# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/03/18 21:27:49*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR536753.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_SRR536753 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536753.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Mar 18 21:27:47 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR536753.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 22,981,238 |
| Mapped reads | 22,150,289 / 96.38% |
| Unmapped reads | 830,949 / 3.62% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 493 / 0% |
| Read min/max/mean length | 30 / 50 / 50 |
| Duplicated reads (estimated) | 189,349 / 0.82% |
| Duplication rate | 0.85% |
| Clipped reads | 354,835 / 1.54% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 340,493,835 / 30.83% |
| Number/percentage of C's | 210,139,406 / 19.02% |
| Number/percentage of T's | 340,887,669 / 30.86% |
| Number/percentage of G's | 212,581,457 / 19.25% |
| Number/percentage of N's | 445,258 / 0.04% |
| GC Percentage | 38.27% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.3568 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6619 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.4 |

## 2.5. Mismatches and indels

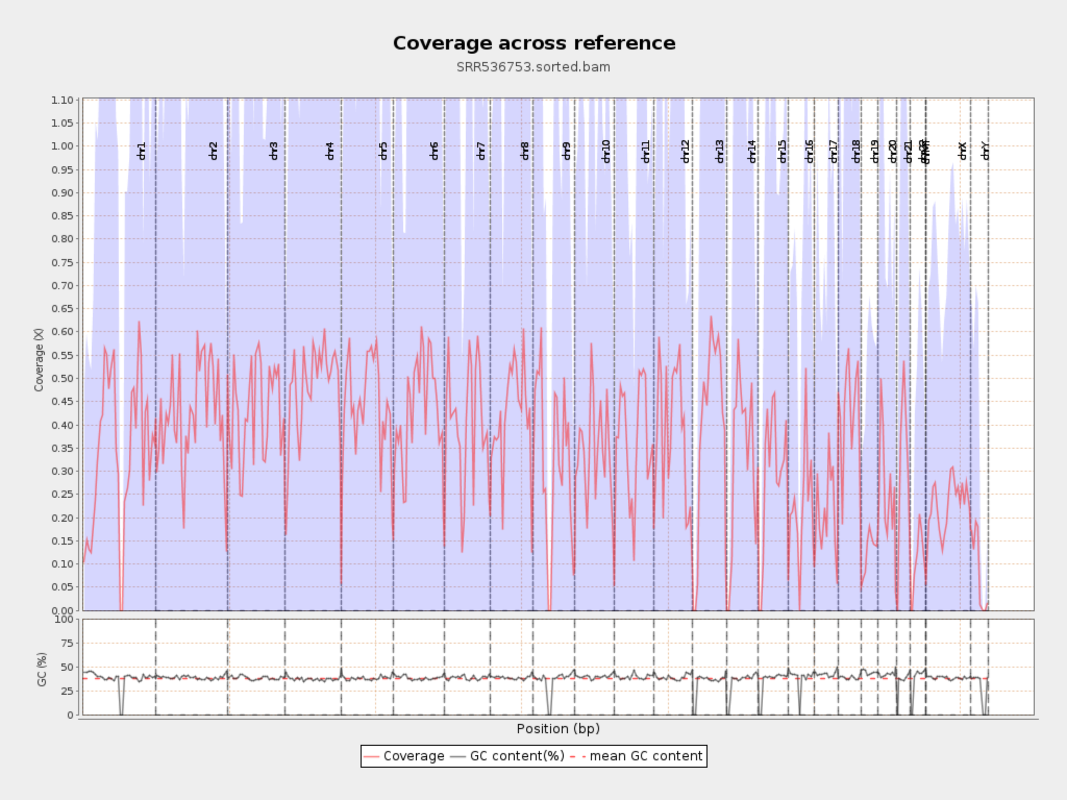
| | |
|---|---|
| General error rate | 0.36% |
| Mismatches | 3,908,064 |
| Insertions | 57,314 |
| Mapped reads with at least one insertion | 0.26% |
| Deletions | 55,862 |
| Mapped reads with at least one deletion | 0.25% |
| Homopolymer indels | 48.02% |

## 2.6. Chromosome stats

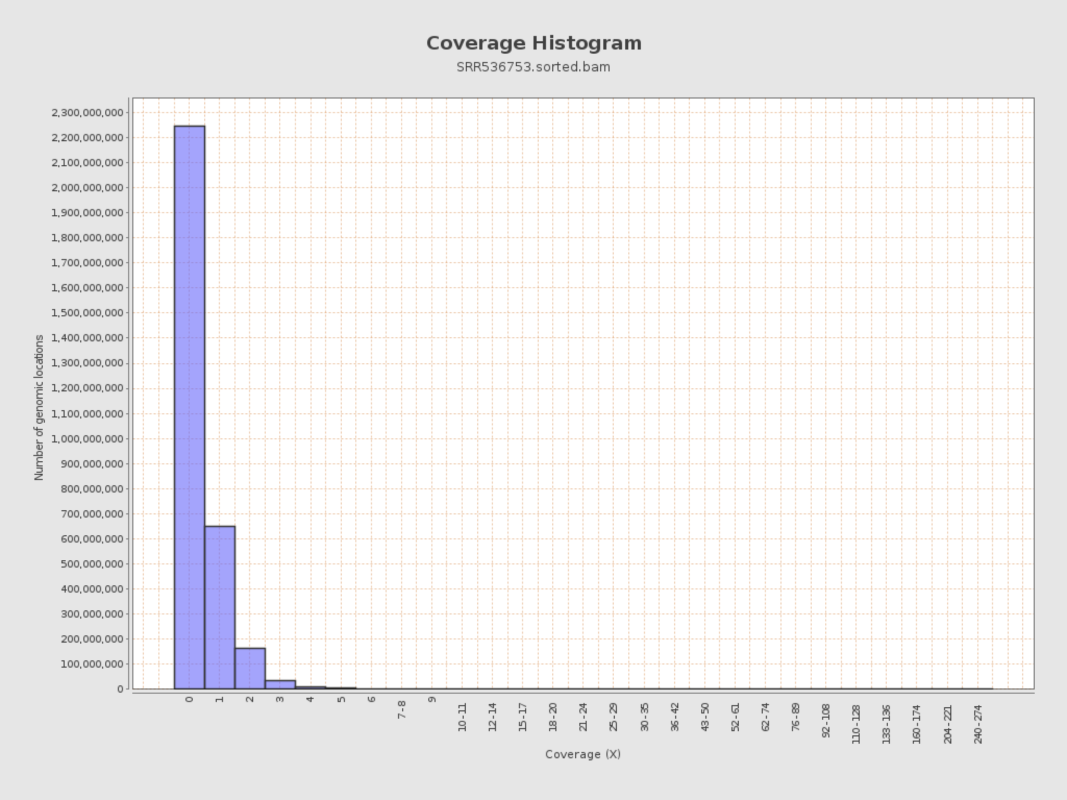
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 84664562 | 0.3397 | 0.6577 |
| chr2 | 243199373 | 102437743 | 0.4212 | 0.7061 |
| chr3 | 198022430 | 85562790 | 0.4321 | 0.7093 |
| chr4 | 191154276 | 92184902 | 0.4823 | 0.7484 |
| chr5 | 180915260 | 79233463 | 0.438 | 0.7158 |
| chr6 | 171115067 | 74975623 | 0.4382 | 0.7192 |
| chr7 | 159138663 | 63239391 | 0.3974 | 0.695 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 61761315 | 0.422 | 0.705 |
| chr9 | 141213431 | 46068237 | 0.3262 | 0.6405 |
| chr10 | 135534747 | 47216602 | 0.3484 | 0.6406 |
| chr11 | 135006516 | 49225404 | 0.3646 | 0.6681 |
| chr12 | 133851895 | 51025899 | 0.3812 | 0.6815 |
| chr13 | 115169878 | 46702518 | 0.4055 | 0.7076 |
| chr14 | 107349540 | 35261969 | 0.3285 | 0.6419 |
| chr15 | 102531392 | 29600985 | 0.2887 | 0.6063 |
| chr16 | 90354753 | 19814417 | 0.2193 | 0.5195 |
| chr17 | 81195210 | 17471454 | 0.2152 | 0.519 |
| chr18 | 78077248 | 33495392 | 0.429 | 0.7114 |
| chr19 | 59128983 | 7634516 | 0.1291 | 0.3901 |
| chr20 | 63025520 | 16866154 | 0.2676 | 0.5745 |
| chr21 | 48129895 | 14228013 | 0.2956 | 0.6299 |
| chr22 | 51304566 | 5586025 | 0.1089 | 0.3647 |
| chrMT | 16571 | 918 | 0.0554 | 0.2288 |
| chrX | 155270560 | 35350255 | 0.2277 | 0.5017 |
| chrY | 59373566 | 5032145 | 0.0848 | 0.3261 |

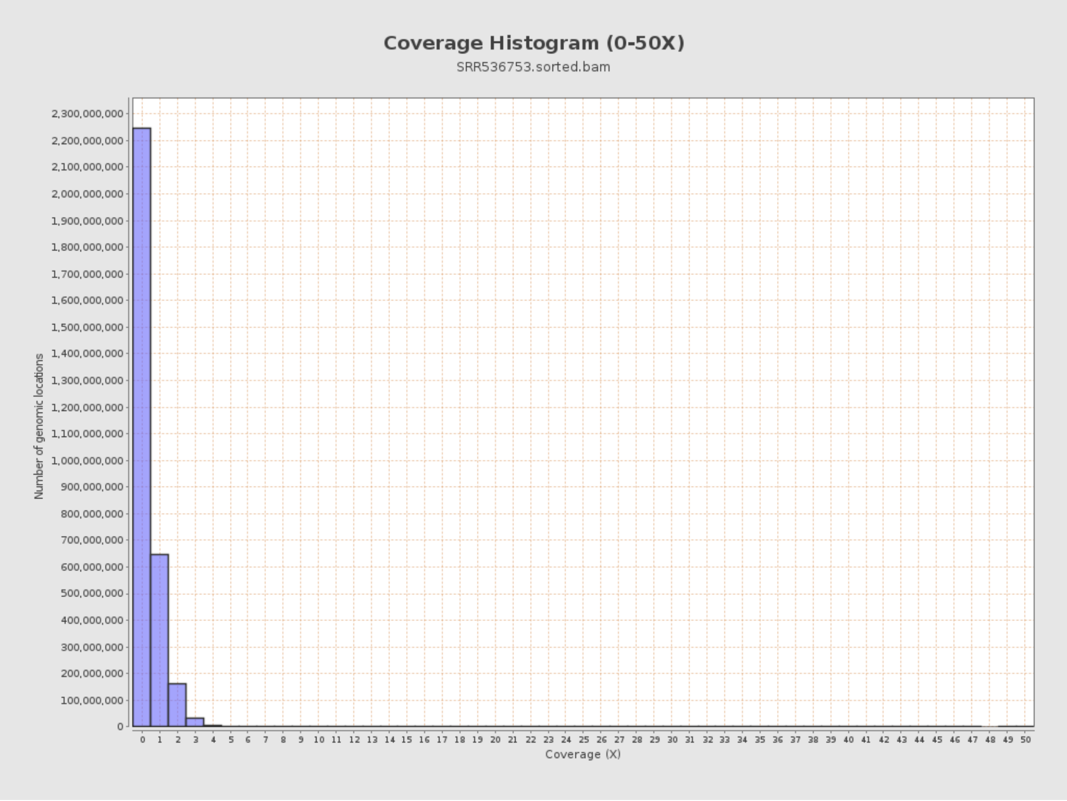
# 3. Results : Coverage across reference



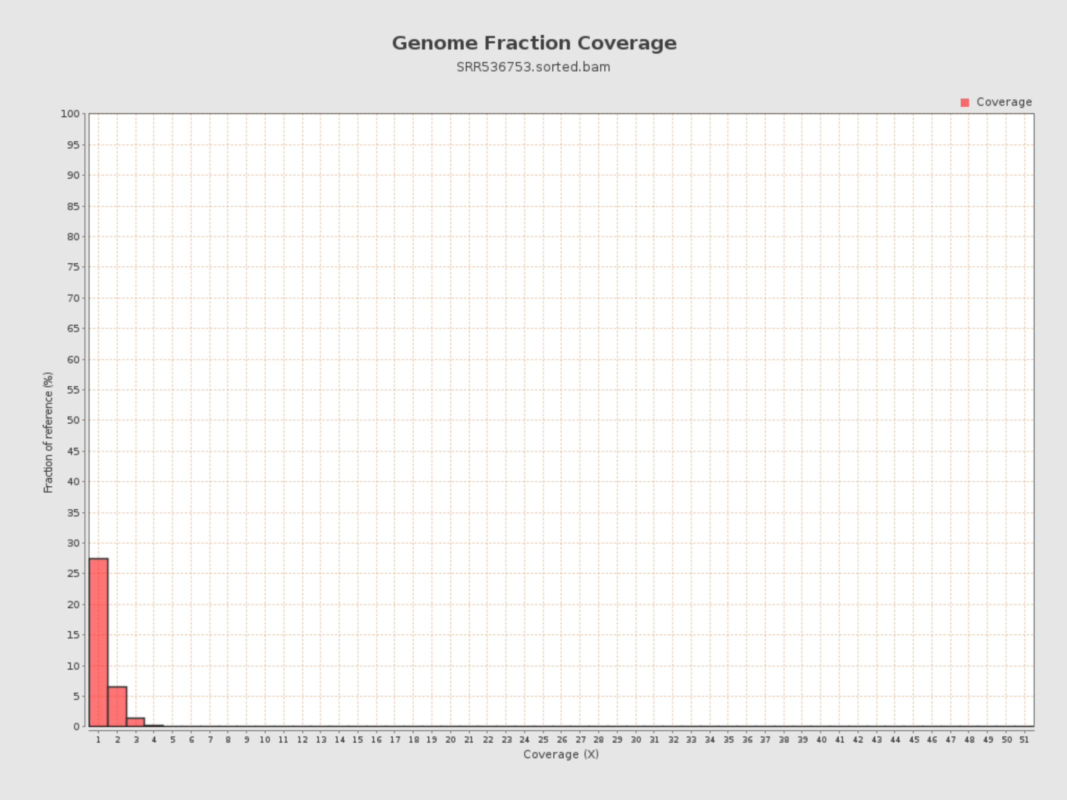
# 4. Results : Coverage Histogram



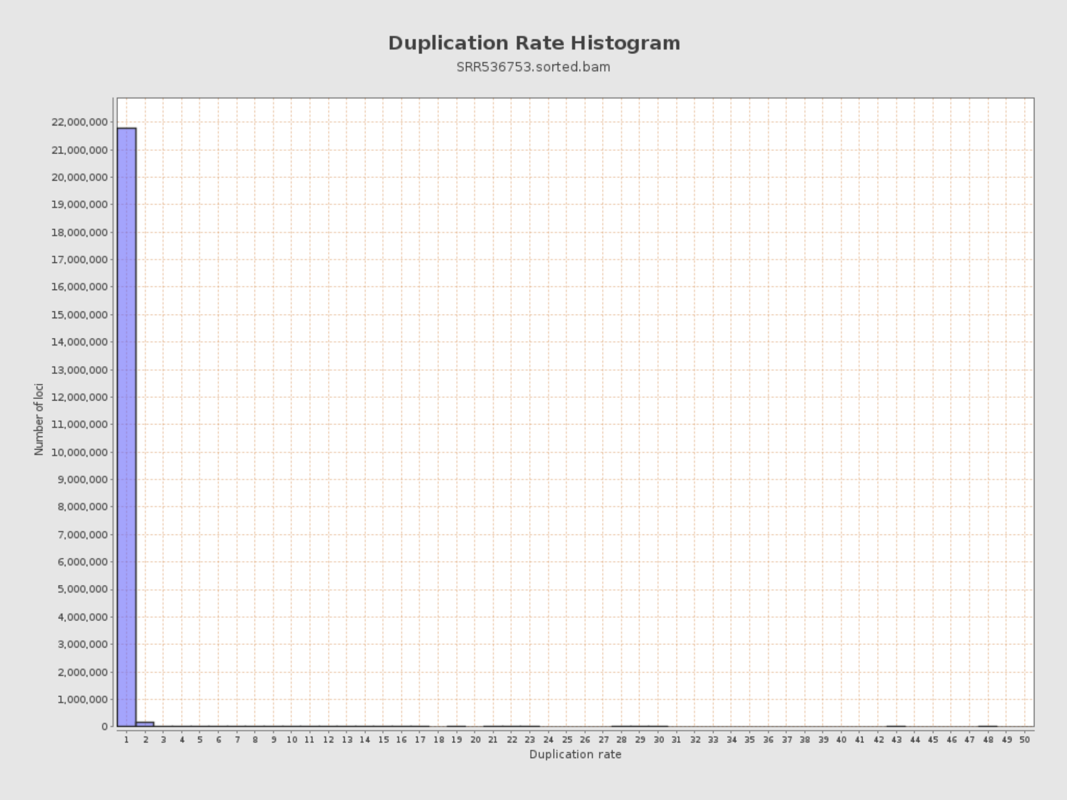
# 5. Results : Coverage Histogram (0-50X)



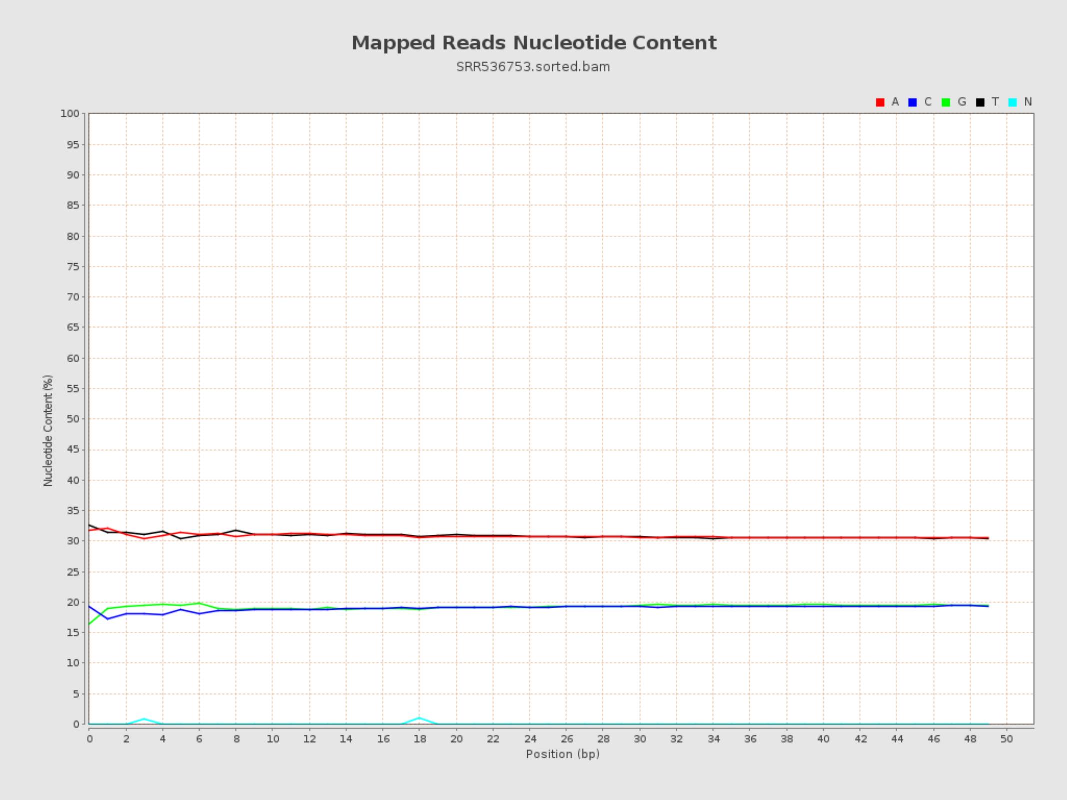
# 6. Results : Genome Fraction Coverage



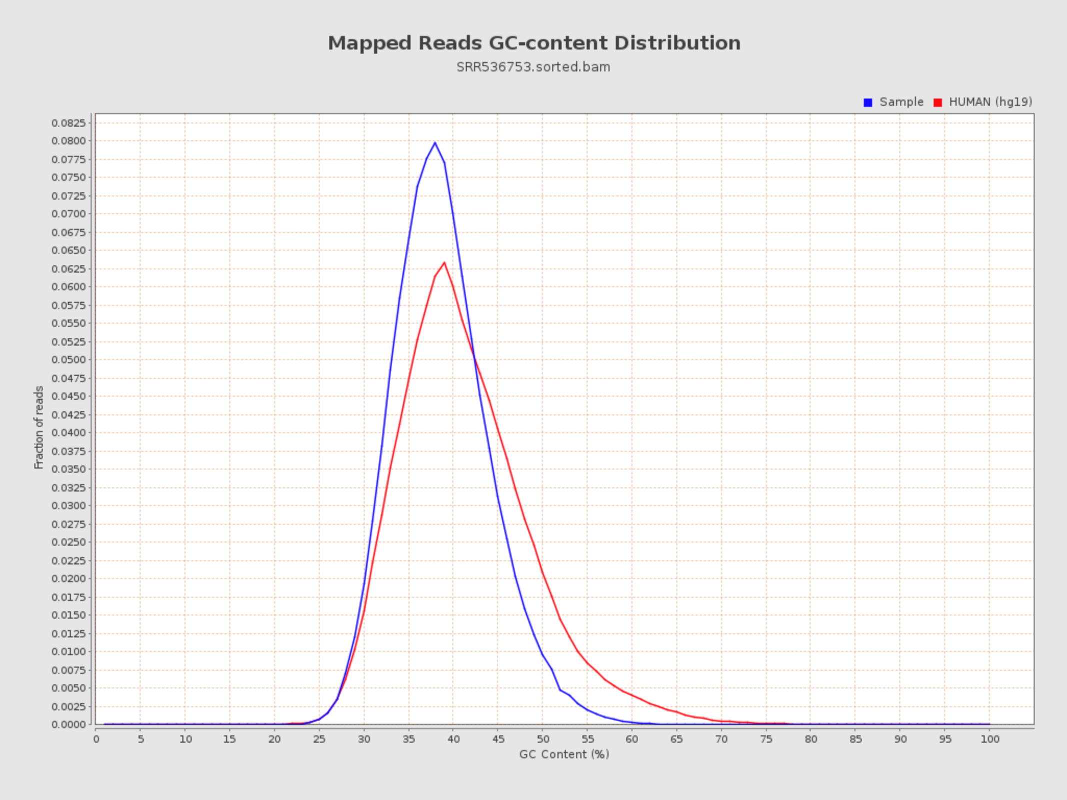
# 7. Results : Duplication Rate Histogram



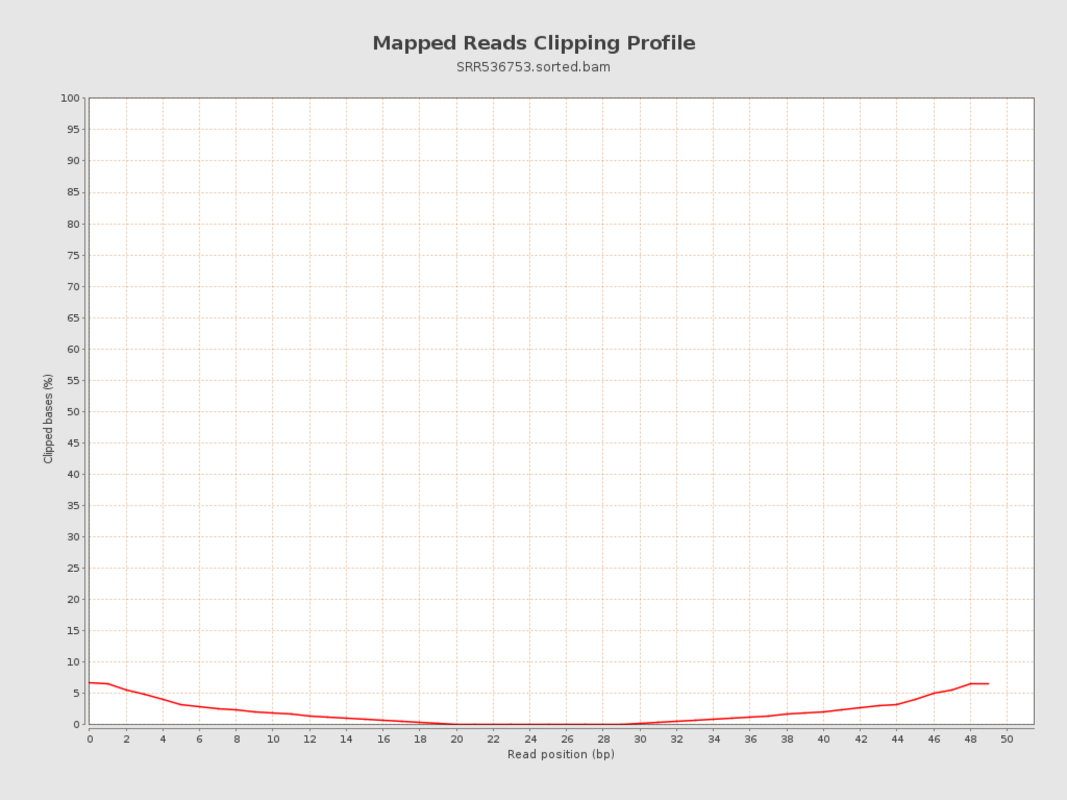
# 8. Results : Mapped Reads Nucleotide Content



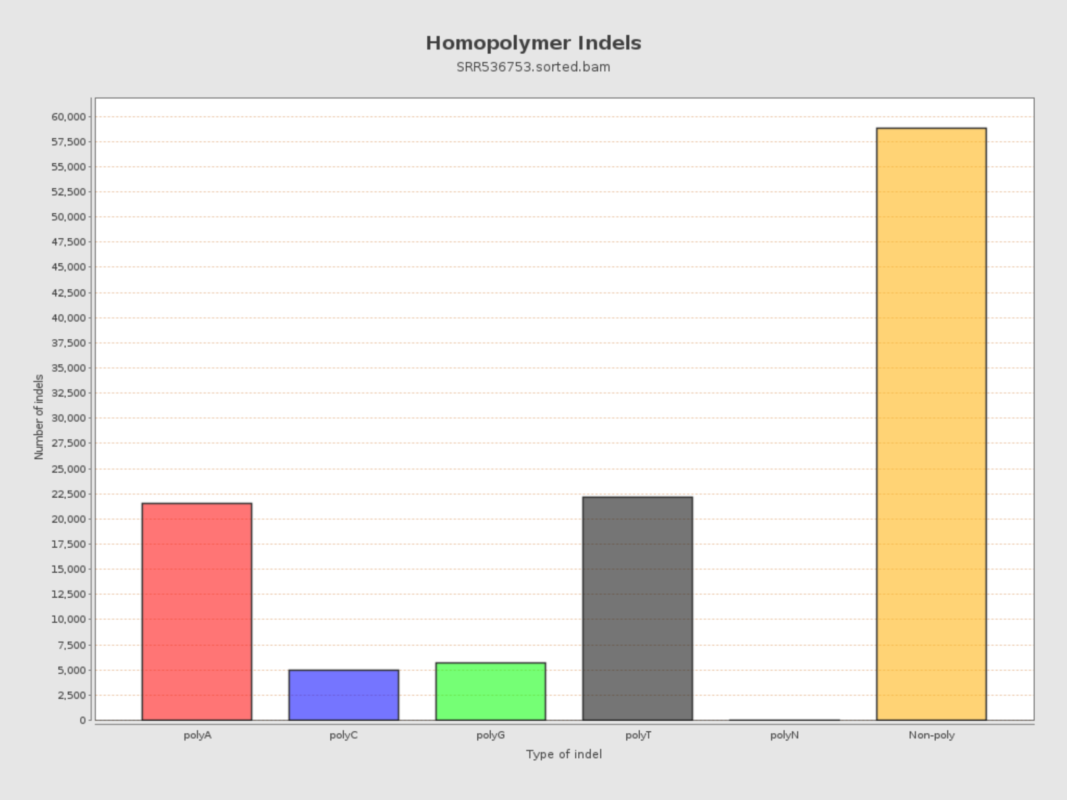
# 9. Results : Mapped Reads GC-content Distribution



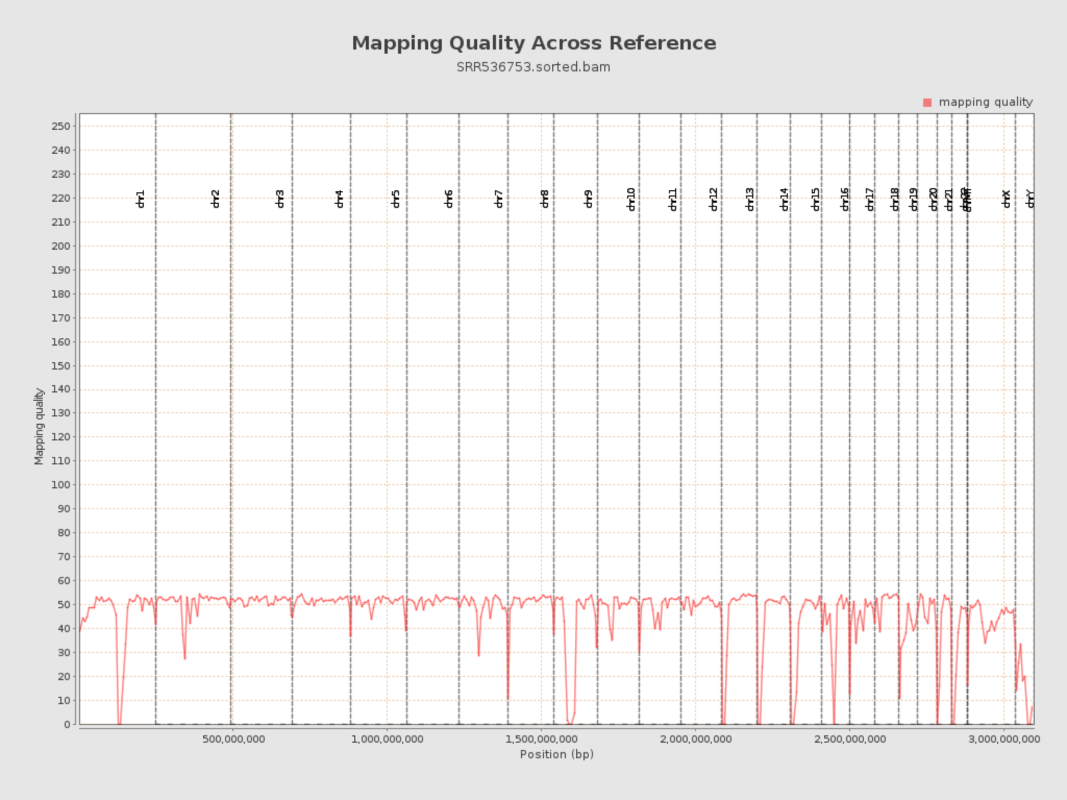
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram