# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 16:31:22*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525077.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_SRR10525077 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525077.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 16:31:21 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525077.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 7,284,967 |
| Mapped reads | 6,785,613 / 93.15% |
| Unmapped reads | 499,354 / 6.85% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 29,207 / 0.4% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 837,290 / 11.49% |
| Duplication rate | 8.85% |
| Clipped reads | 6,791,898 / 93.23% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 105,668,855 / 26.29% |
| Number/percentage of C's | 68,610,575 / 17.07% |
| Number/percentage of T's | 127,967,348 / 31.84% |
| Number/percentage of G's | 99,598,302 / 24.78% |
| Number/percentage of N's | 43,385 / 0.01% |
| GC Percentage | 41.85% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1299 |
| | |

| | |
|---|---|
| Standard Deviation | 1.0033 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.2 |

## 2.5. Mismatches and indels

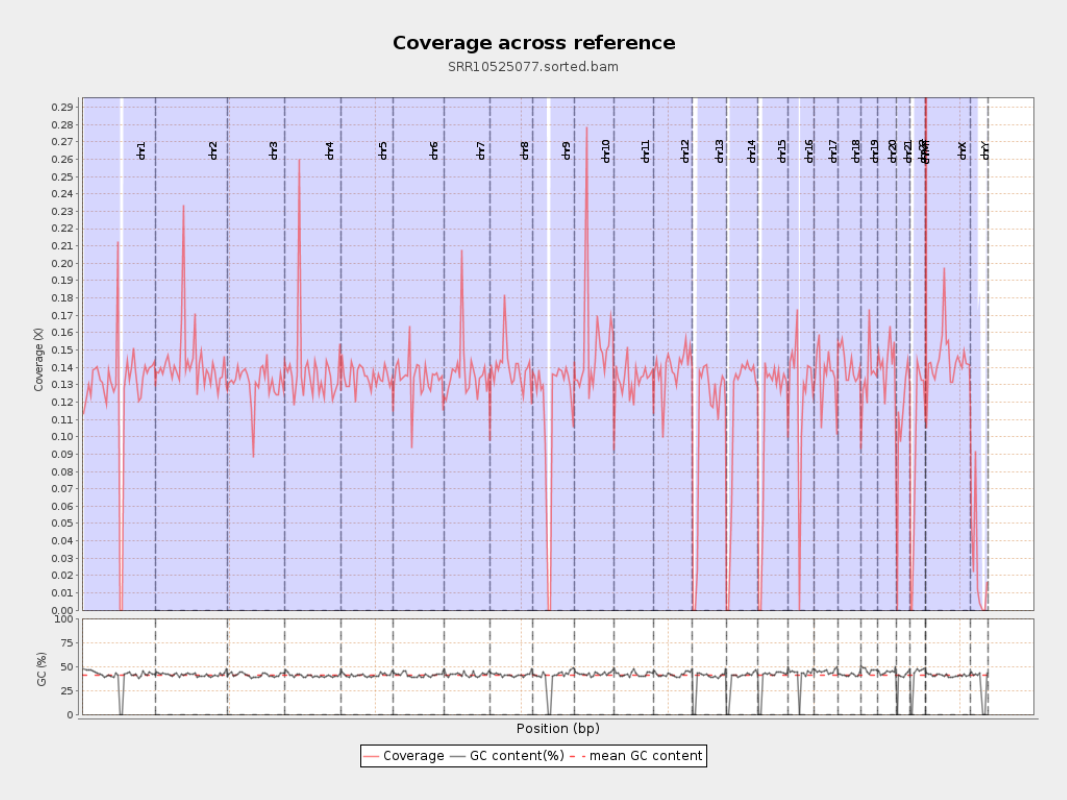
| | |
|---|---|
| General error rate | 0.49% |
| Mismatches | 1,905,581 |
| Insertions | 30,199 |
| Mapped reads with at least one insertion | 0.44% |
| Deletions | 79,681 |
| Mapped reads with at least one deletion | 1.17% |
| Homopolymer indels | 42.54% |

## 2.6. Chromosome stats

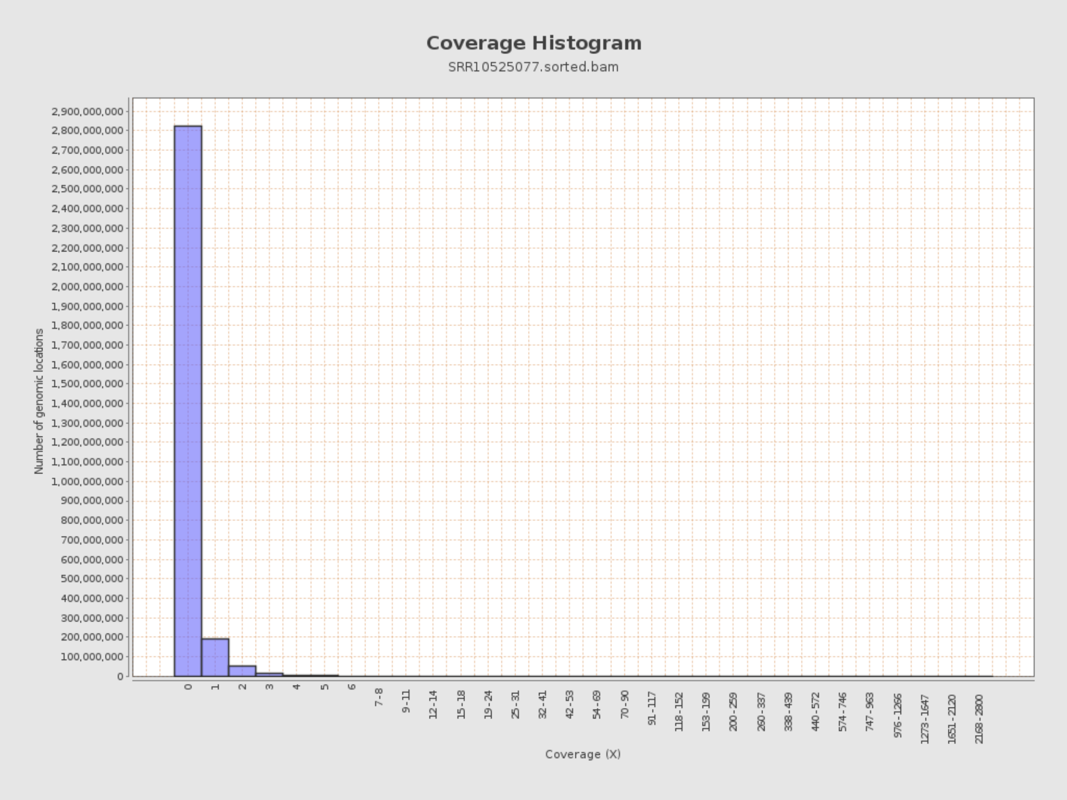
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 31671829 | 0.1271 | 2.0822 |
| chr2 | 243199373 | 34712643 | 0.1427 | 1.2654 |
| chr3 | 198022430 | 25901223 | 0.1308 | 0.509 |
| chr4 | 191154276 | 26571510 | 0.139 | 0.7426 |
| chr5 | 180915260 | 24352713 | 0.1346 | 0.5206 |
| chr6 | 171115067 | 22912176 | 0.1339 | 0.6126 |
| chr7 | 159138663 | 21850899 | 0.1373 | 1.2275 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 20403434 | 0.1394 | 1.13 |
| chr9 | 141213431 | 16364856 | 0.1159 | 0.7544 |
| chr10 | 135534747 | 20451188 | 0.1509 | 1.1169 |
| chr11 | 135006516 | 17912896 | 0.1327 | 0.7206 |
| chr12 | 133851895 | 18722234 | 0.1399 | 0.5581 |
| chr13 | 115169878 | 12456646 | 0.1082 | 0.462 |
| chr14 | 107349540 | 12307056 | 0.1146 | 0.5119 |
| chr15 | 102531392 | 11228708 | 0.1095 | 0.4681 |
| chr16 | 90354753 | 11110572 | 0.123 | 0.5839 |
| chr17 | 81195210 | 11078842 | 0.1364 | 0.5894 |
| chr18 | 78077248 | 11049660 | 0.1415 | 1.5137 |
| chr19 | 59128983 | 8005354 | 0.1354 | 1.4293 |
| chr20 | 63025520 | 8988072 | 0.1426 | 0.5757 |
| chr21 | 48129895 | 5344368 | 0.111 | 0.647 |
| chr22 | 51304566 | 4808908 | 0.0937 | 0.4286 |
| chrMT | 16571 | 67057 | 4.0466 | 3.3198 |
| chrX | 155270560 | 22348753 | 0.1439 | 0.6656 |
| chrY | 59373566 | 1397258 | 0.0235 | 0.7515 |

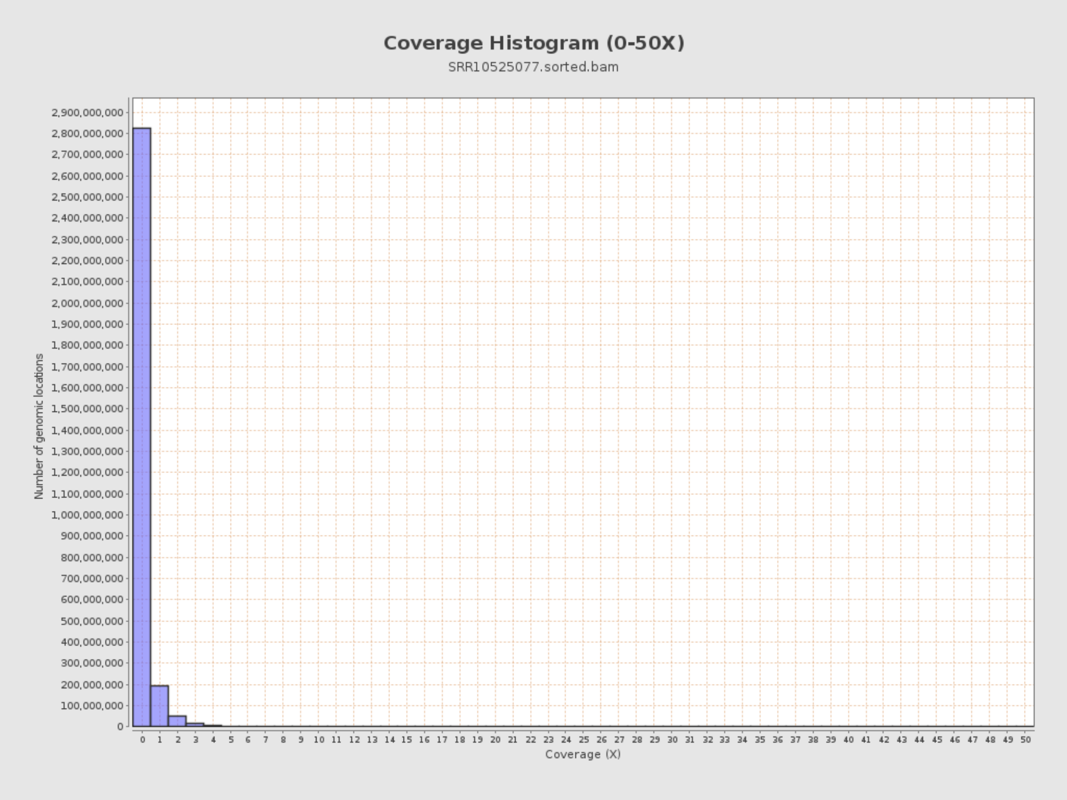
# 3. Results : Coverage across reference



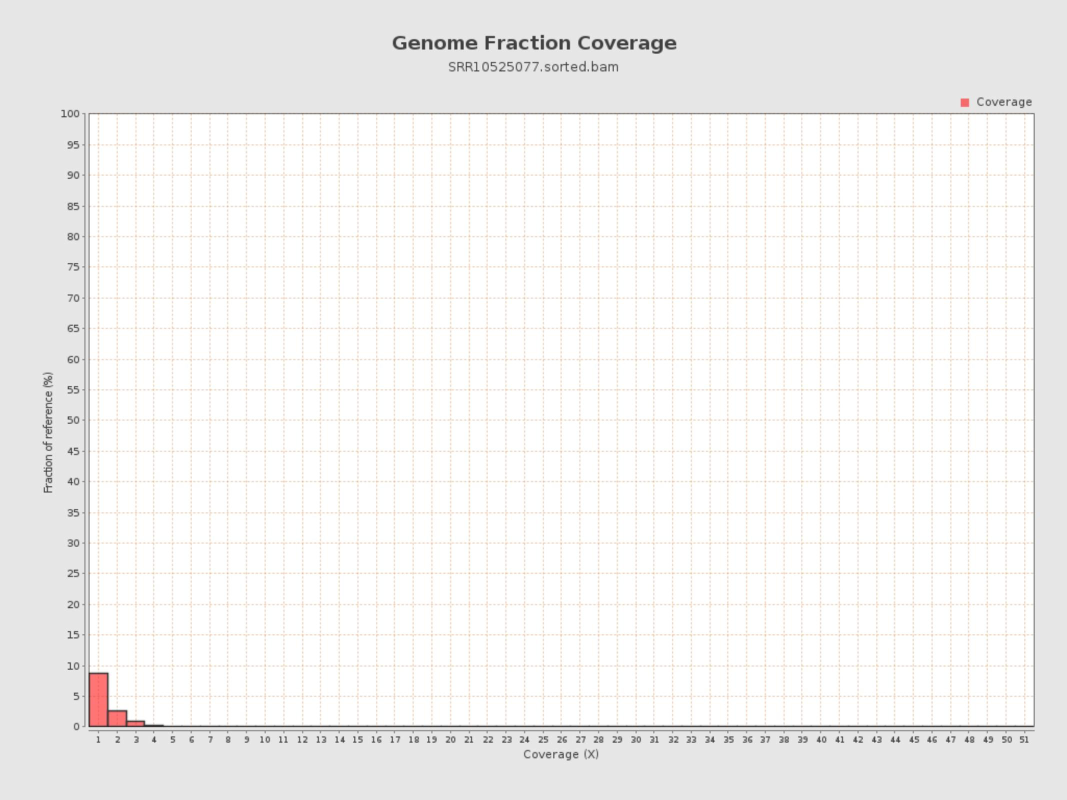
# 4. Results : Coverage Histogram



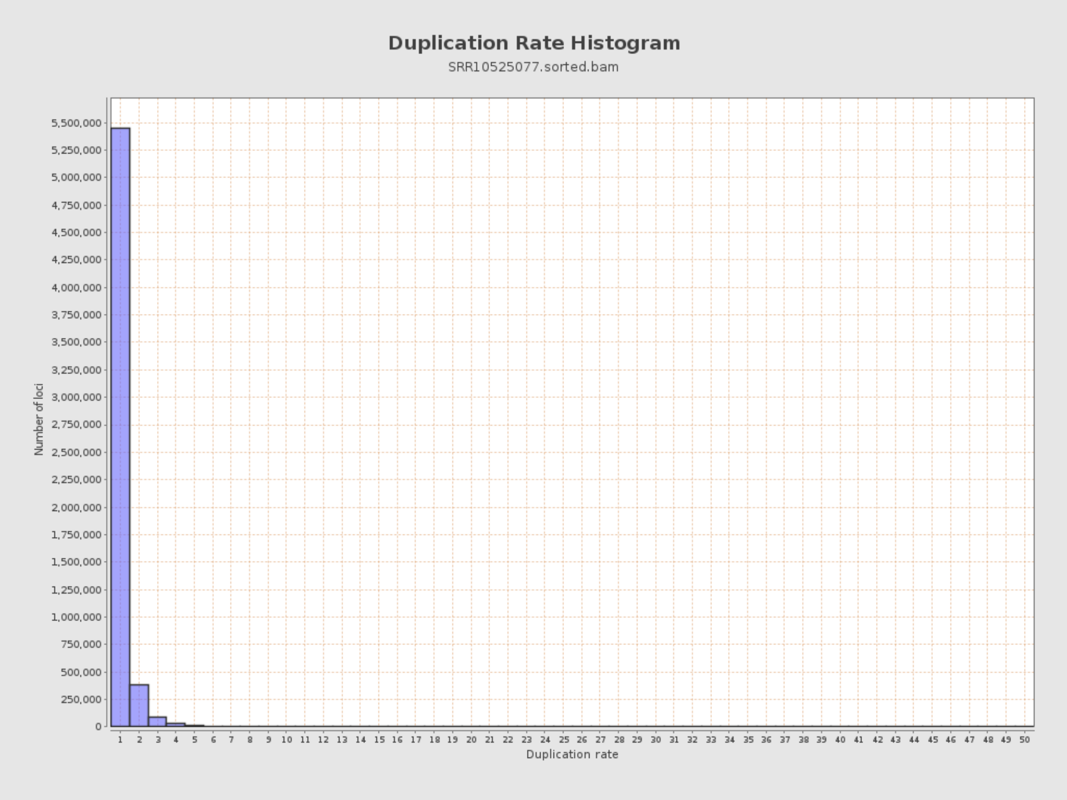
# 5. Results : Coverage Histogram (0-50X)



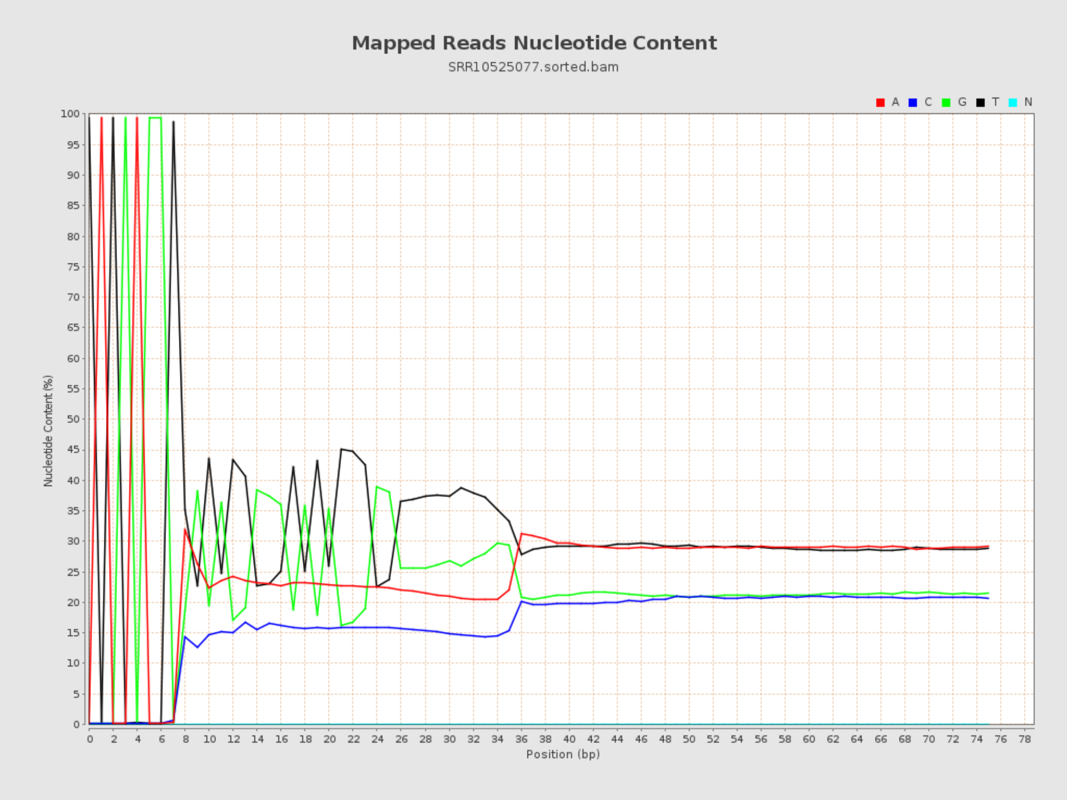
# 6. Results : Genome Fraction Coverage



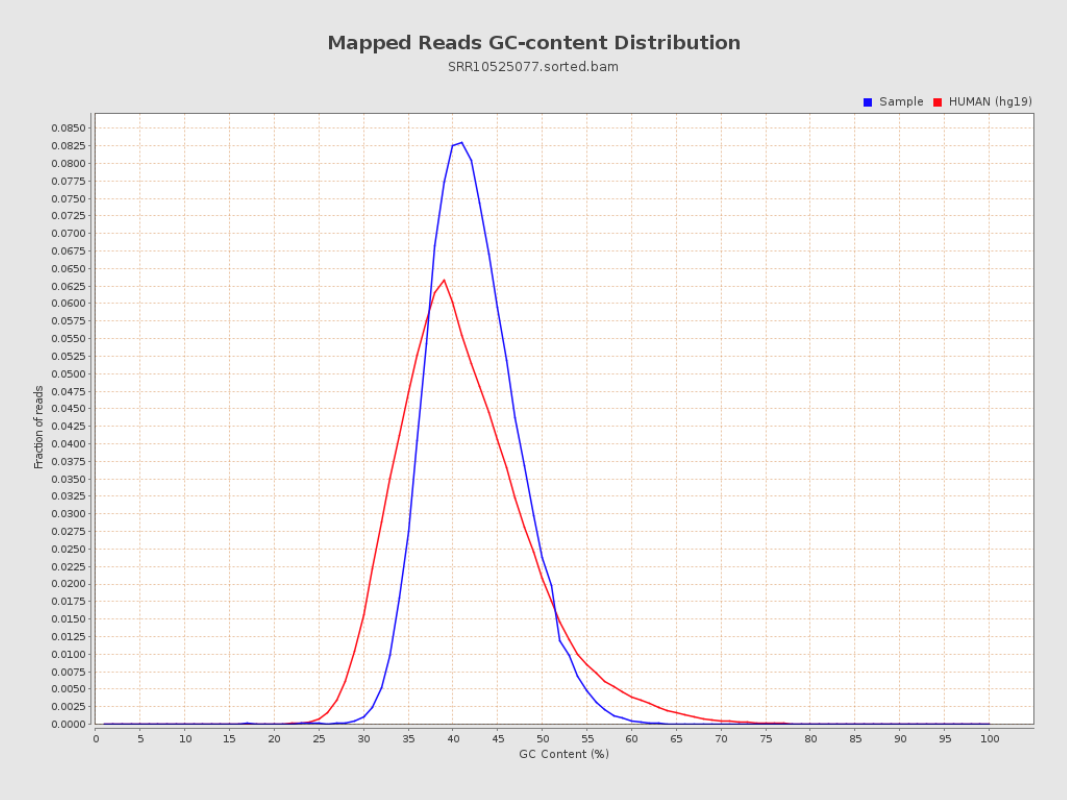
# 7. Results : Duplication Rate Histogram



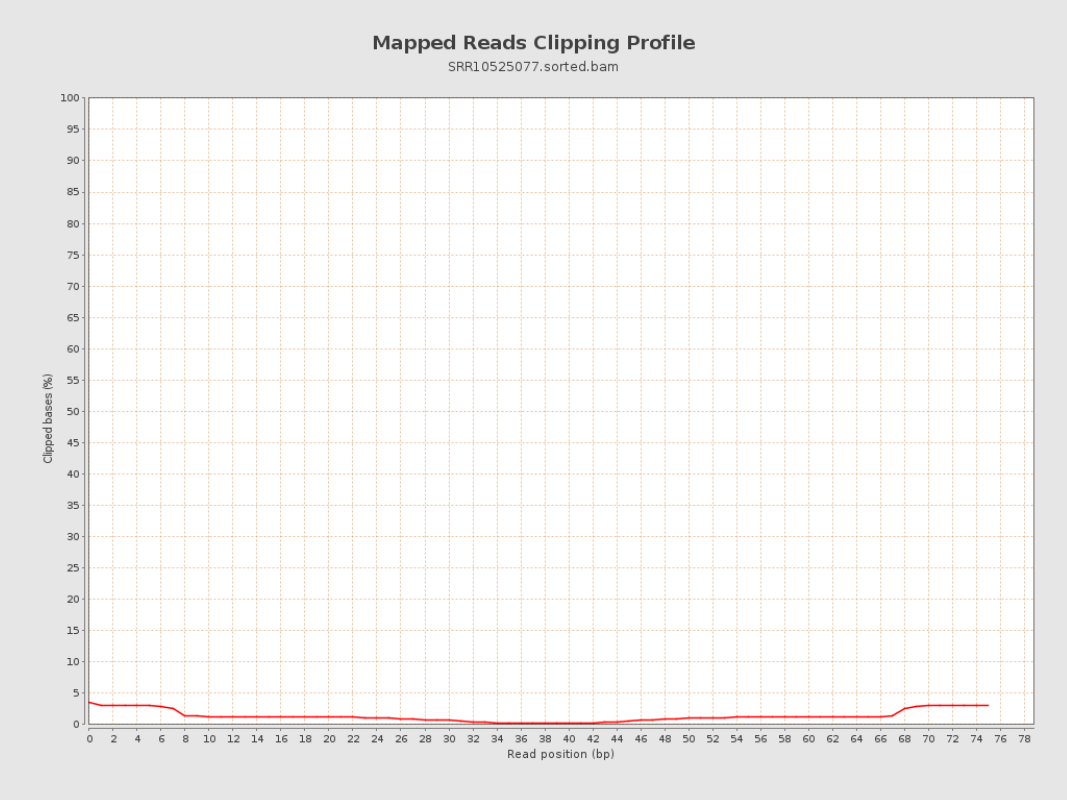
# 8. Results : Mapped Reads Nucleotide Content



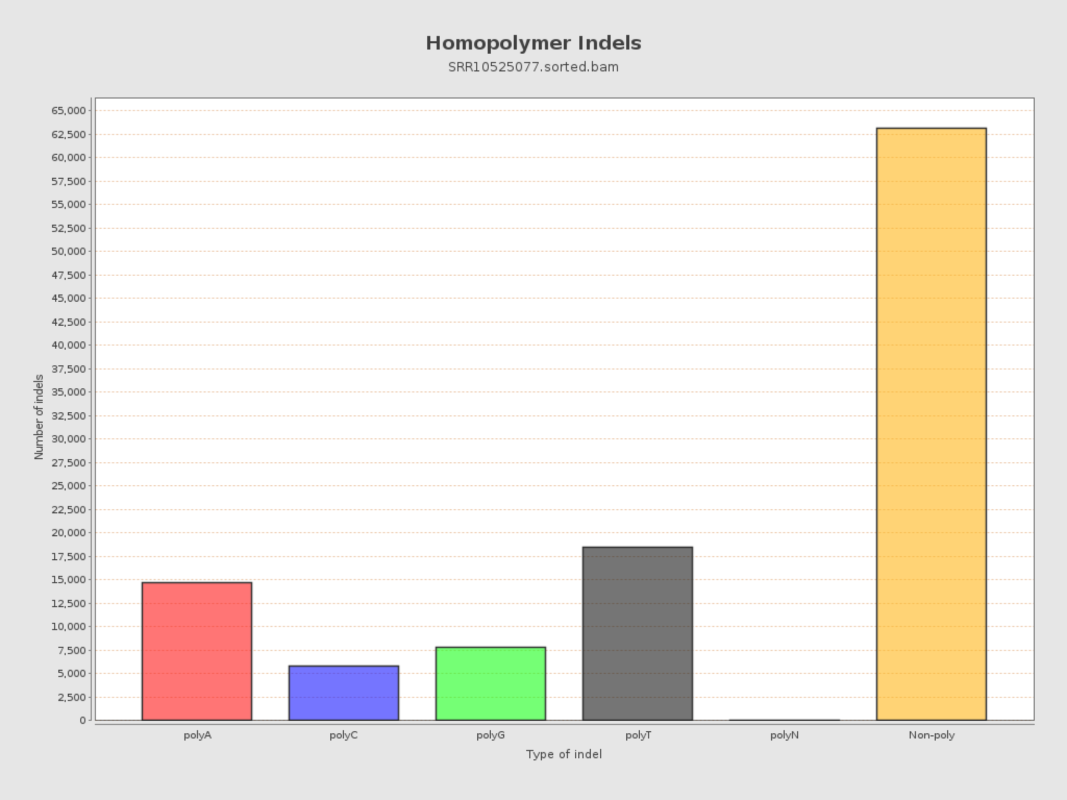
# 9. Results : Mapped Reads GC-content Distribution



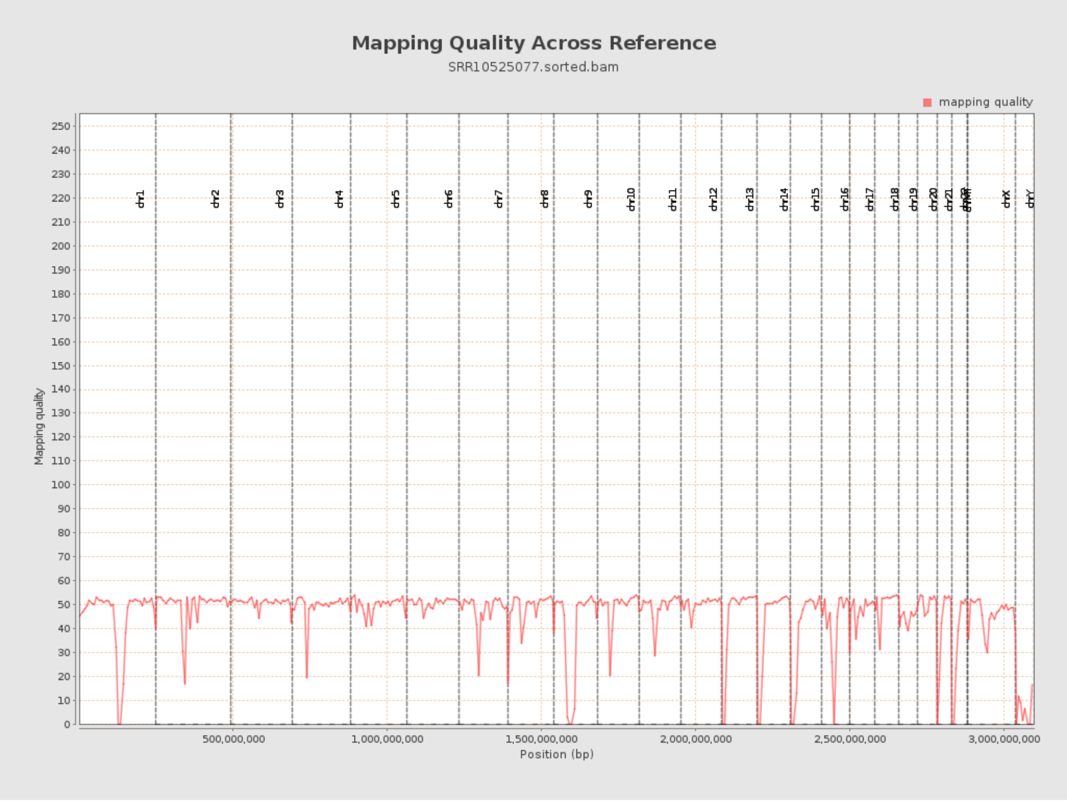
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram