# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 18:45:22*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819065.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_SRR1819065 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819065.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 18:45:20 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1819065.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,017,064 |
| Mapped reads | 930,502 / 91.49% |
| Unmapped reads | 86,562 / 8.51% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,883 / 0.38% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 19,037 / 1.87% |
| Duplication rate | 1.59% |
| Clipped reads | 931,955 / 91.63% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 12,730,798 / 23.81% |
| Number/percentage of C's | 9,875,106 / 18.47% |
| Number/percentage of T's | 17,193,407 / 32.16% |
| Number/percentage of G's | 13,666,300 / 25.56% |
| Number/percentage of N's | 1,154 / 0% |
| GC Percentage | 44.03% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0173 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1614 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.5 |

## 2.5. Mismatches and indels

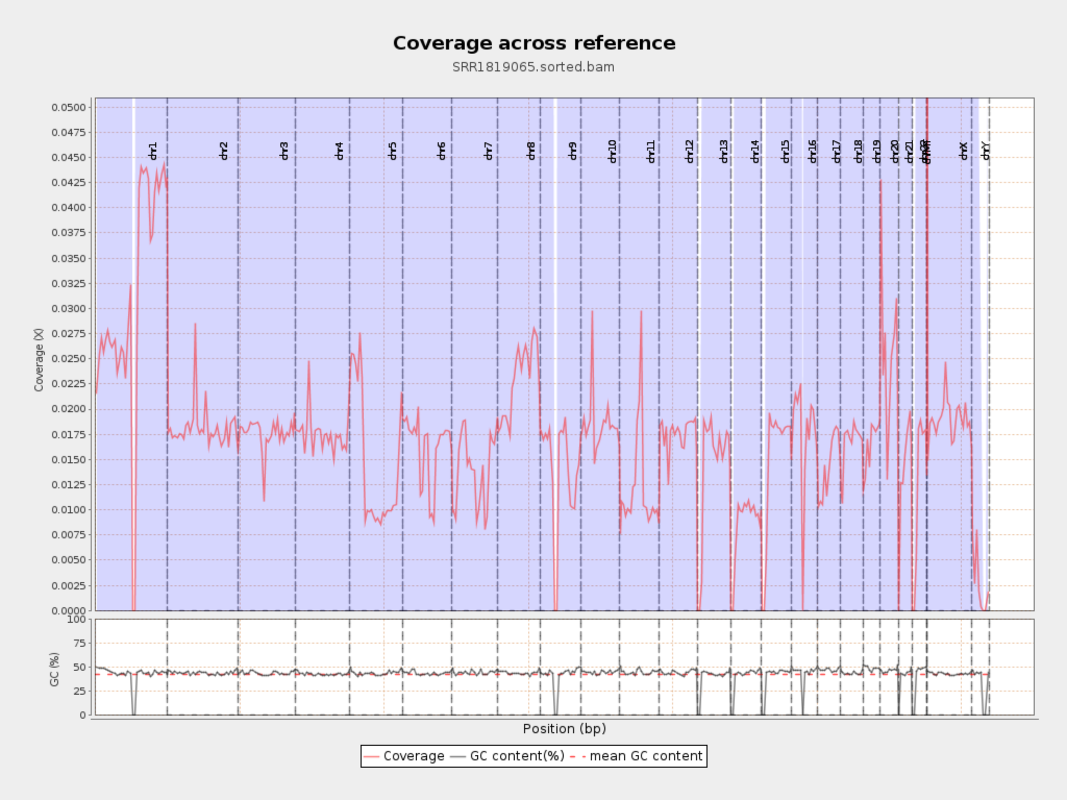
| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 261,019 |
| Insertions | 3,323 |
| Mapped reads with at least one insertion | 0.35% |
| Deletions | 8,224 |
| Mapped reads with at least one deletion | 0.88% |
| Homopolymer indels | 39.36% |

## 2.6. Chromosome stats

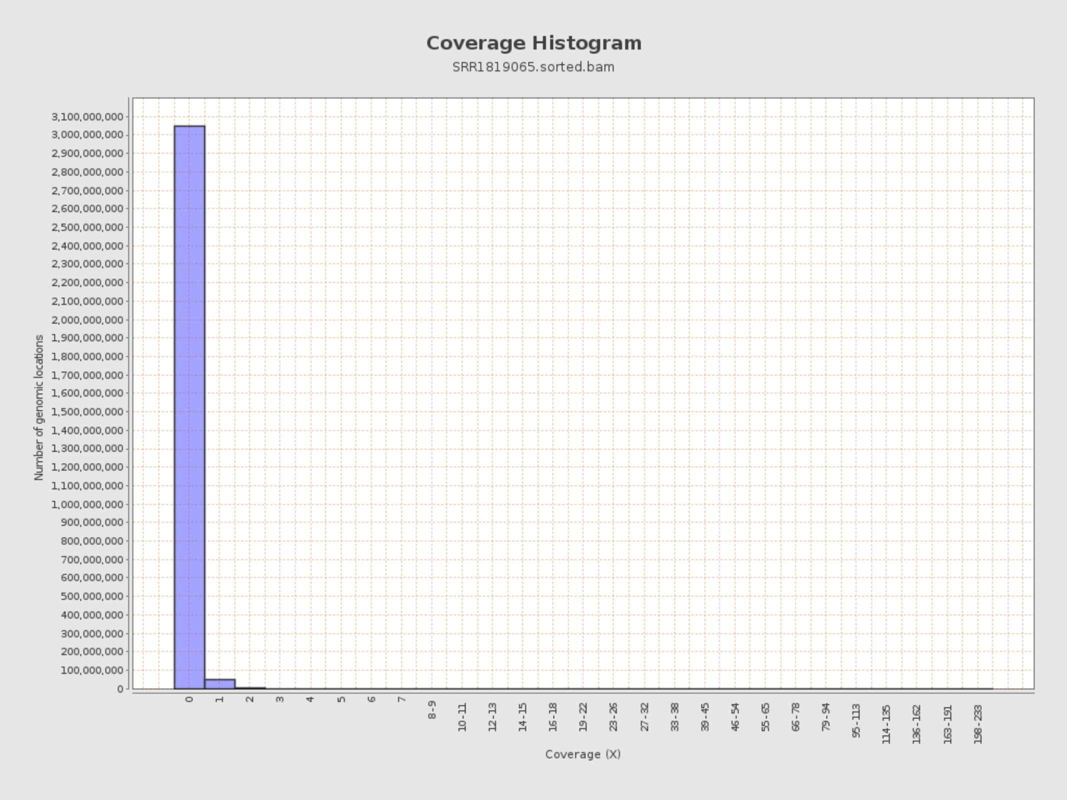
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7729707 | 0.031 | 0.259 |
| chr2 | 243199373 | 4425362 | 0.0182 | 0.172 |
| chr3 | 198022430 | 3473597 | 0.0175 | 0.1399 |
| chr4 | 191154276 | 3350609 | 0.0175 | 0.1439 |
| chr5 | 180915260 | 2603522 | 0.0144 | 0.1273 |
| chr6 | 171115067 | 2759338 | 0.0161 | 0.1388 |
| chr7 | 159138663 | 2204048 | 0.0138 | 0.1402 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3354928 | 0.0229 | 0.1756 |
| chr9 | 141213431 | 1927856 | 0.0137 | 0.1533 |
| chr10 | 135534747 | 2518825 | 0.0186 | 0.177 |
| chr11 | 135006516 | 1680415 | 0.0124 | 0.142 |
| chr12 | 133851895 | 2358021 | 0.0176 | 0.1409 |
| chr13 | 115169878 | 1633476 | 0.0142 | 0.125 |
| chr14 | 107349540 | 899904 | 0.0084 | 0.1025 |
| chr15 | 102531392 | 1514333 | 0.0148 | 0.1283 |
| chr16 | 90354753 | 1561912 | 0.0173 | 0.1462 |
| chr17 | 81195210 | 1161187 | 0.0143 | 0.1281 |
| chr18 | 78077248 | 1298517 | 0.0166 | 0.2383 |
| chr19 | 59128983 | 981747 | 0.0166 | 0.1962 |
| chr20 | 63025520 | 1605411 | 0.0255 | 0.1707 |
| chr21 | 48129895 | 687797 | 0.0143 | 0.1321 |
| chr22 | 51304566 | 631294 | 0.0123 | 0.117 |
| chrMT | 16571 | 3714 | 0.2241 | 0.5221 |
| chrX | 155270560 | 2963072 | 0.0191 | 0.1557 |
| chrY | 59373566 | 152117 | 0.0026 | 0.0676 |

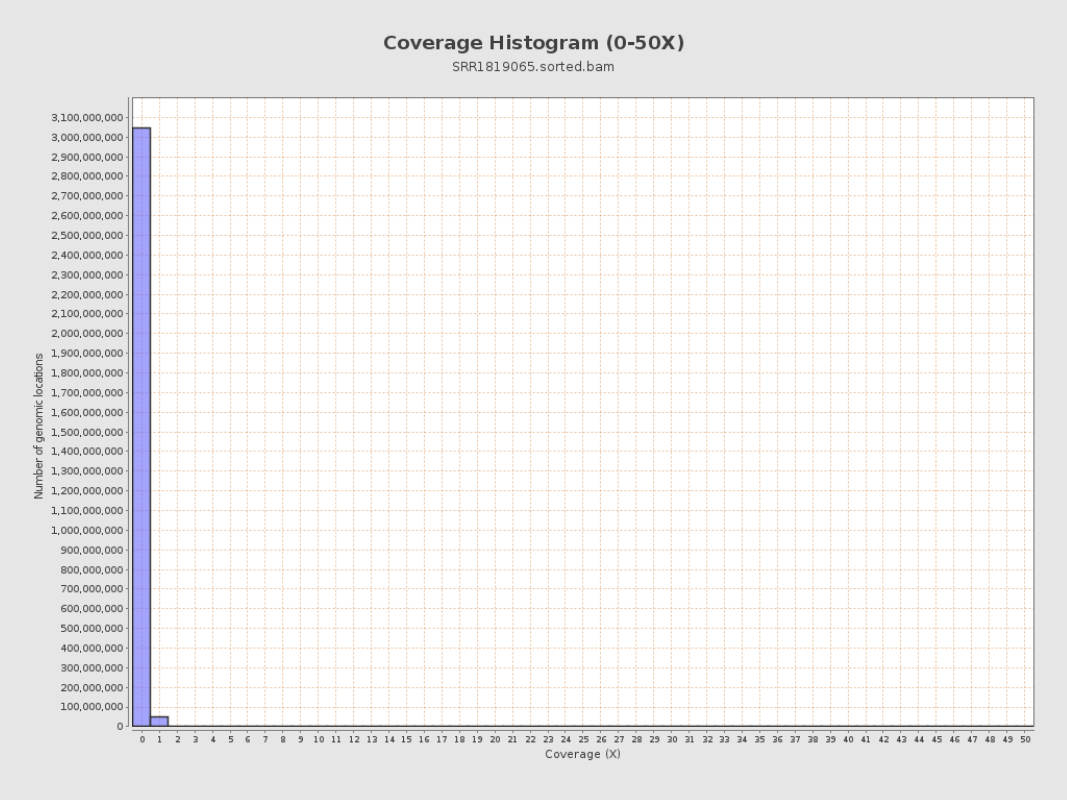
# 3. Results : Coverage across reference



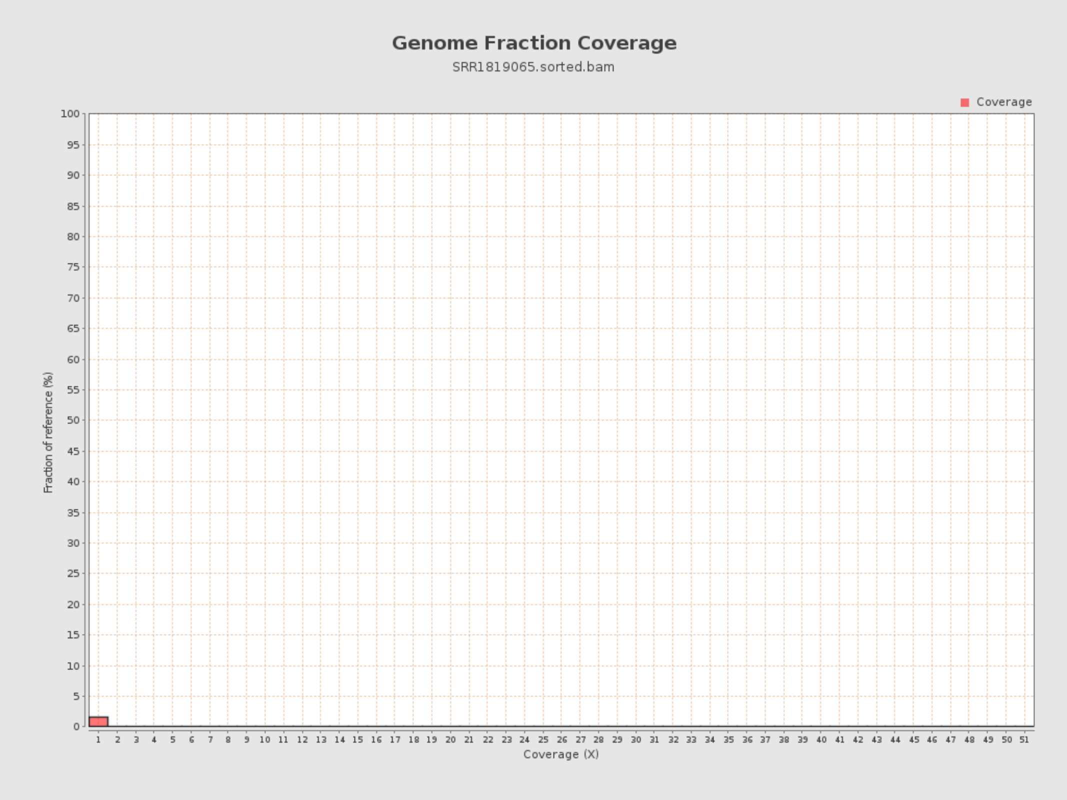
# 4. Results : Coverage Histogram



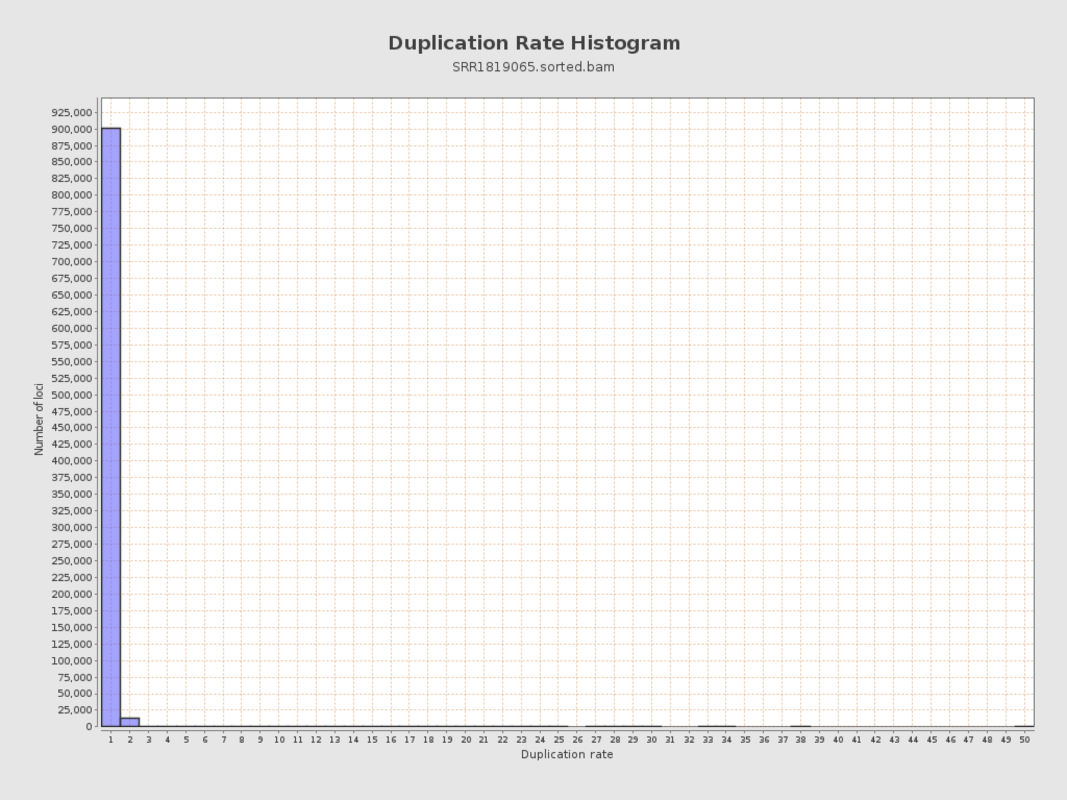
# 5. Results : Coverage Histogram (0-50X)



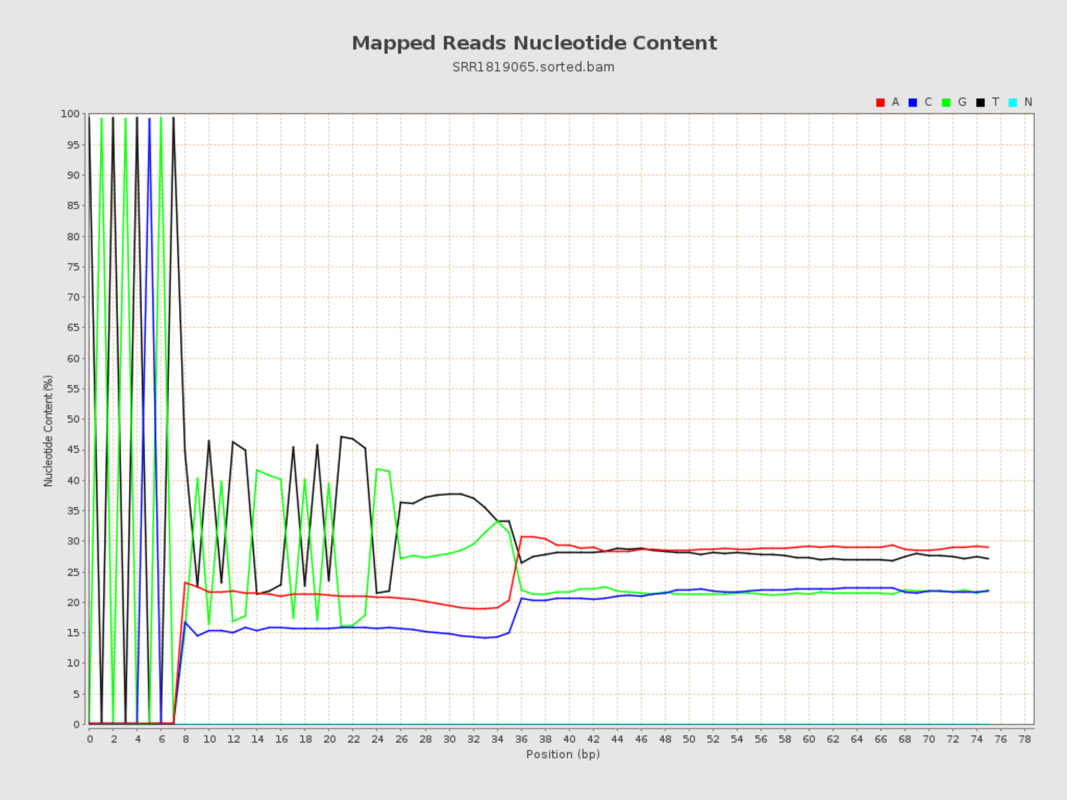
# 6. Results : Genome Fraction Coverage



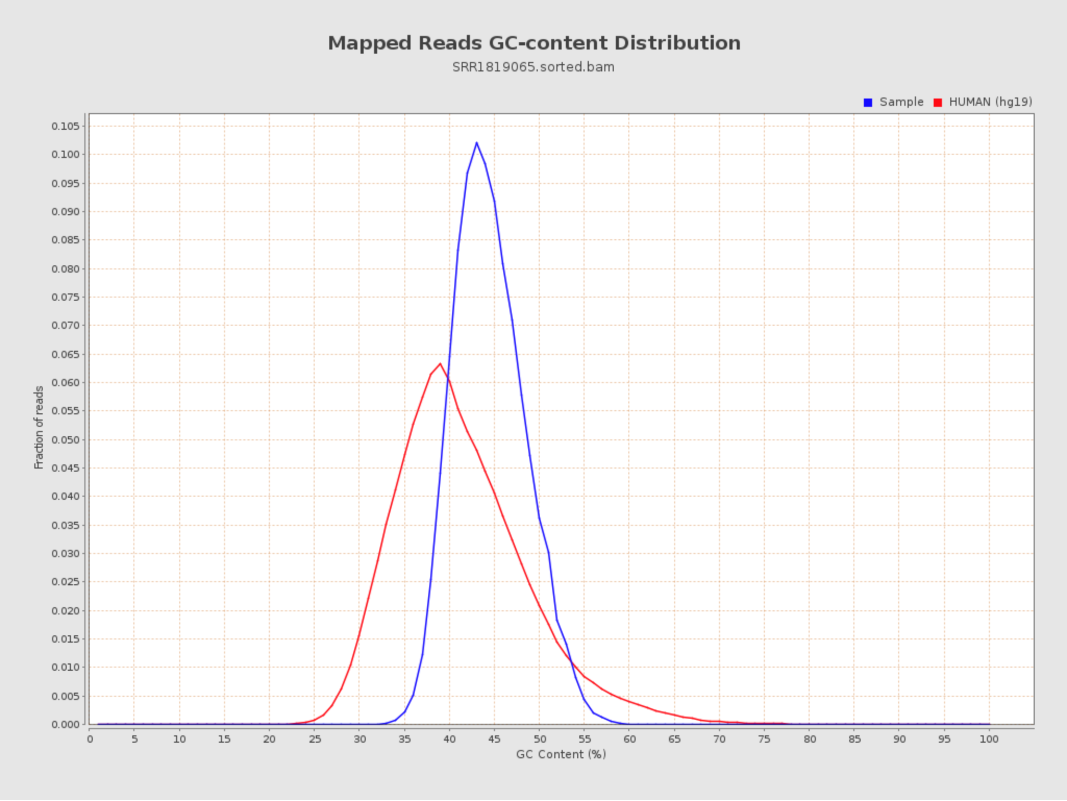
# 7. Results : Duplication Rate Histogram



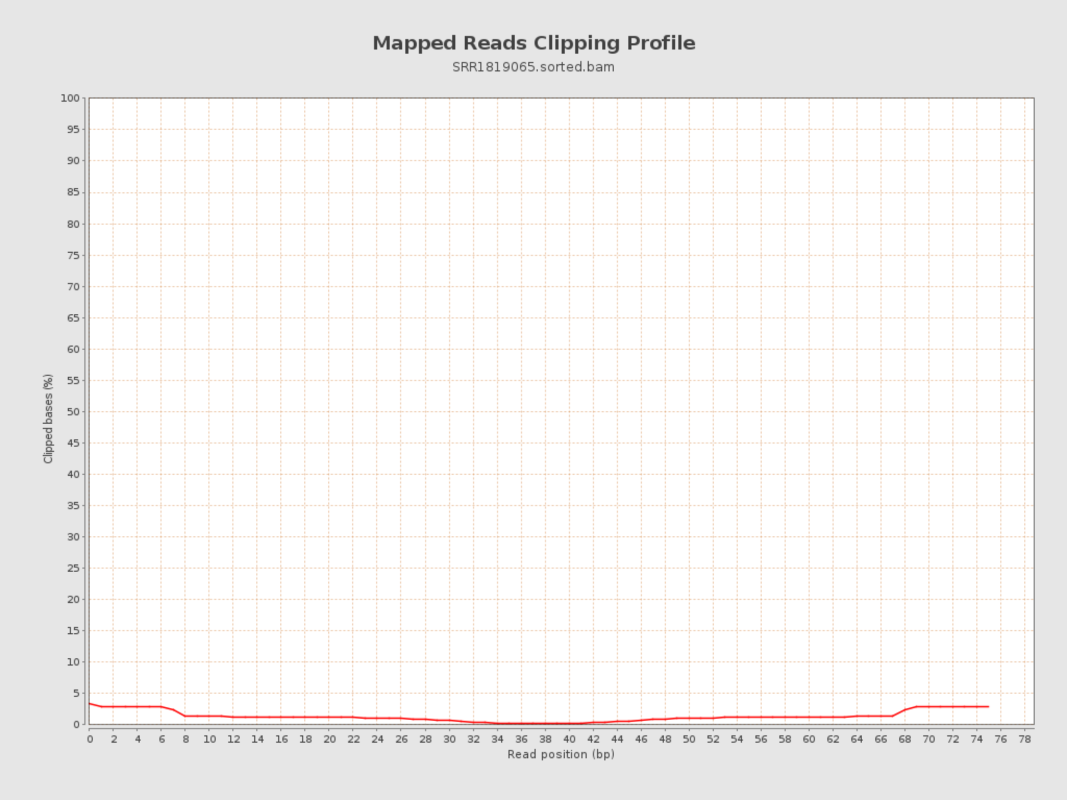
# 8. Results : Mapped Reads Nucleotide Content



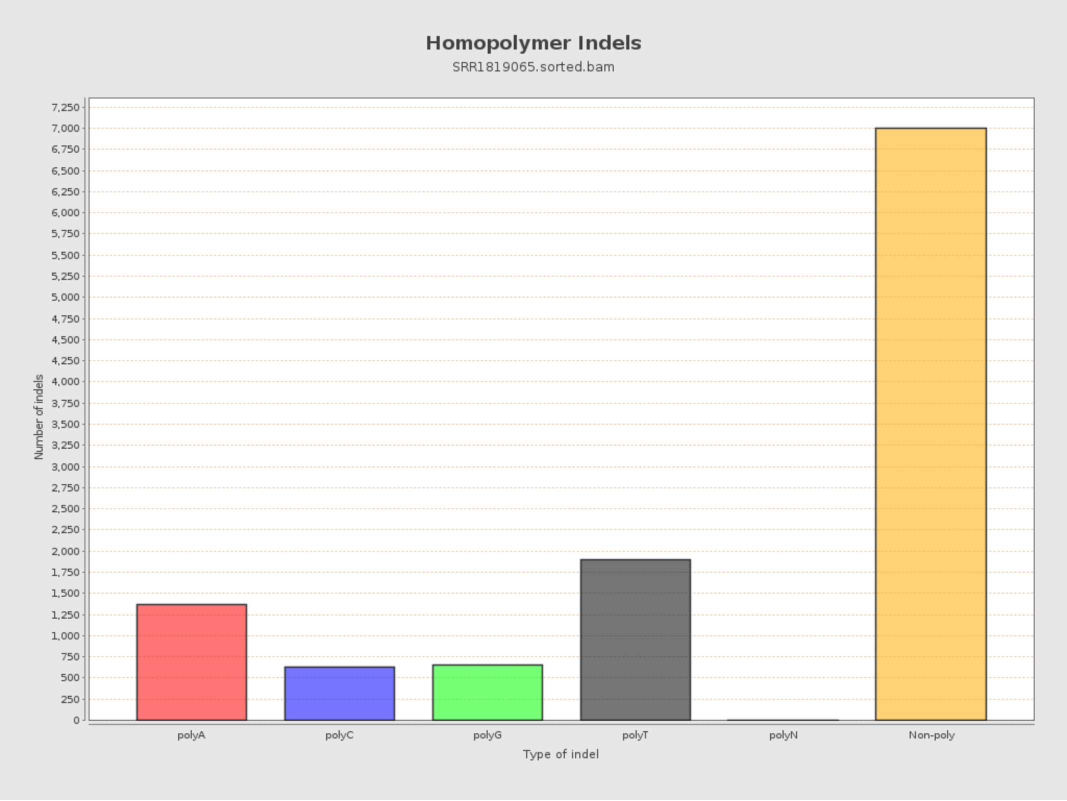
# 9. Results : Mapped Reads GC-content Distribution



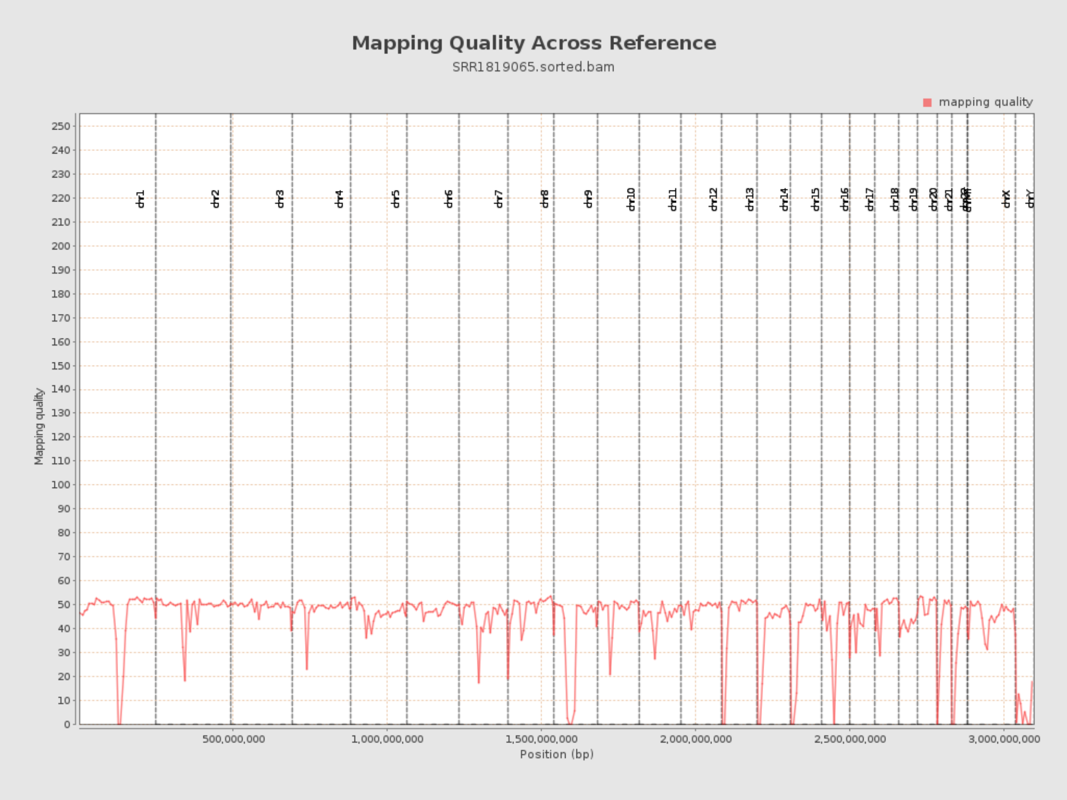
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram