# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 20:49:15*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819082.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_SRR1819082 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819082.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 20:48:45 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1819082.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,962,283 |
| Mapped reads | 1,806,899 / 92.08% |
| Unmapped reads | 155,384 / 7.92% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 6,928 / 0.35% |
| Read min/max/mean length | 30 / 76 / 76.12 |
| Duplicated reads (estimated) | 82,893 / 4.22% |
| Duplication rate | 3.52% |
| Clipped reads | 1,809,192 / 92.2% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 26,001,722 / 24.72% |
| Number/percentage of C's | 19,761,484 / 18.79% |
| Number/percentage of T's | 33,681,780 / 32.03% |
| Number/percentage of G's | 25,724,865 / 24.46% |
| Number/percentage of N's | 1,446 / 0% |
| GC Percentage | 43.25% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.034 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2975 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.74 |

## 2.5. Mismatches and indels

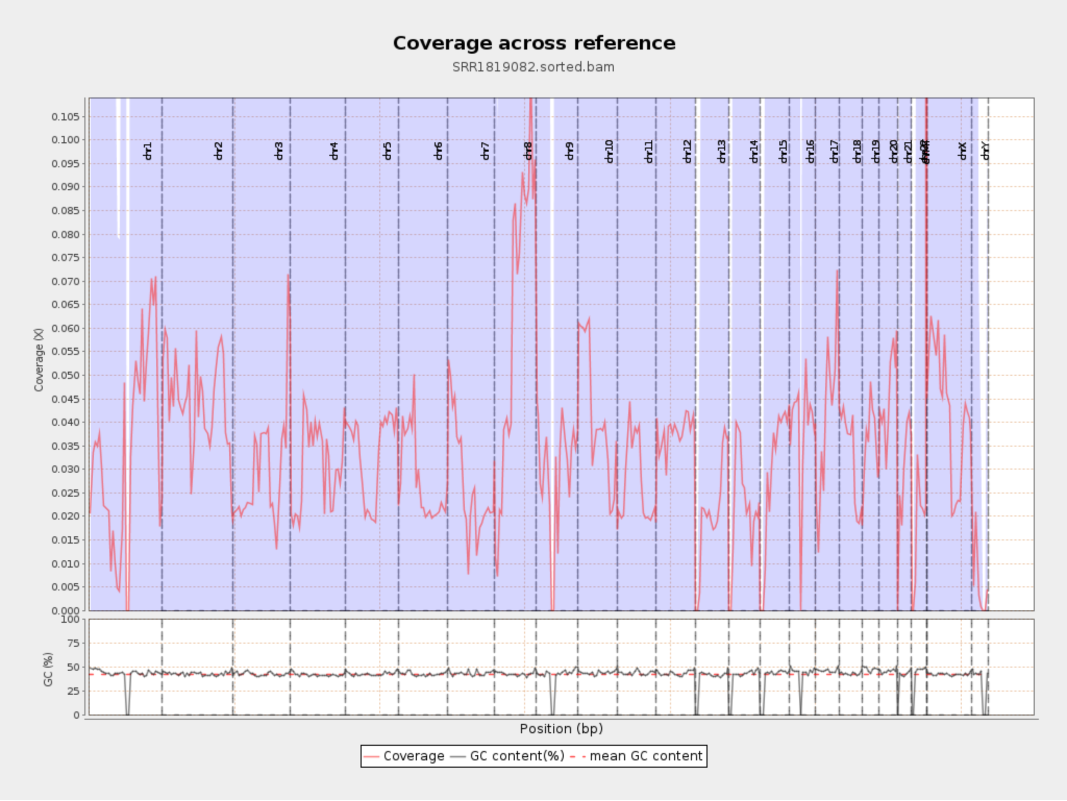
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 521,478 |
| Insertions | 7,415 |
| Mapped reads with at least one insertion | 0.41% |
| Deletions | 19,940 |
| Mapped reads with at least one deletion | 1.1% |
| Homopolymer indels | 43.34% |

## 2.6. Chromosome stats

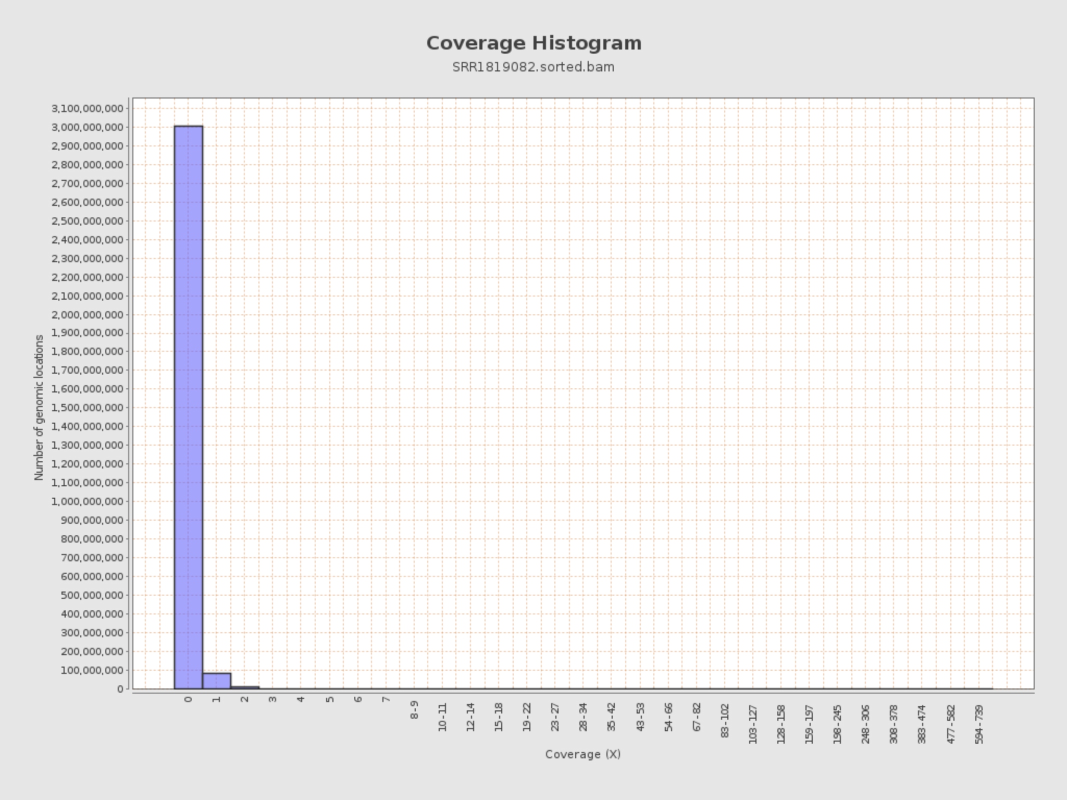
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8400581 | 0.0337 | 0.5643 |
| chr2 | 243199373 | 10981345 | 0.0452 | 0.3724 |
| chr3 | 198022430 | 5809945 | 0.0293 | 0.1924 |
| chr4 | 191154276 | 5859314 | 0.0307 | 0.2238 |
| chr5 | 180915260 | 6083797 | 0.0336 | 0.2061 |
| chr6 | 171115067 | 4717318 | 0.0276 | 0.241 |
| chr7 | 159138663 | 4264709 | 0.0268 | 0.2066 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 9136368 | 0.0624 | 0.3409 |
| chr9 | 141213431 | 3997810 | 0.0283 | 0.2459 |
| chr10 | 135534747 | 5694279 | 0.042 | 0.3076 |
| chr11 | 135006516 | 3719341 | 0.0275 | 0.271 |
| chr12 | 133851895 | 5083733 | 0.038 | 0.218 |
| chr13 | 115169878 | 2374774 | 0.0206 | 0.1611 |
| chr14 | 107349540 | 2306336 | 0.0215 | 0.1684 |
| chr15 | 102531392 | 2964106 | 0.0289 | 0.1966 |
| chr16 | 90354753 | 3482748 | 0.0385 | 0.2305 |
| chr17 | 81195210 | 3447670 | 0.0425 | 0.248 |
| chr18 | 78077248 | 2583569 | 0.0331 | 0.4565 |
| chr19 | 59128983 | 2161849 | 0.0366 | 0.3974 |
| chr20 | 63025520 | 2870201 | 0.0455 | 0.239 |
| chr21 | 48129895 | 1382208 | 0.0287 | 0.208 |
| chr22 | 51304566 | 844510 | 0.0165 | 0.1426 |
| chrMT | 16571 | 59832 | 3.6106 | 2.7339 |
| chrX | 155270560 | 6619059 | 0.0426 | 0.2581 |
| chrY | 59373566 | 358989 | 0.006 | 0.1702 |

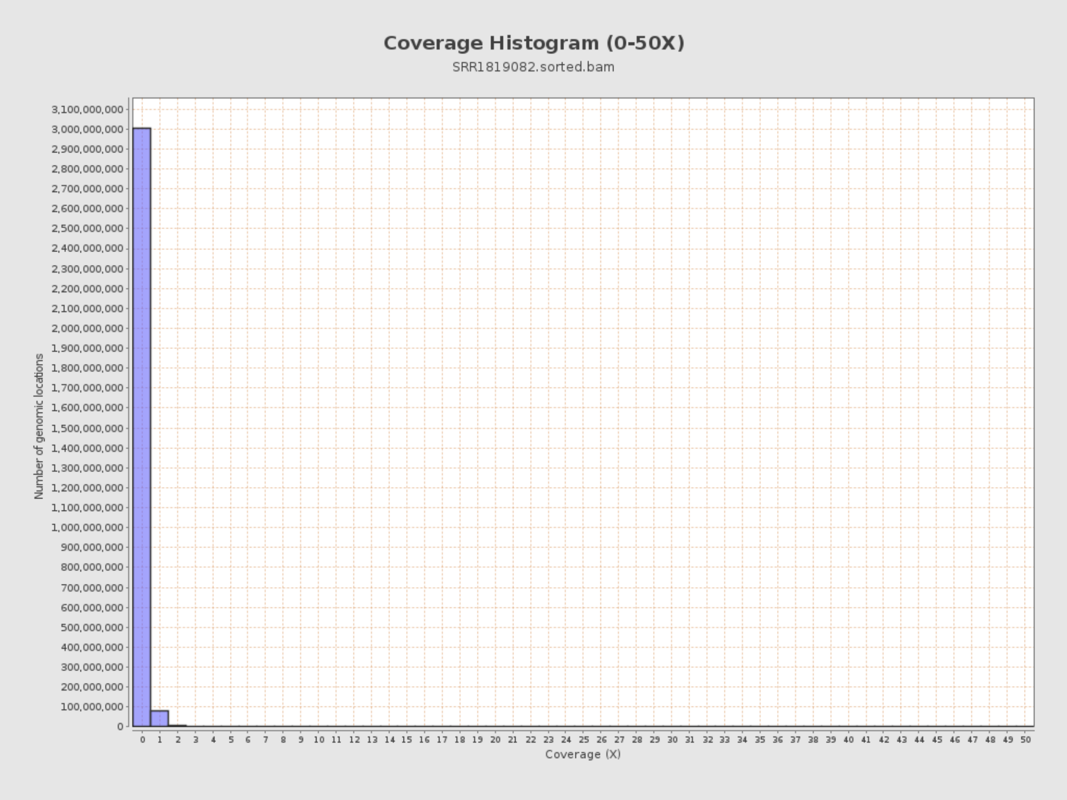
# 3. Results : Coverage across reference



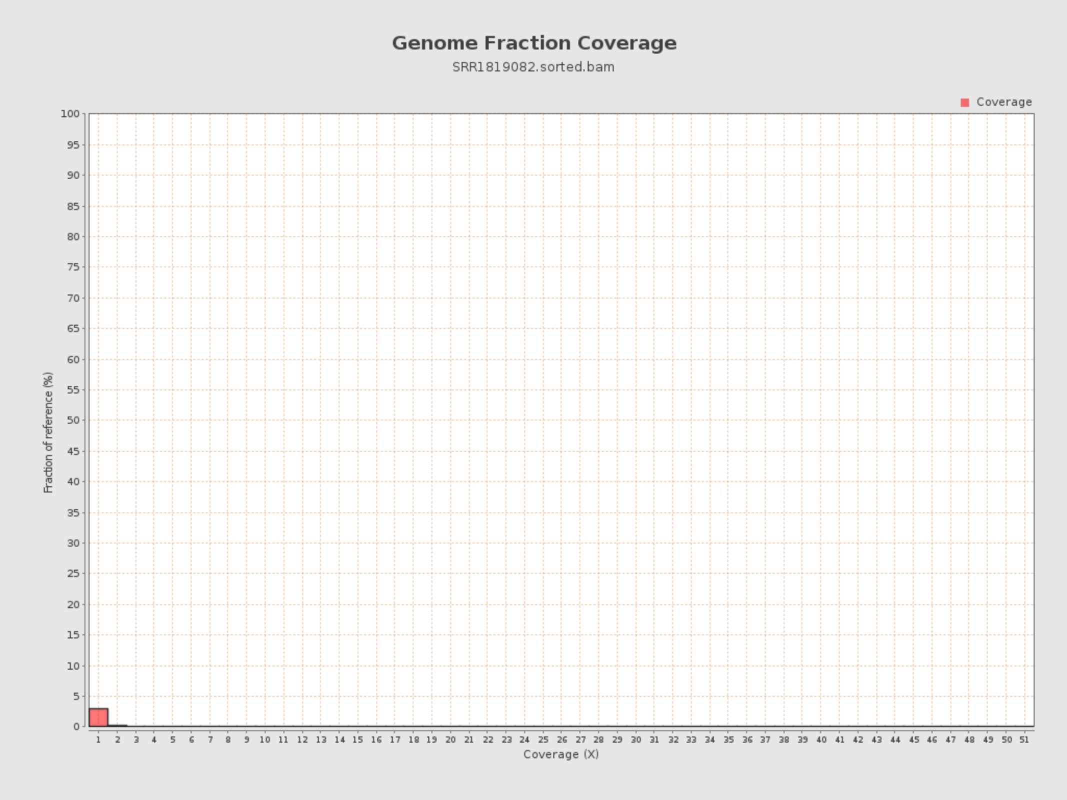
# 4. Results : Coverage Histogram



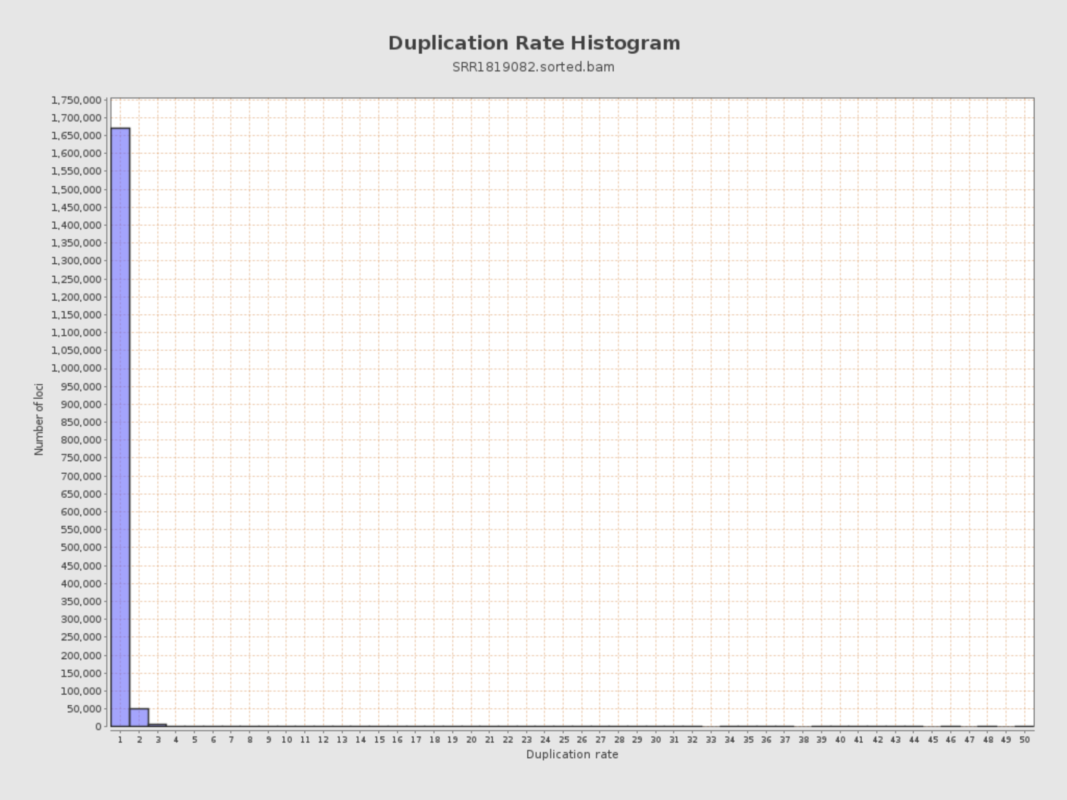
# 5. Results : Coverage Histogram (0-50X)



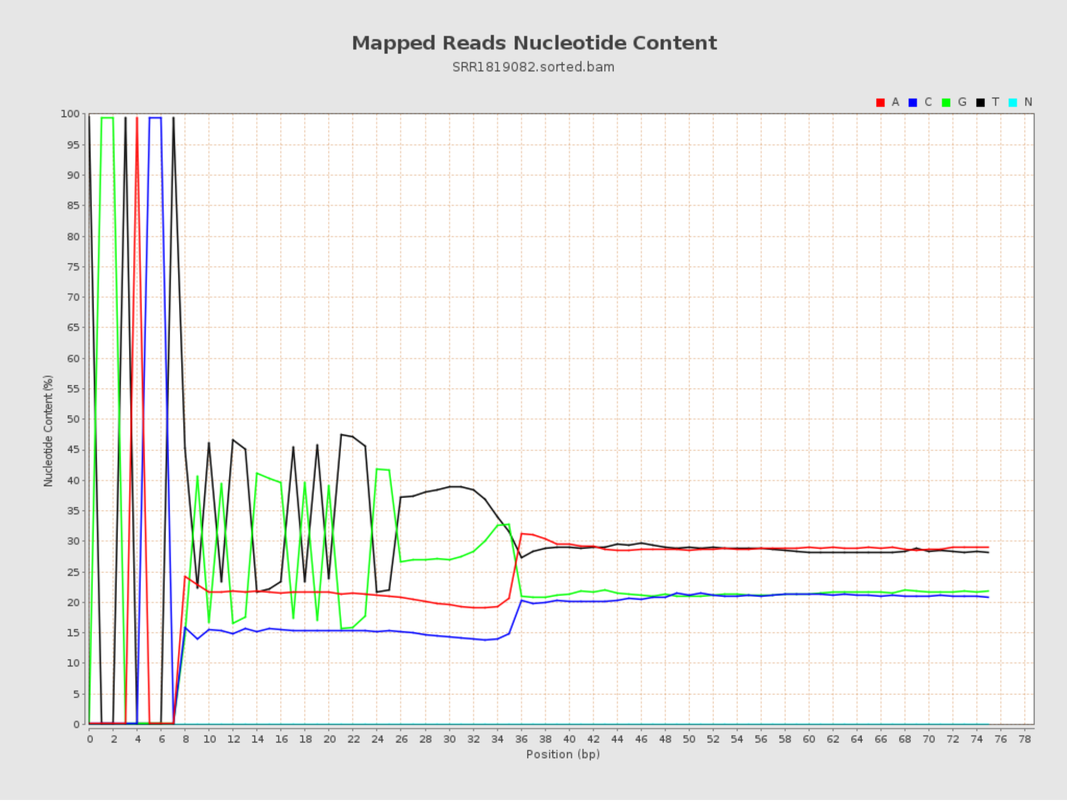
# 6. Results : Genome Fraction Coverage



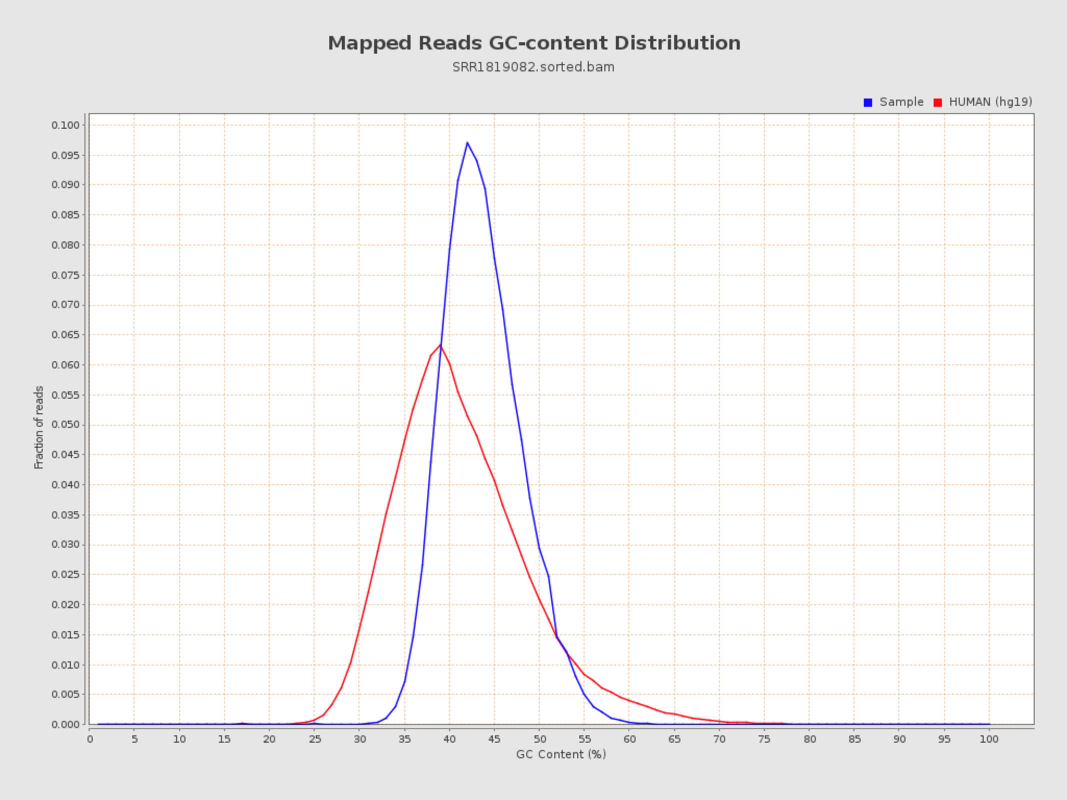
# 7. Results : Duplication Rate Histogram



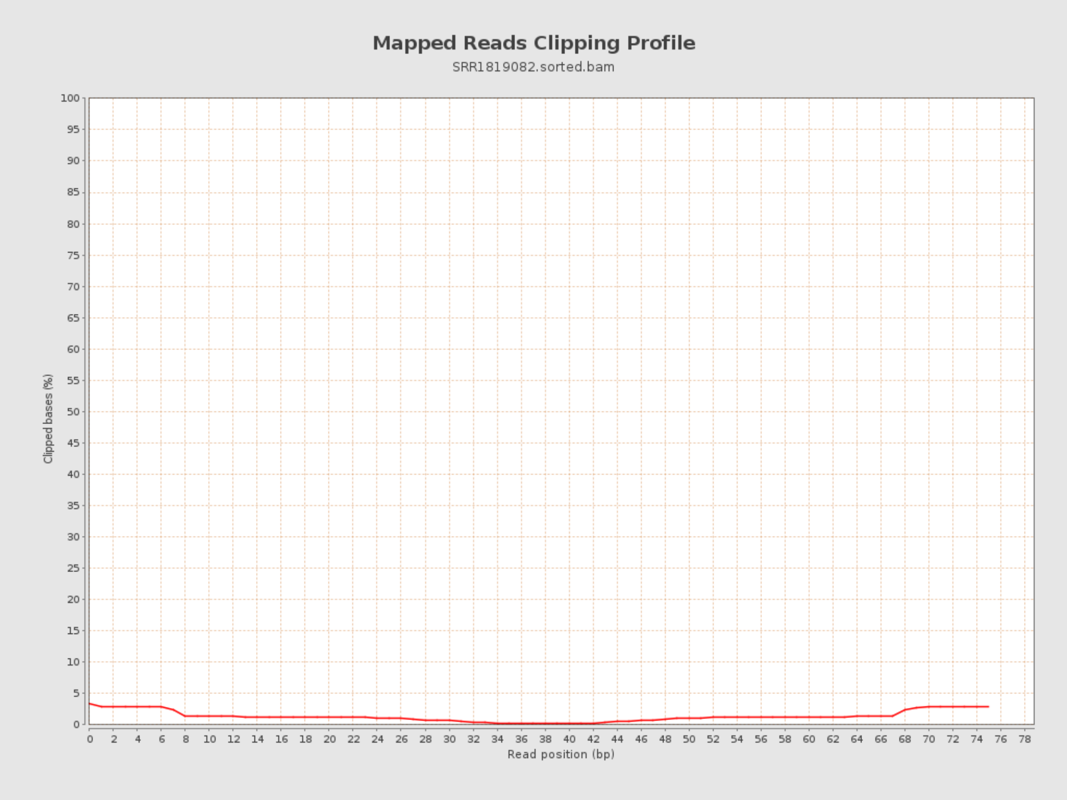
# 8. Results : Mapped Reads Nucleotide Content



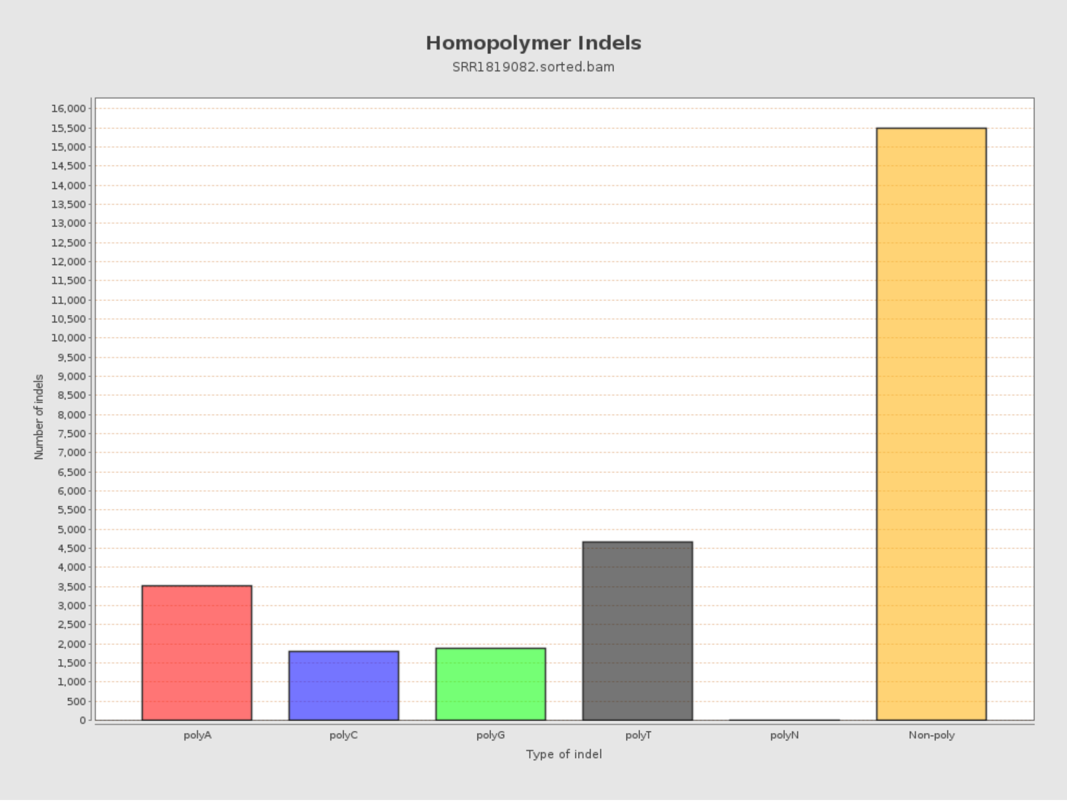
# 9. Results : Mapped Reads GC-content Distribution



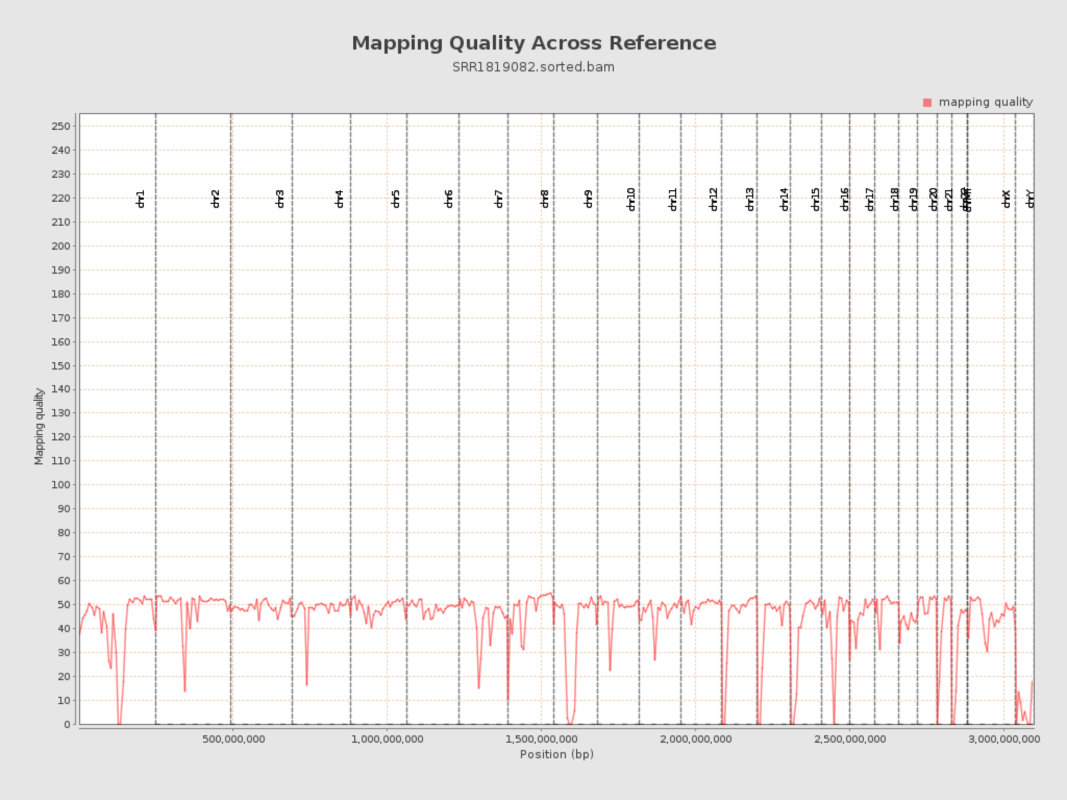
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram