# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/22 09:12:21*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080645.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_SRR3080645 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080645.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 22 09:12:18 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3080645.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,410,298 |
| Mapped reads | 1,266,208 / 89.78% |
| Unmapped reads | 144,090 / 10.22% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 10,558 / 0.75% |
| Read min/max/mean length | 30 / 76 / 76.26 |
| Duplicated reads (estimated) | 44,069 / 3.12% |
| Duplication rate | 3.03% |
| Clipped reads | 594,757 / 42.17% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 22,403,256 / 26.81% |
| Number/percentage of C's | 15,611,471 / 18.68% |
| Number/percentage of T's | 26,226,171 / 31.38% |
| Number/percentage of G's | 19,327,816 / 23.13% |
| Number/percentage of N's | 3,599 / 0% |
| GC Percentage | 41.81% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.027 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2209 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.23 |

## 2.5. Mismatches and indels

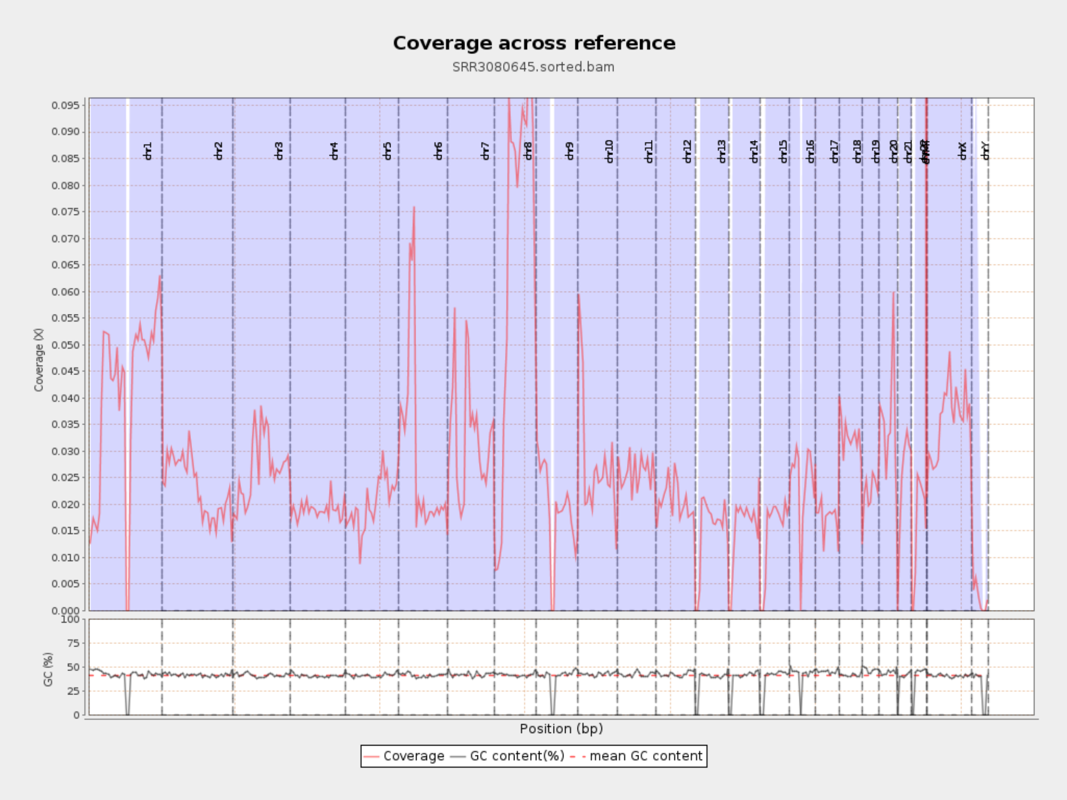
| | |
|---|---|
| General error rate | 0.69% |
| Mismatches | 566,050 |
| Insertions | 6,198 |
| Mapped reads with at least one insertion | 0.49% |
| Deletions | 19,515 |
| Mapped reads with at least one deletion | 1.53% |
| Homopolymer indels | 48.08% |

## 2.6. Chromosome stats

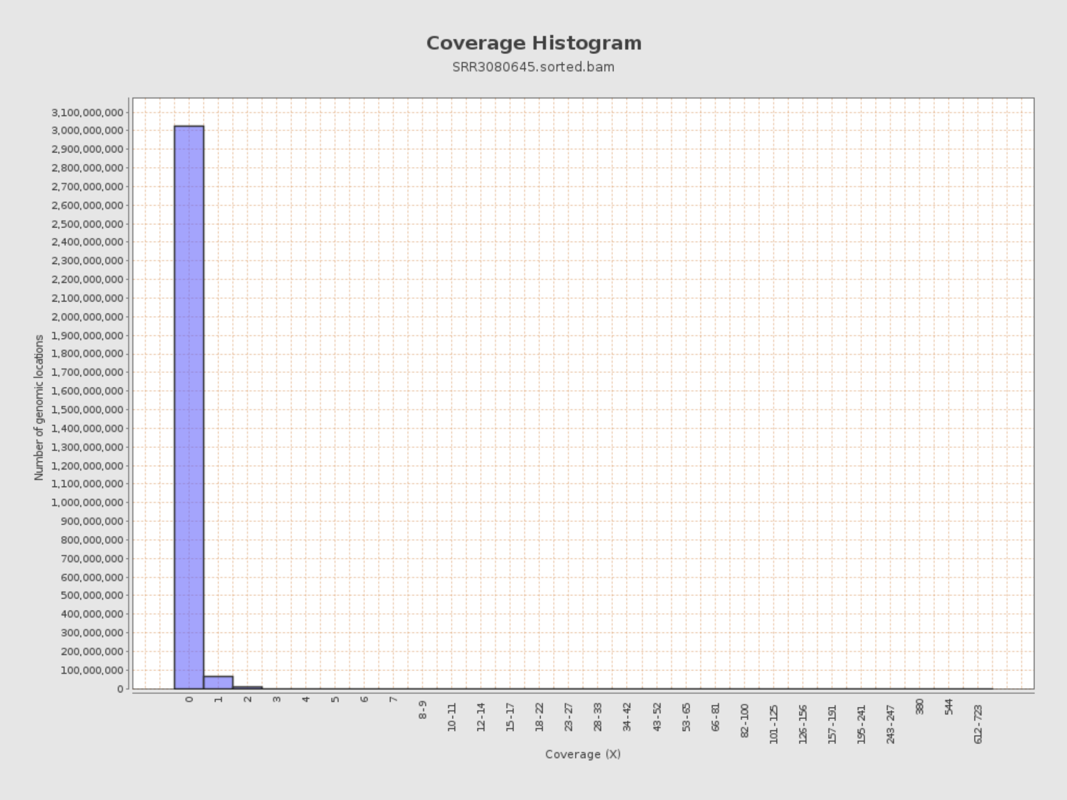
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 10160286 | 0.0408 | 0.2516 |
| chr2 | 243199373 | 5655062 | 0.0233 | 0.3464 |
| chr3 | 198022430 | 5301748 | 0.0268 | 0.1814 |
| chr4 | 191154276 | 3624733 | 0.019 | 0.1544 |
| chr5 | 180915260 | 3654114 | 0.0202 | 0.1579 |
| chr6 | 171115067 | 5007431 | 0.0293 | 0.2246 |
| chr7 | 159138663 | 5269207 | 0.0331 | 0.3453 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 9894722 | 0.0676 | 0.3157 |
| chr9 | 141213431 | 2649958 | 0.0188 | 0.1704 |
| chr10 | 135534747 | 3852762 | 0.0284 | 0.1966 |
| chr11 | 135006516 | 3488594 | 0.0258 | 0.1919 |
| chr12 | 133851895 | 2744408 | 0.0205 | 0.1593 |
| chr13 | 115169878 | 1743009 | 0.0151 | 0.1372 |
| chr14 | 107349540 | 1605474 | 0.015 | 0.1385 |
| chr15 | 102531392 | 1513619 | 0.0148 | 0.1423 |
| chr16 | 90354753 | 2178112 | 0.0241 | 0.1758 |
| chr17 | 81195210 | 1402305 | 0.0173 | 0.1485 |
| chr18 | 78077248 | 2566909 | 0.0329 | 0.2378 |
| chr19 | 59128983 | 1332537 | 0.0225 | 0.1823 |
| chr20 | 63025520 | 2218678 | 0.0352 | 0.2121 |
| chr21 | 48129895 | 1187998 | 0.0247 | 0.1772 |
| chr22 | 51304566 | 803940 | 0.0157 | 0.1386 |
| chrMT | 16571 | 17375 | 1.0485 | 1.1767 |
| chrX | 155270560 | 5560632 | 0.0358 | 0.2169 |
| chrY | 59373566 | 170036 | 0.0029 | 0.0608 |

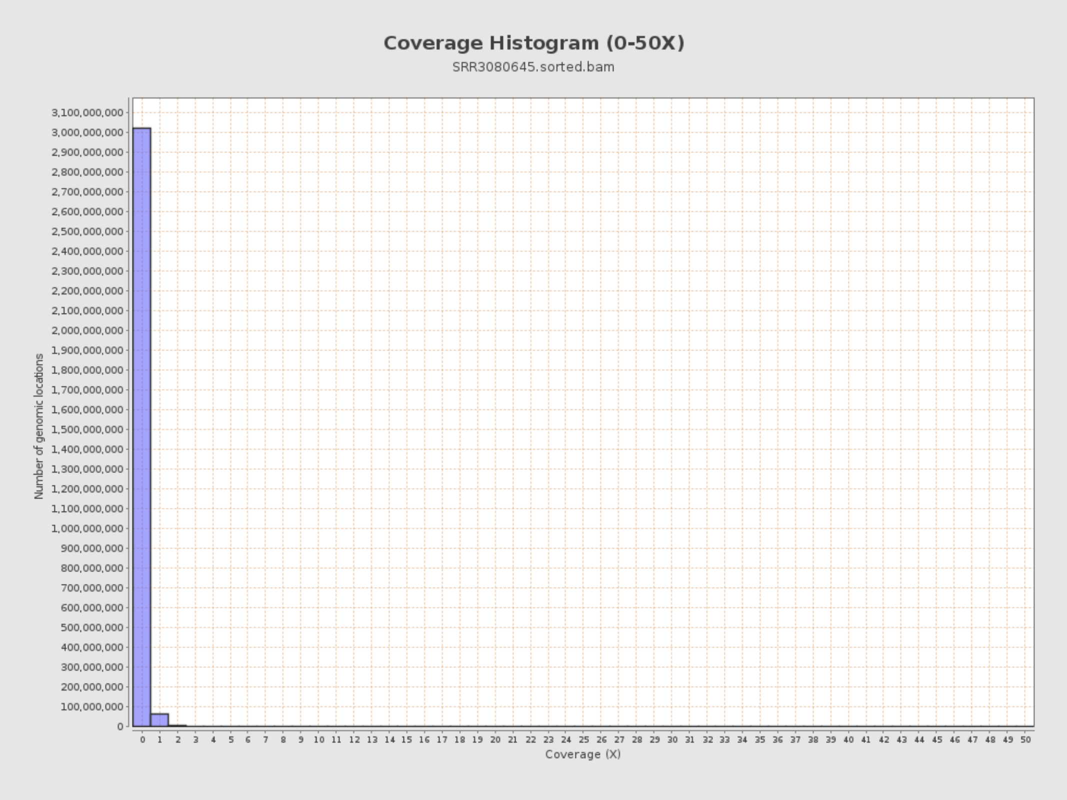
# 3. Results : Coverage across reference



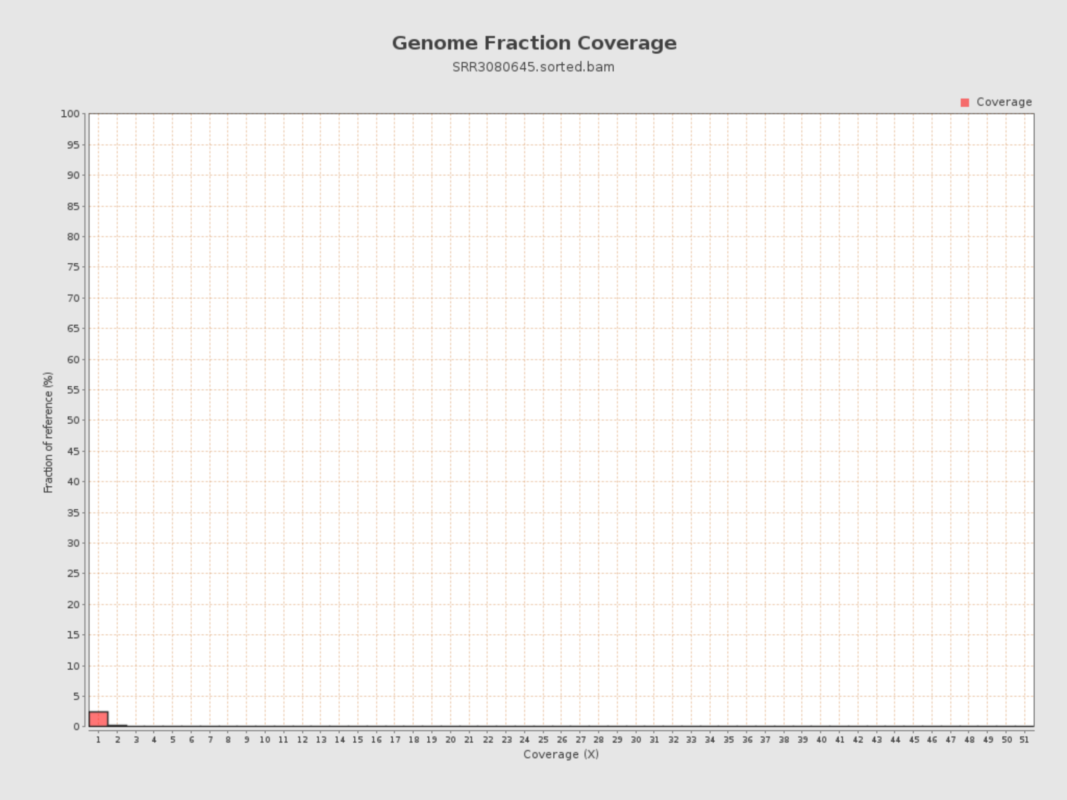
# 4. Results : Coverage Histogram



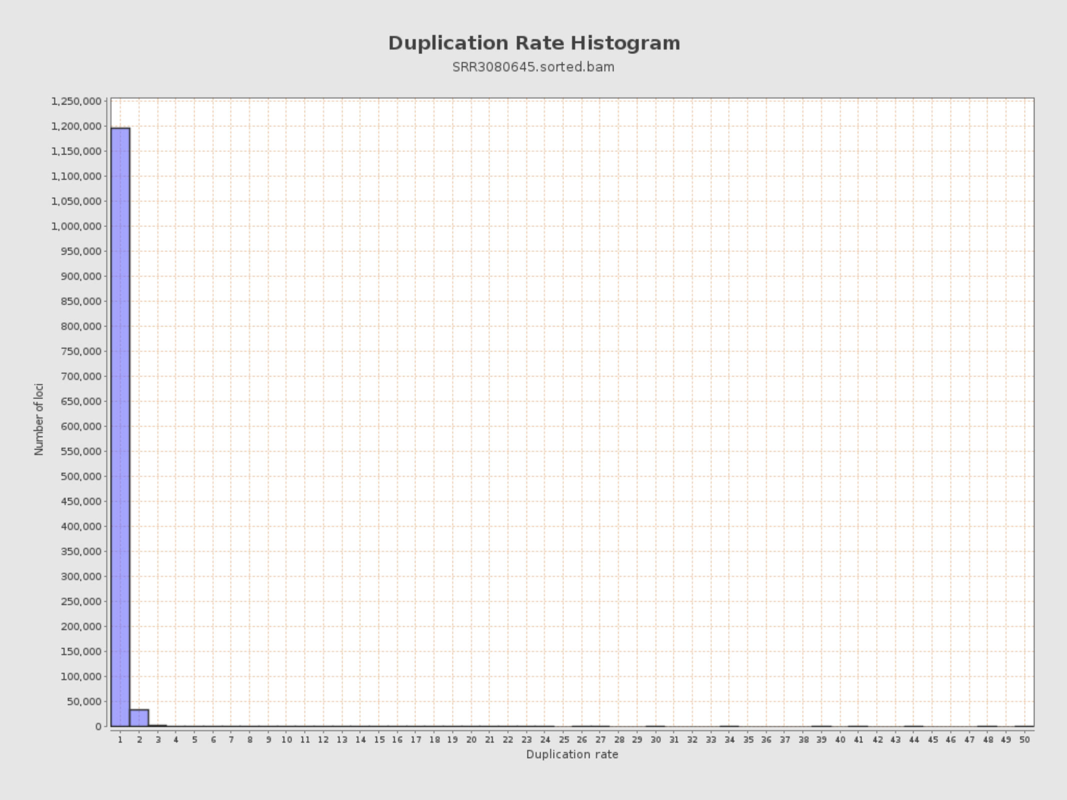
# 5. Results : Coverage Histogram (0-50X)



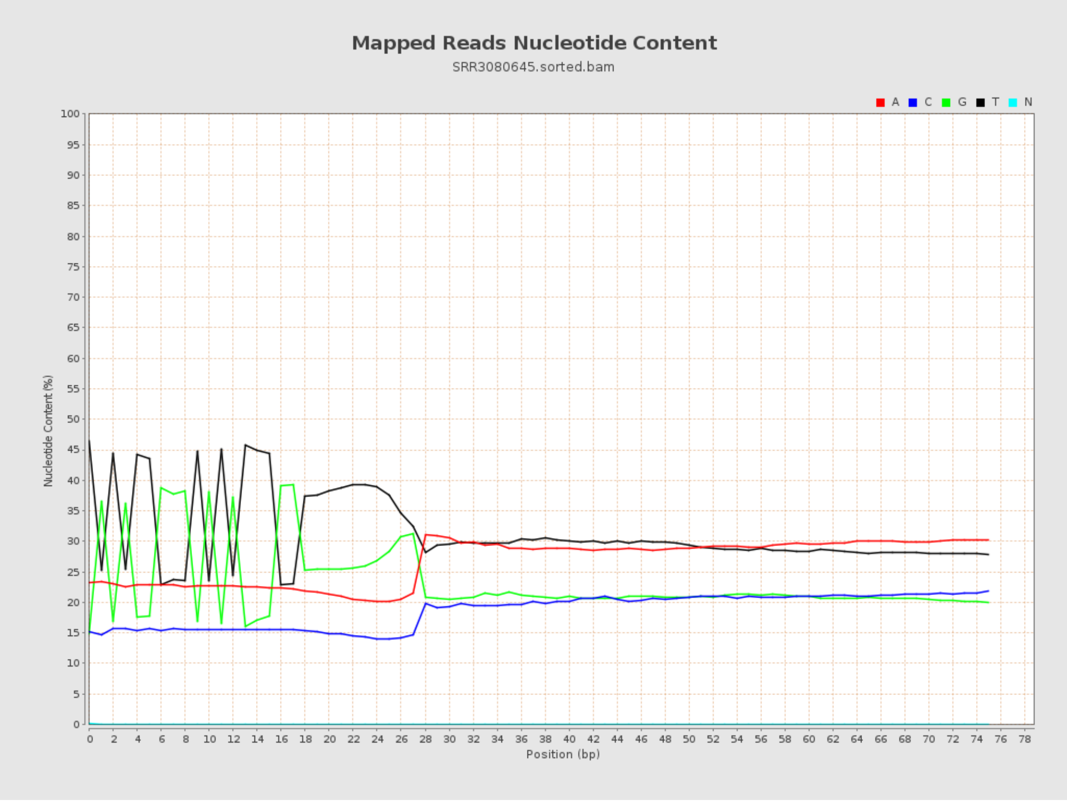
# 6. Results : Genome Fraction Coverage



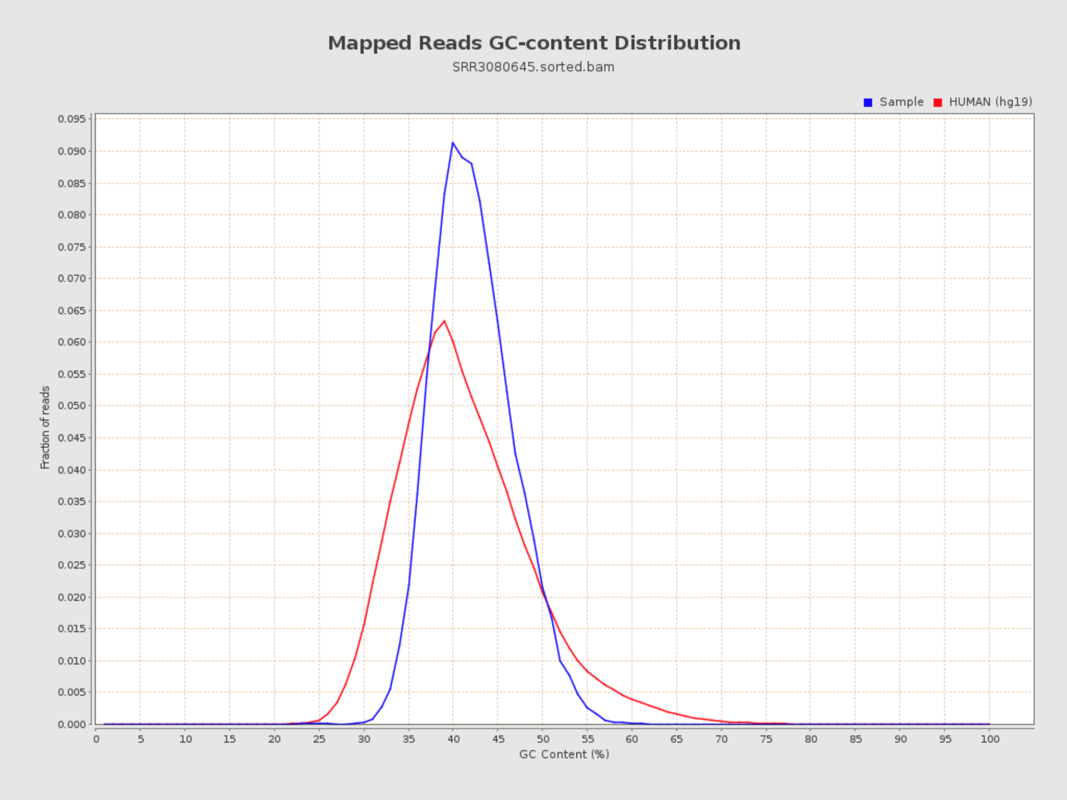
# 7. Results : Duplication Rate Histogram



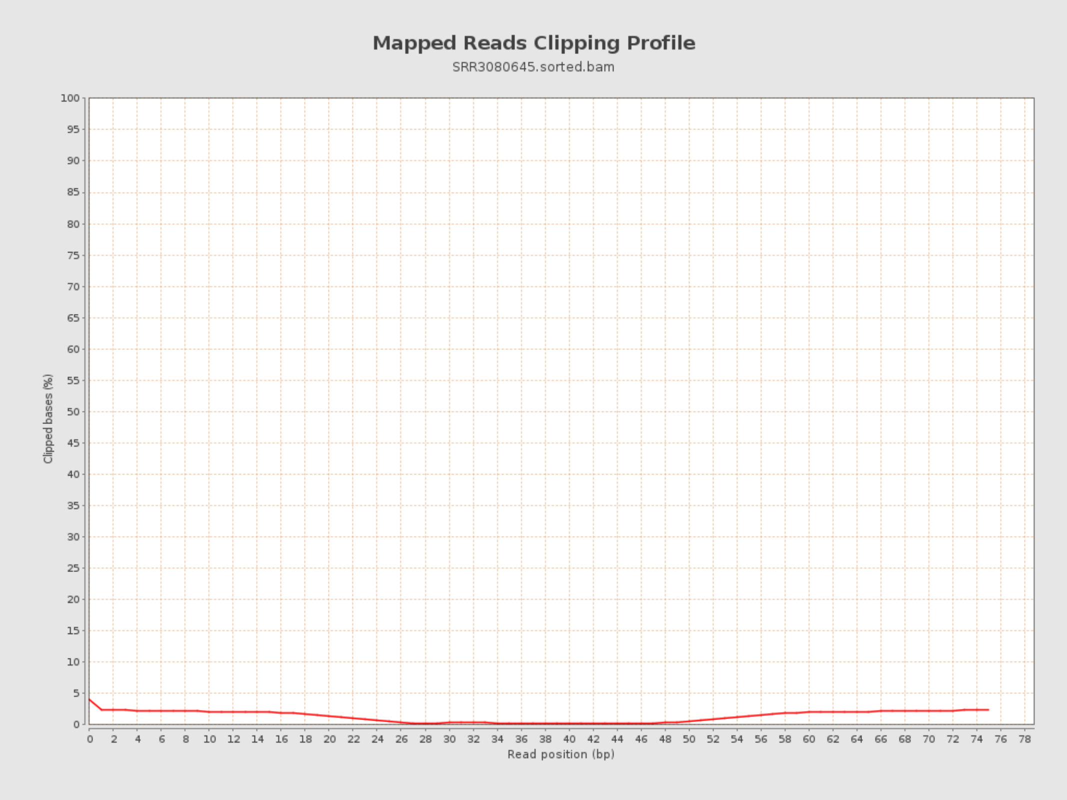
# 8. Results : Mapped Reads Nucleotide Content



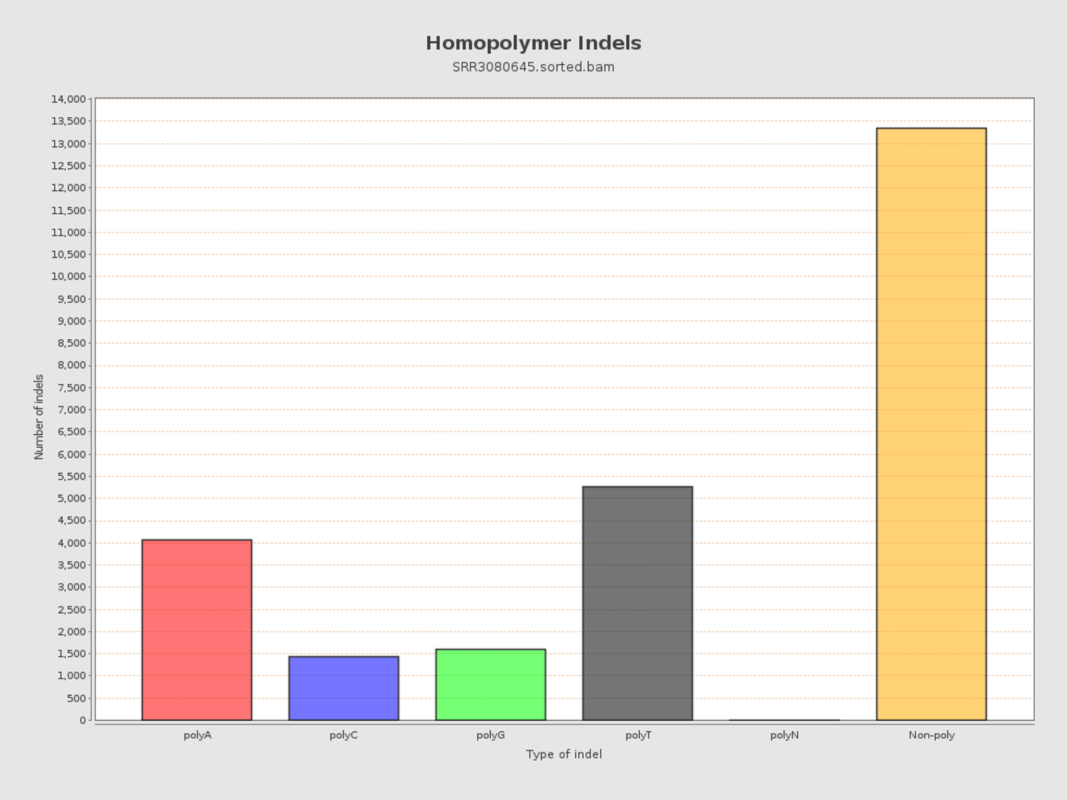
# 9. Results : Mapped Reads GC-content Distribution



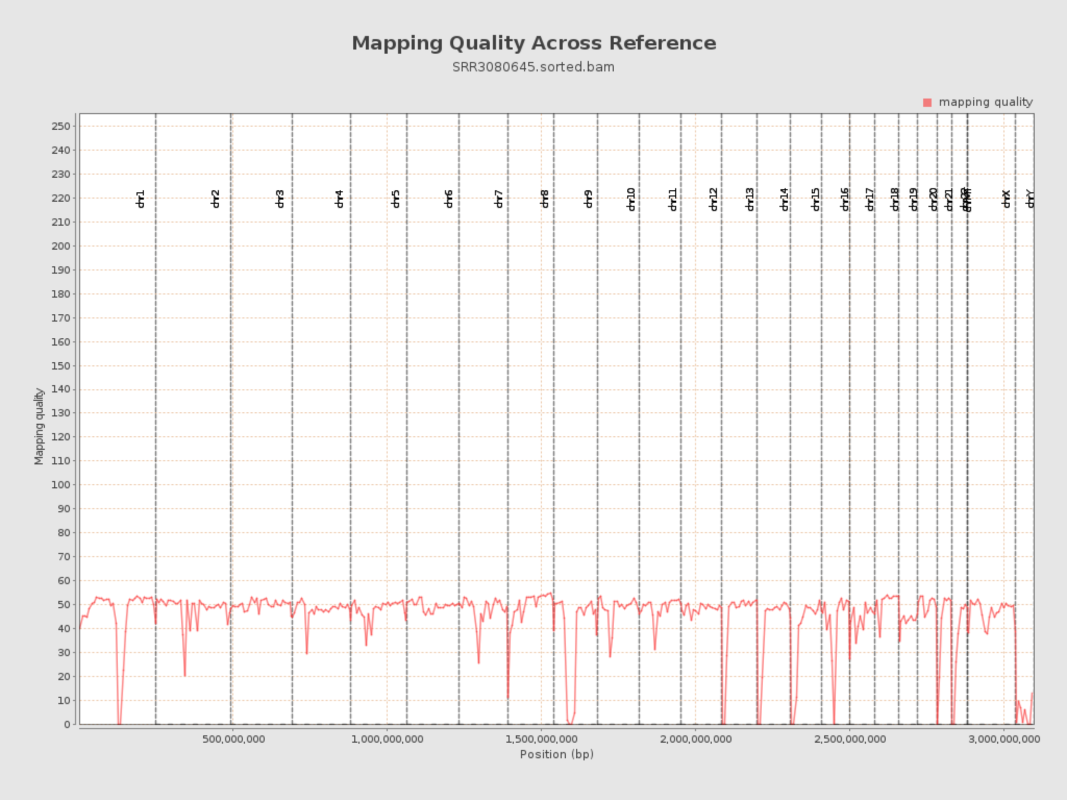
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram