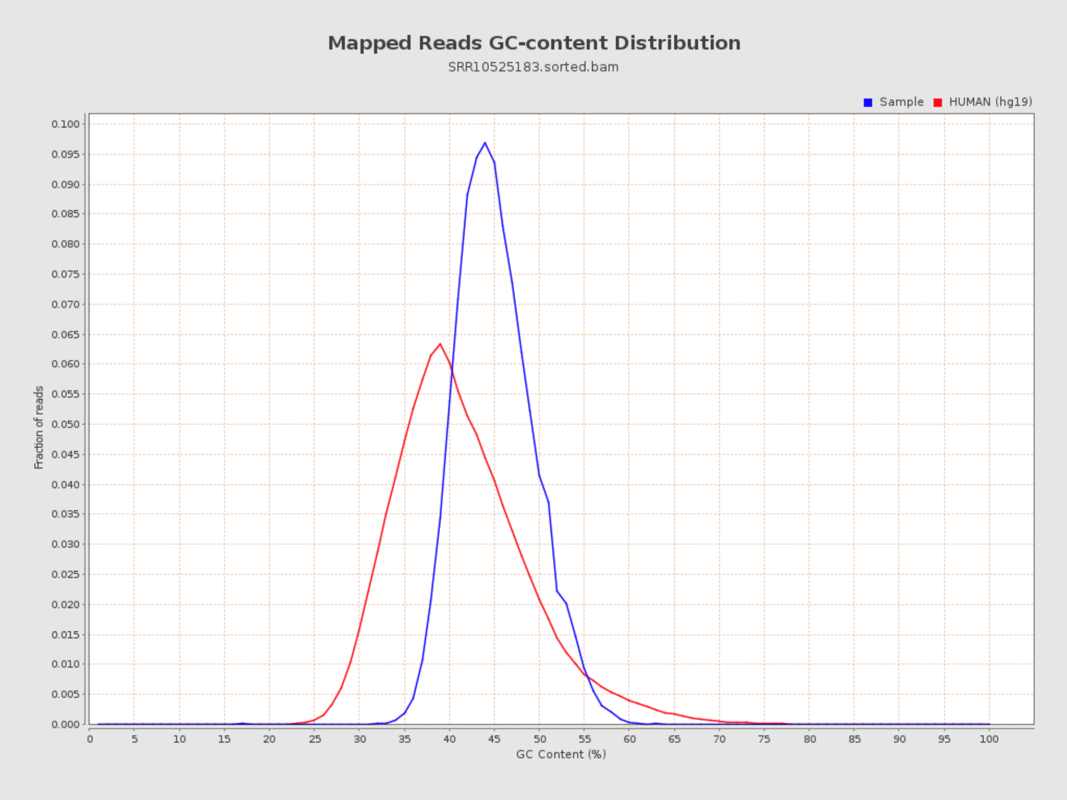
# 7. Results : Duplication Rate Histogram



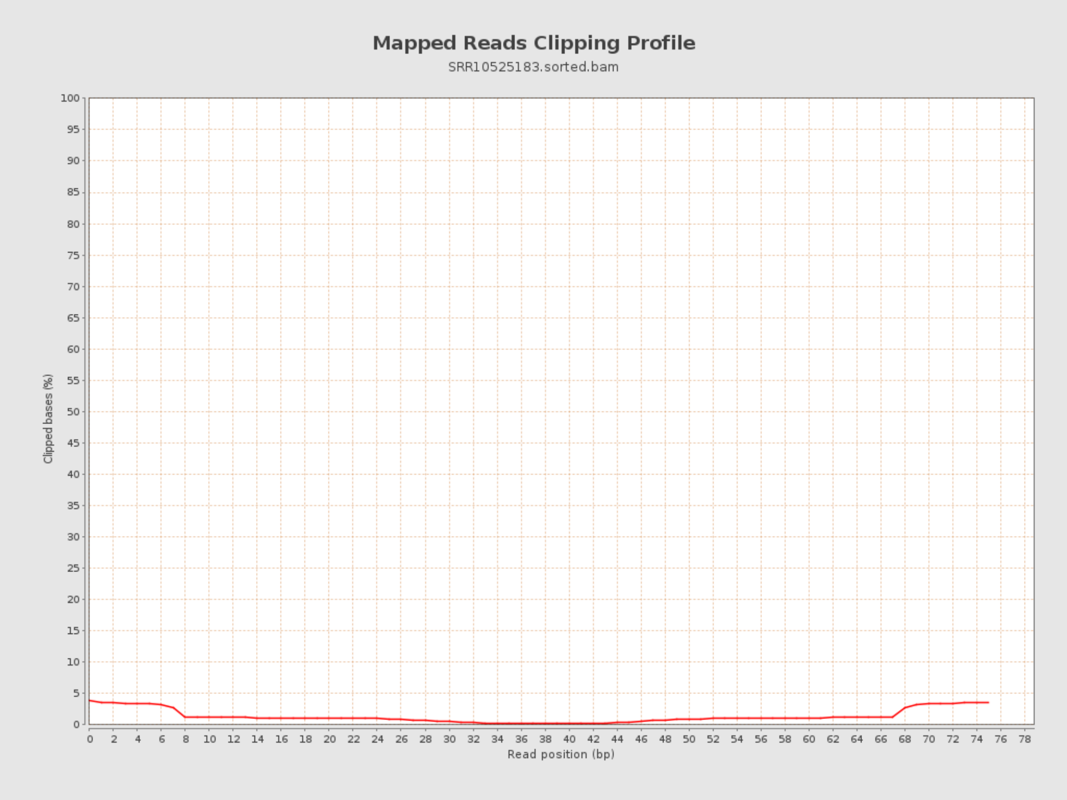
# 8. Results : Mapped Reads Nucleotide Content



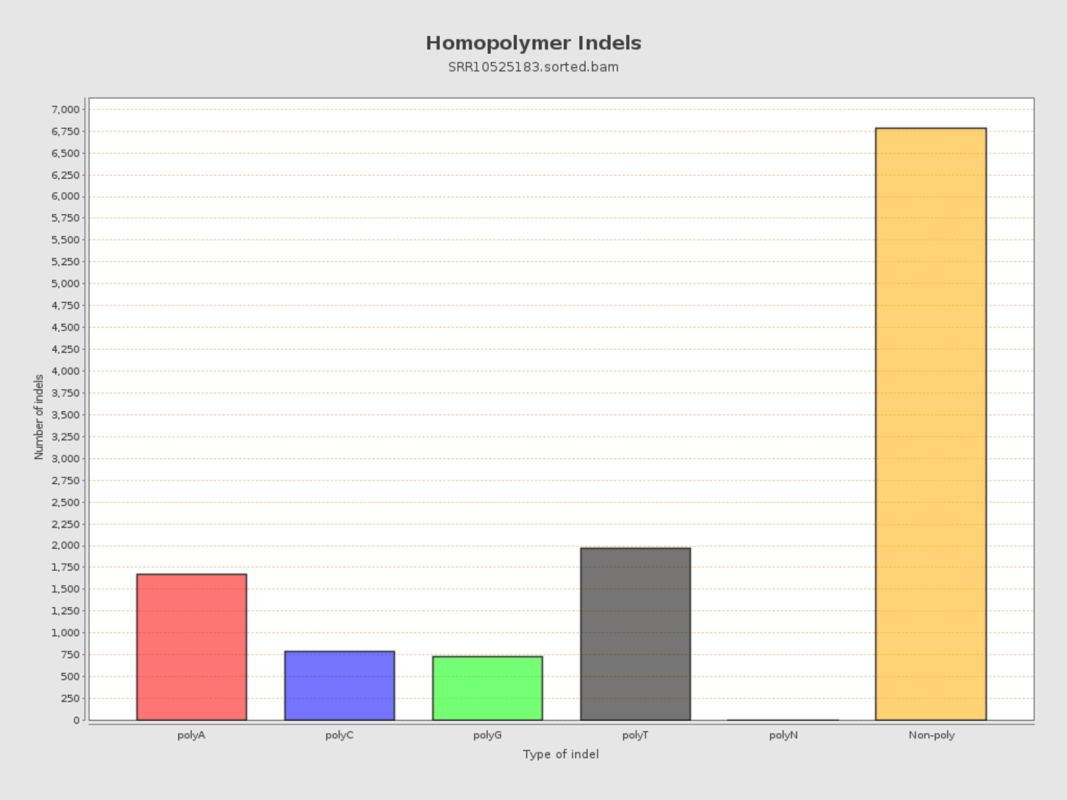
# 9. Results : Mapped Reads GC-content Distribution



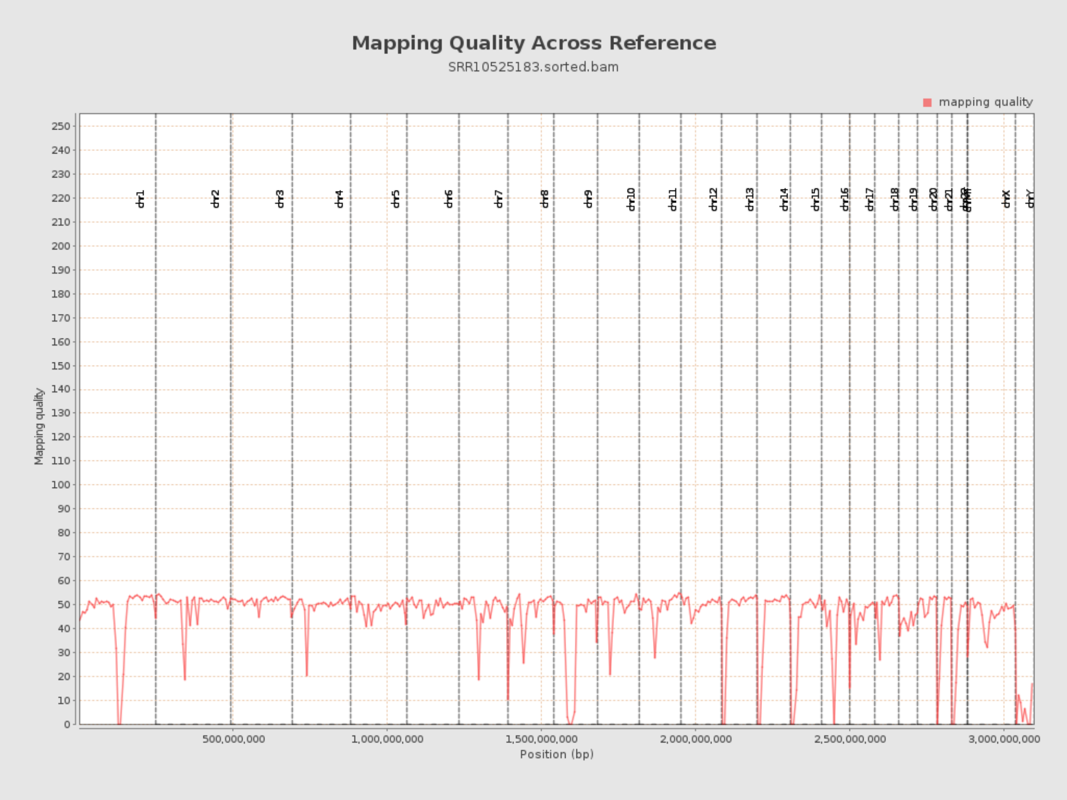
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram