# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/22 12:45:43*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818797.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_SRR1818797 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818797.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 22 12:45:41 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1818797.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,814,430 |
| Mapped reads | 1,766,647 / 97.37% |
| Unmapped reads | 47,783 / 2.63% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 13,037 / 0.72% |
| Read min/max/mean length | 30 / 76 / 76.24 |
| Duplicated reads (estimated) | 787,625 / 43.41% |
| Duplication rate | 37.2% |
| Clipped reads | 1,771,622 / 97.64% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 35,552,292 / 29.64% |
| Number/percentage of C's | 27,410,785 / 22.85% |
| Number/percentage of T's | 32,773,686 / 27.33% |
| Number/percentage of G's | 24,193,438 / 20.17% |
| Number/percentage of N's | 7,679 / 0.01% |
| GC Percentage | 43.03% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0388 |
| | |

| | |
|---|---|
| Standard Deviation | 0.5211 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.62 |

## 2.5. Mismatches and indels

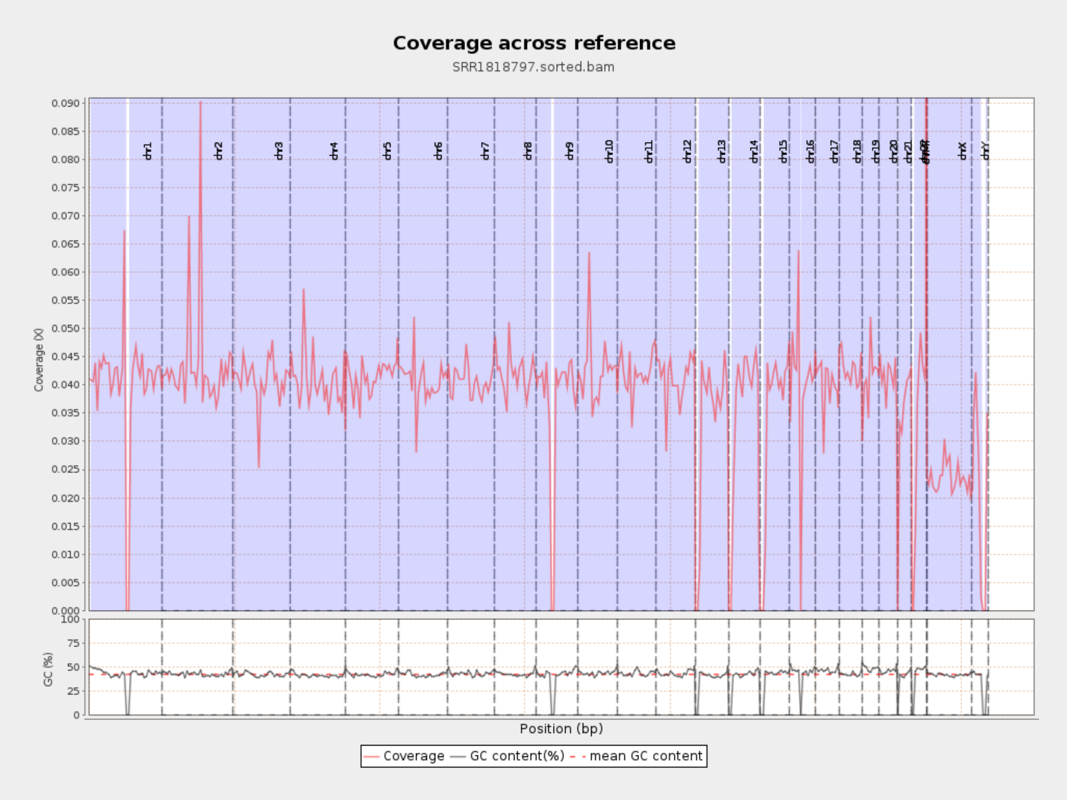
| | |
|---|---|
| General error rate | 0.55% |
| Mismatches | 636,075 |
| Insertions | 13,747 |
| Mapped reads with at least one insertion | 0.77% |
| Deletions | 30,934 |
| Mapped reads with at least one deletion | 1.73% |
| Homopolymer indels | 40.24% |

## 2.6. Chromosome stats

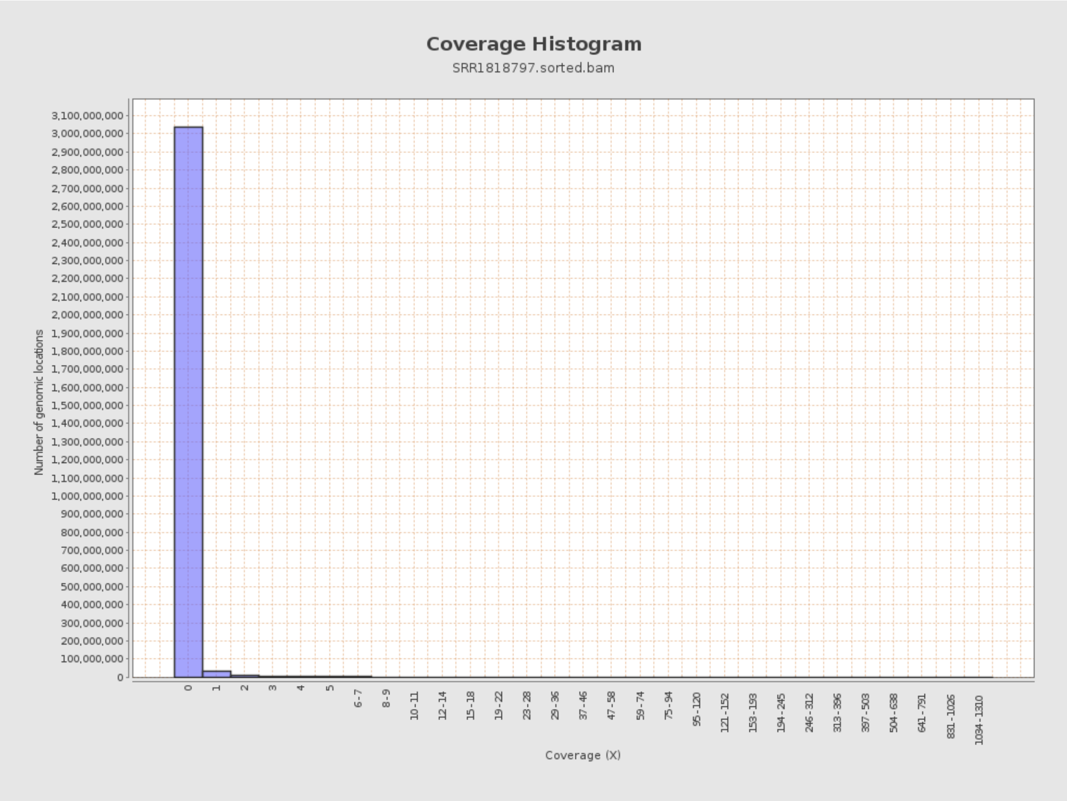
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 9983578 | 0.0401 | 0.7038 |
| chr2 | 243199373 | 10633499 | 0.0437 | 0.9147 |
| chr3 | 198022430 | 8121495 | 0.041 | 0.3698 |
| chr4 | 191154276 | 7782687 | 0.0407 | 0.4133 |
| chr5 | 180915260 | 7489984 | 0.0414 | 0.3995 |
| chr6 | 171115067 | 6971269 | 0.0407 | 0.4056 |
| chr7 | 159138663 | 6461515 | 0.0406 | 0.4316 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6187673 | 0.0423 | 0.4214 |
| chr9 | 141213431 | 5120463 | 0.0363 | 0.4424 |
| chr10 | 135534747 | 5752851 | 0.0424 | 0.5767 |
| chr11 | 135006516 | 5695765 | 0.0422 | 0.4284 |
| chr12 | 133851895 | 5503005 | 0.0411 | 0.4198 |
| chr13 | 115169878 | 3816790 | 0.0331 | 0.3391 |
| chr14 | 107349540 | 3741998 | 0.0349 | 0.3921 |
| chr15 | 102531392 | 3417344 | 0.0333 | 0.3317 |
| chr16 | 90354753 | 3622214 | 0.0401 | 0.61 |
| chr17 | 81195210 | 3230381 | 0.0398 | 0.3904 |
| chr18 | 78077248 | 3341995 | 0.0428 | 0.5295 |
| chr19 | 59128983 | 2459585 | 0.0416 | 0.5919 |
| chr20 | 63025520 | 2619637 | 0.0416 | 0.4055 |
| chr21 | 48129895 | 1635344 | 0.034 | 0.3651 |
| chr22 | 51304566 | 1523257 | 0.0297 | 0.3566 |
| chrMT | 16571 | 17761 | 1.0718 | 1.9605 |
| chrX | 155270560 | 3663298 | 0.0236 | 0.3142 |
| chrY | 59373566 | 1195503 | 0.0201 | 0.9347 |

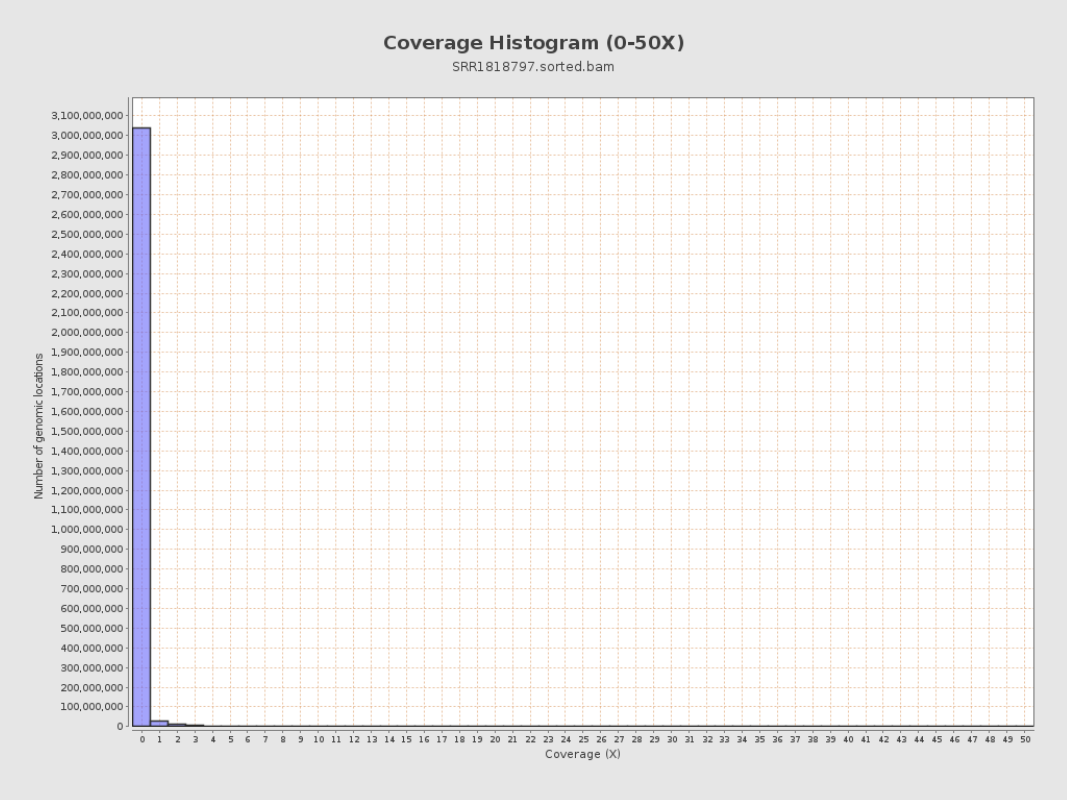
# 3. Results : Coverage across reference



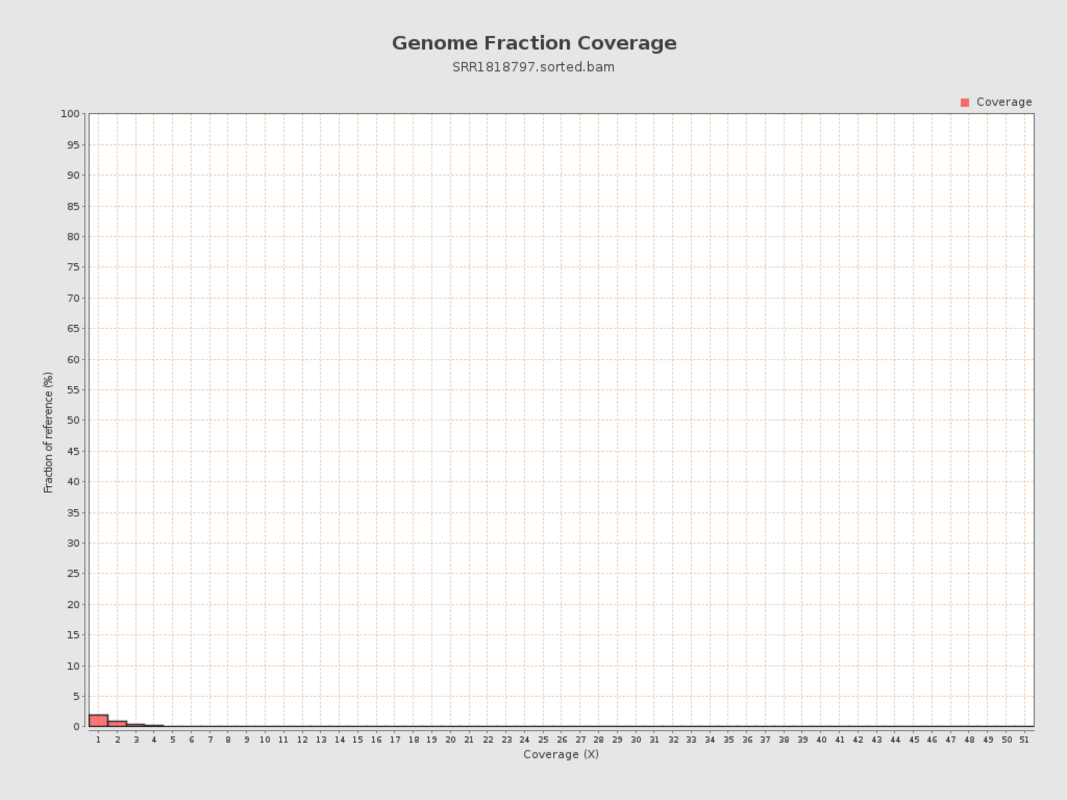
# 4. Results : Coverage Histogram



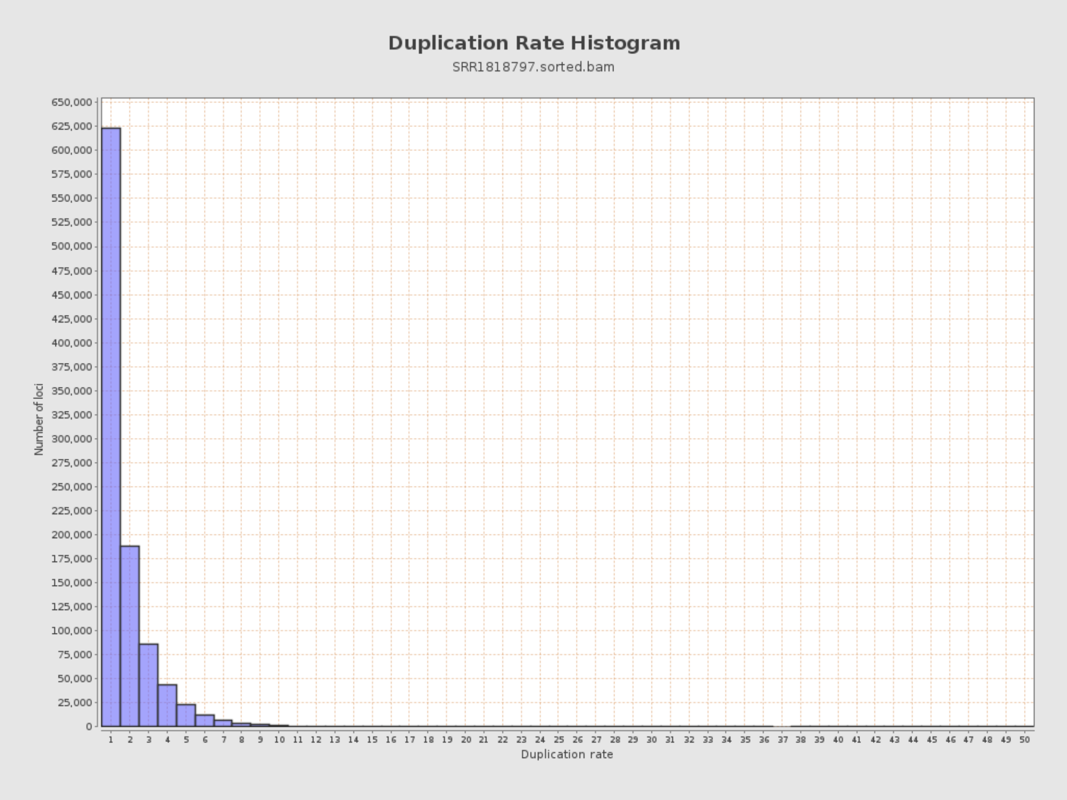
# 5. Results : Coverage Histogram (0-50X)



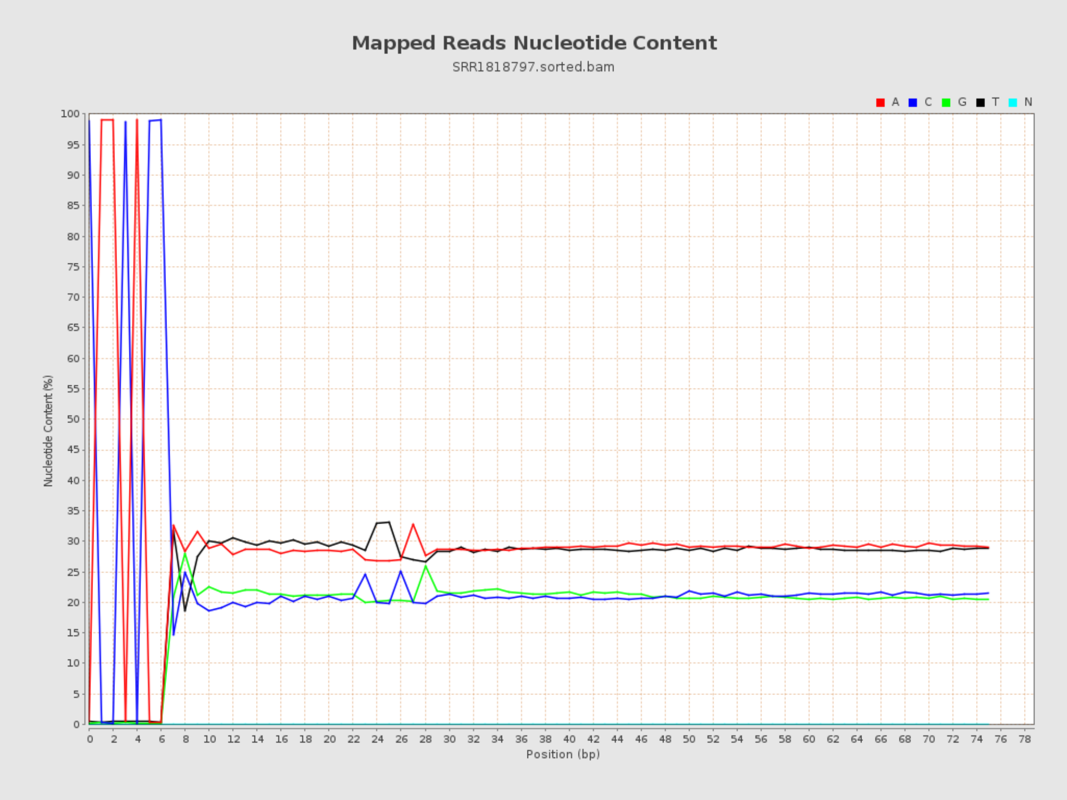
# 6. Results : Genome Fraction Coverage



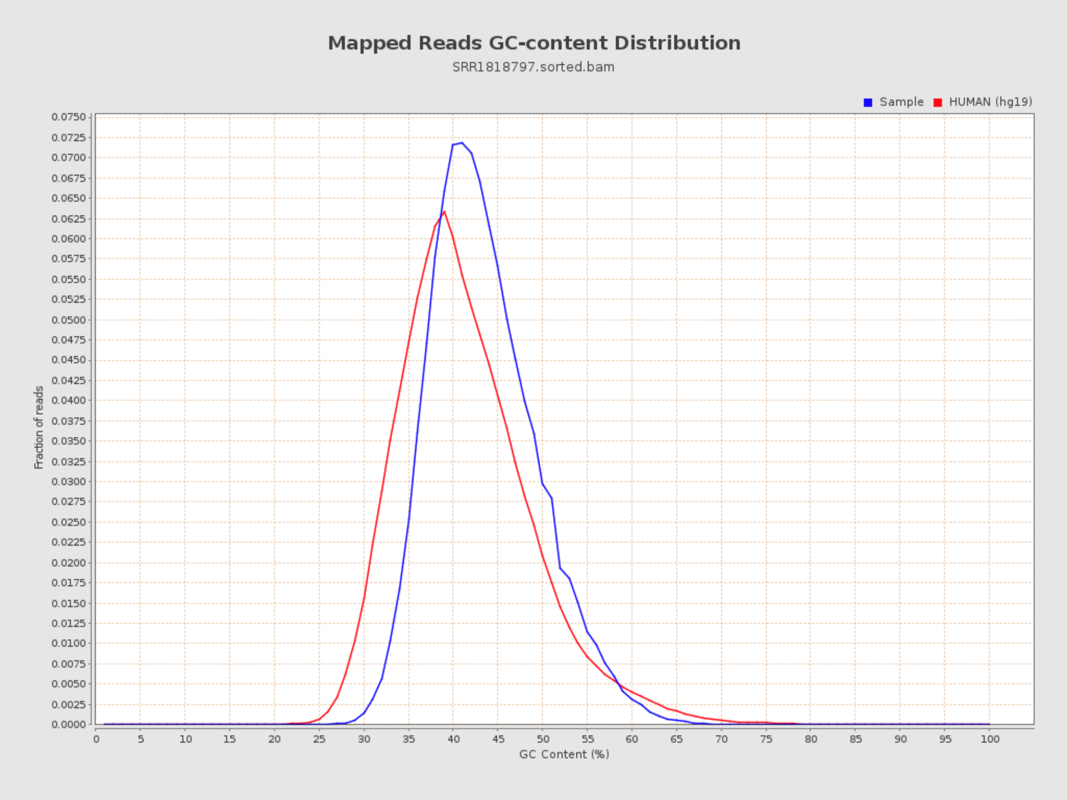
# 7. Results : Duplication Rate Histogram



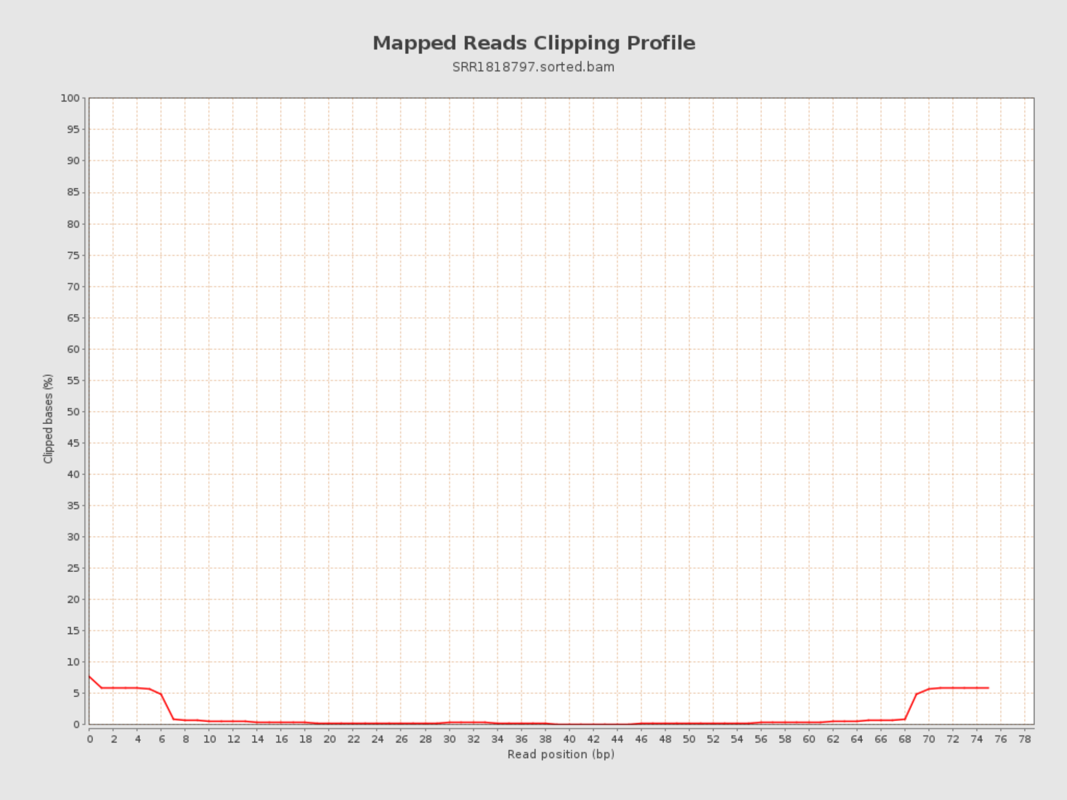
# 8. Results : Mapped Reads Nucleotide Content



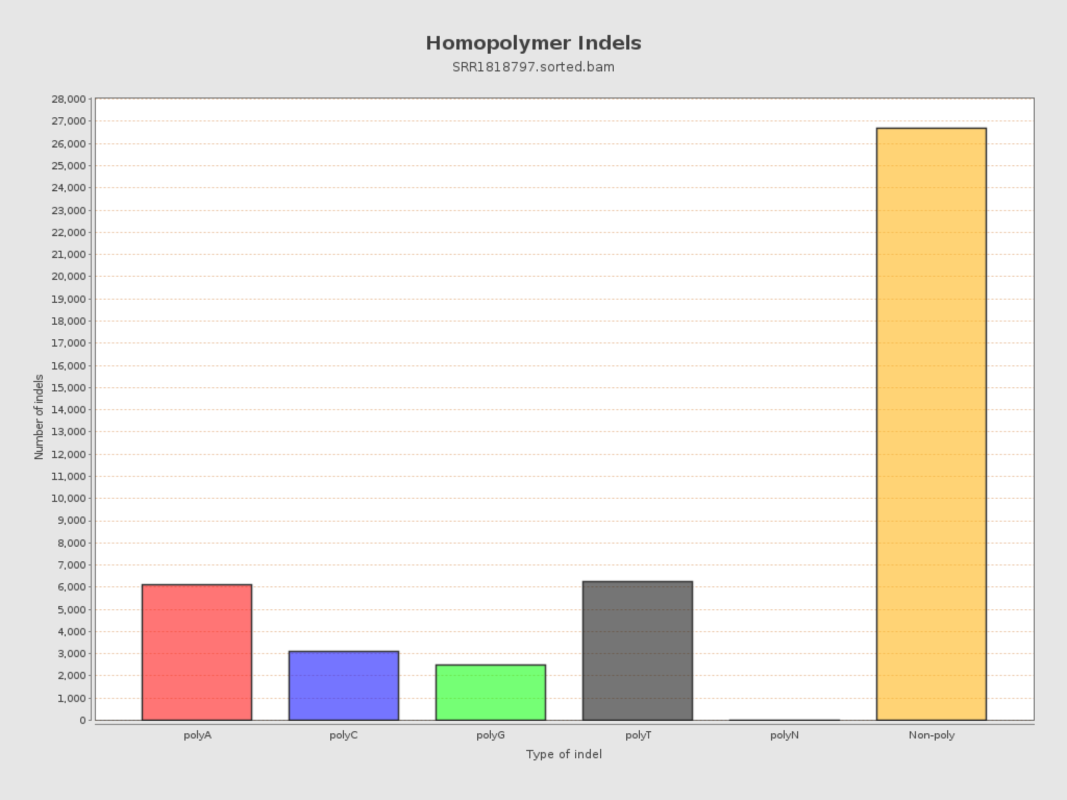
# 9. Results : Mapped Reads GC-content Distribution



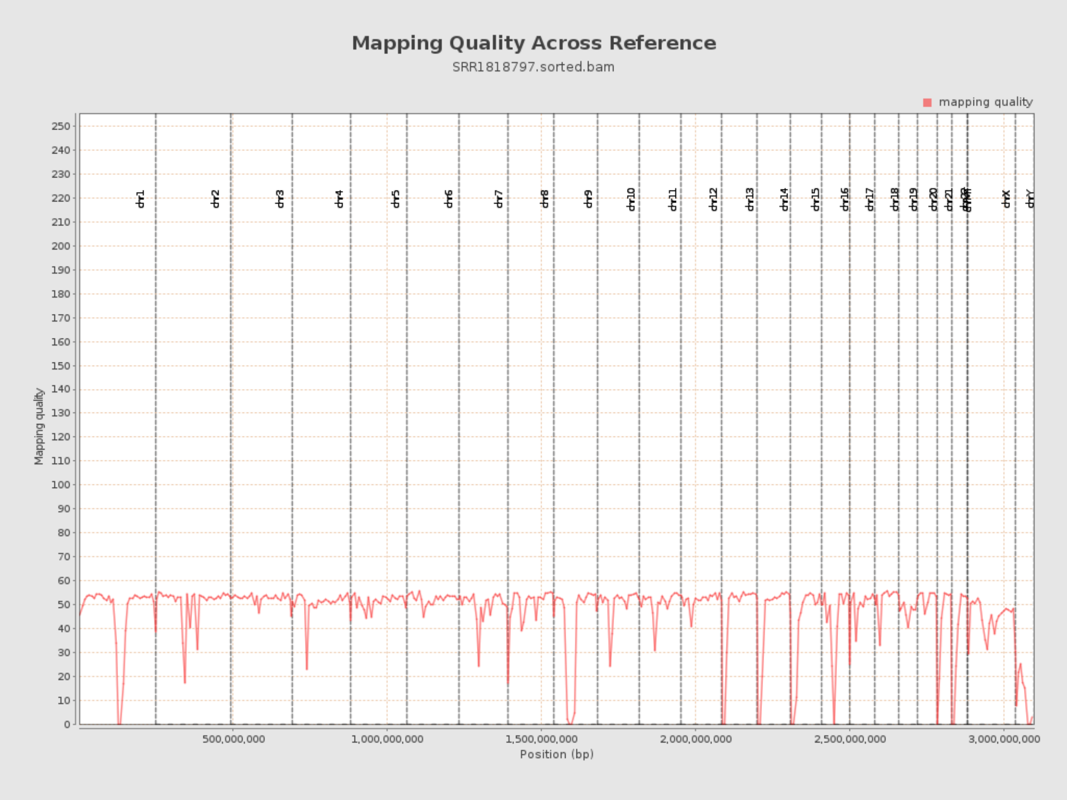
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram