# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/03/18 18:02:11*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR536743.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_SRR536743 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536743.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Mar 18 18:02:10 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR536743.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 19,268,535 |
| Mapped reads | 15,658,881 / 81.27% |
| Unmapped reads | 3,609,654 / 18.73% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 349 / 0% |
| Read min/max/mean length | 30 / 50 / 50 |
| Duplicated reads (estimated) | 150,744 / 0.78% |
| Duplication rate | 0.68% |
| Clipped reads | 285,691 / 1.48% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 245,507,038 / 31.46% |
| Number/percentage of C's | 144,038,316 / 18.46% |
| Number/percentage of T's | 244,779,617 / 31.36% |
| Number/percentage of G's | 146,114,553 / 18.72% |
| Number/percentage of N's | 16,865 / 0% |
| GC Percentage | 37.18% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.2521 |
| | |

| | |
|---|---|
| Standard Deviation | 3.3143 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.44 |

## 2.5. Mismatches and indels

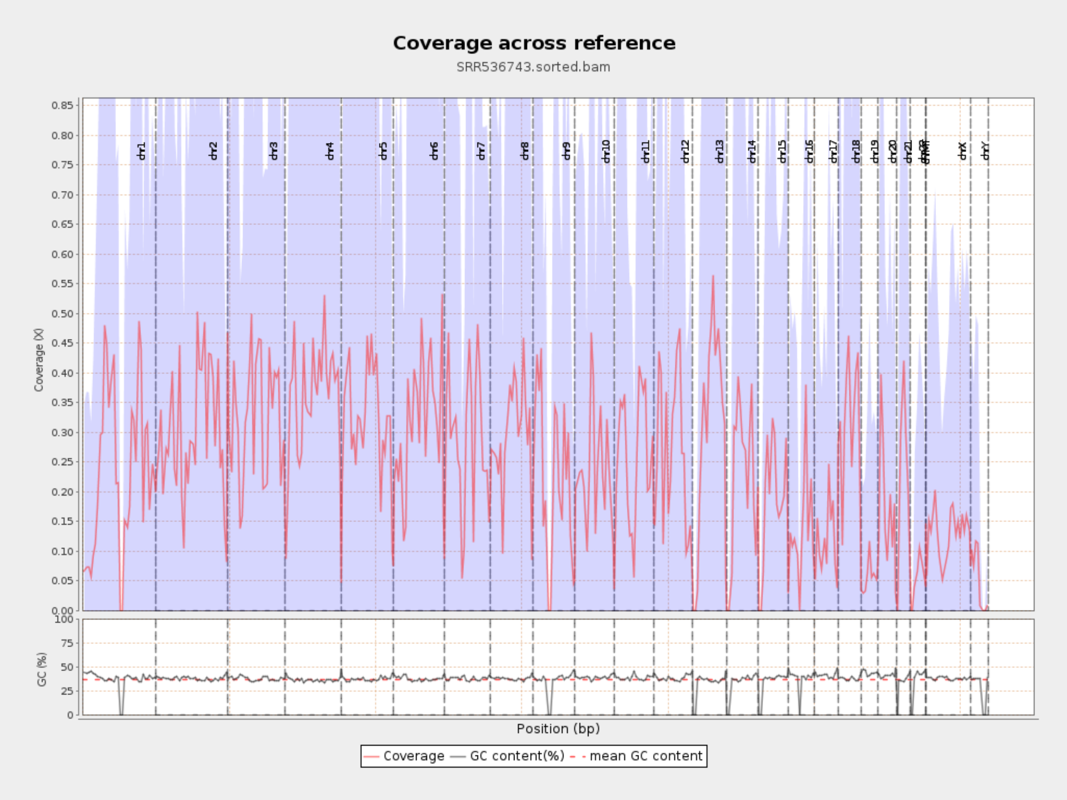
| | |
|---|---|
| General error rate | 0.35% |
| Mismatches | 2,683,780 |
| Insertions | 56,745 |
| Mapped reads with at least one insertion | 0.36% |
| Deletions | 40,075 |
| Mapped reads with at least one deletion | 0.26% |
| Homopolymer indels | 49.32% |

## 2.6. Chromosome stats

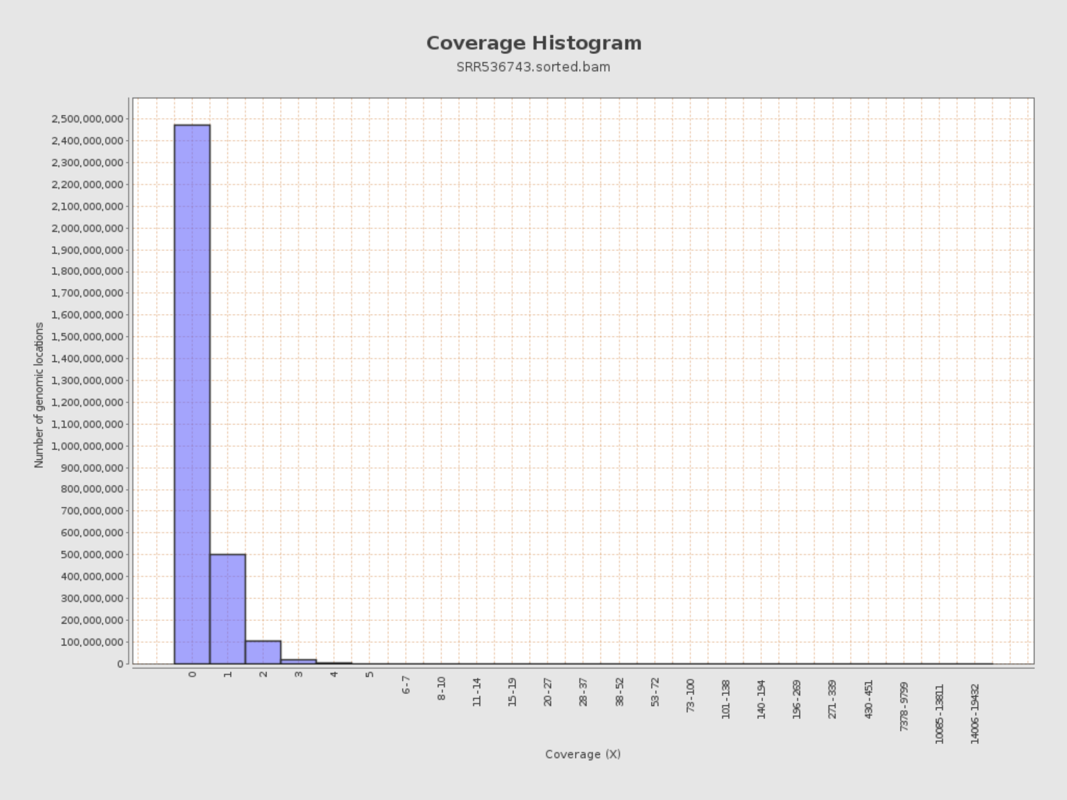
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 58037708 | 0.2328 | 0.5475 |
| chr2 | 243199373 | 73287906 | 0.3013 | 0.6044 |
| chr3 | 198022430 | 64649720 | 0.3265 | 0.6333 |
| chr4 | 191154276 | 69258993 | 0.3623 | 0.6678 |
| chr5 | 180915260 | 57796023 | 0.3195 | 0.6797 |
| chr6 | 171115067 | 55296731 | 0.3232 | 13.9046 |
| chr7 | 159138663 | 45170952 | 0.2838 | 0.5939 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 43759126 | 0.299 | 0.5957 |
| chr9 | 141213431 | 32199658 | 0.228 | 0.5363 |
| chr10 | 135534747 | 32397620 | 0.239 | 0.5342 |
| chr11 | 135006516 | 35137928 | 0.2603 | 0.5638 |
| chr12 | 133851895 | 35374224 | 0.2643 | 0.5686 |
| chr13 | 115169878 | 35998902 | 0.3126 | 0.626 |
| chr14 | 107349540 | 24121986 | 0.2247 | 0.5313 |
| chr15 | 102531392 | 19027444 | 0.1856 | 0.4789 |
| chr16 | 90354753 | 12400965 | 0.1372 | 0.4084 |
| chr17 | 81195210 | 9702320 | 0.1195 | 0.381 |
| chr18 | 78077248 | 25293841 | 0.324 | 0.624 |
| chr19 | 59128983 | 3443815 | 0.0582 | 0.2573 |
| chr20 | 63025520 | 11533399 | 0.183 | 0.4753 |
| chr21 | 48129895 | 10541830 | 0.219 | 0.5399 |
| chr22 | 51304566 | 2885941 | 0.0563 | 0.2545 |
| chrMT | 16571 | 2430 | 0.1466 | 0.3762 |
| chrX | 155270560 | 20171982 | 0.1299 | 0.3761 |
| chrY | 59373566 | 3031432 | 0.0511 | 0.2449 |

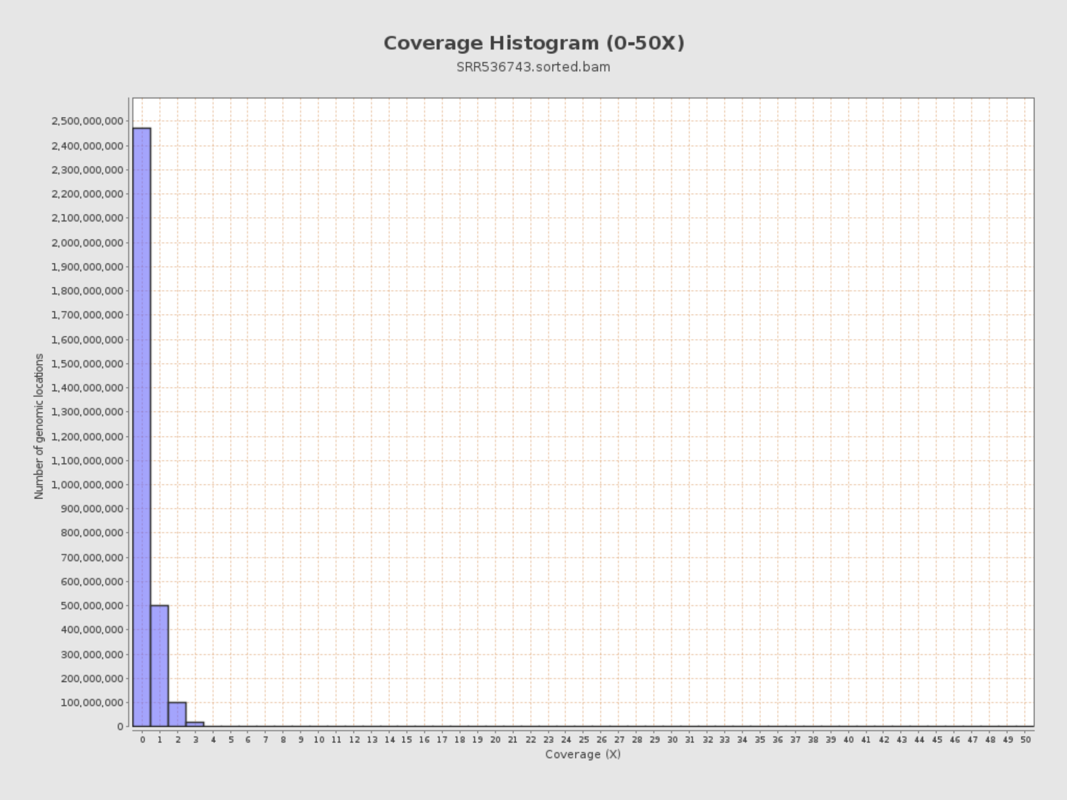
# 3. Results : Coverage across reference



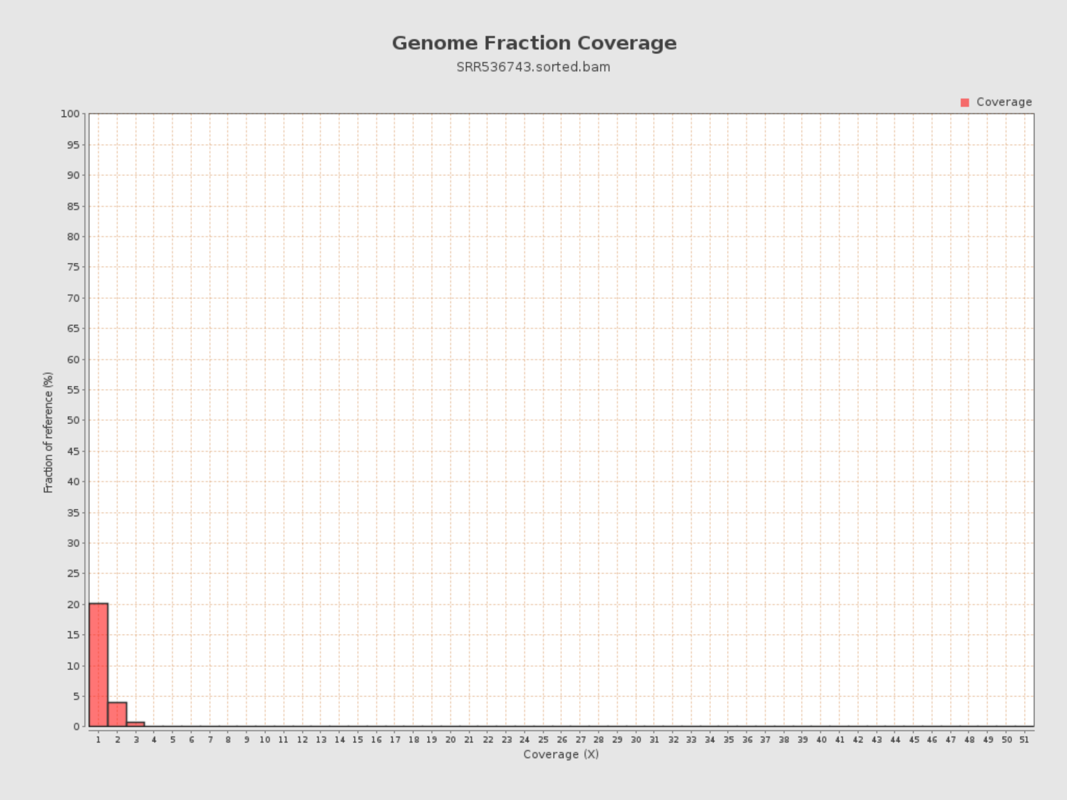
# 4. Results : Coverage Histogram



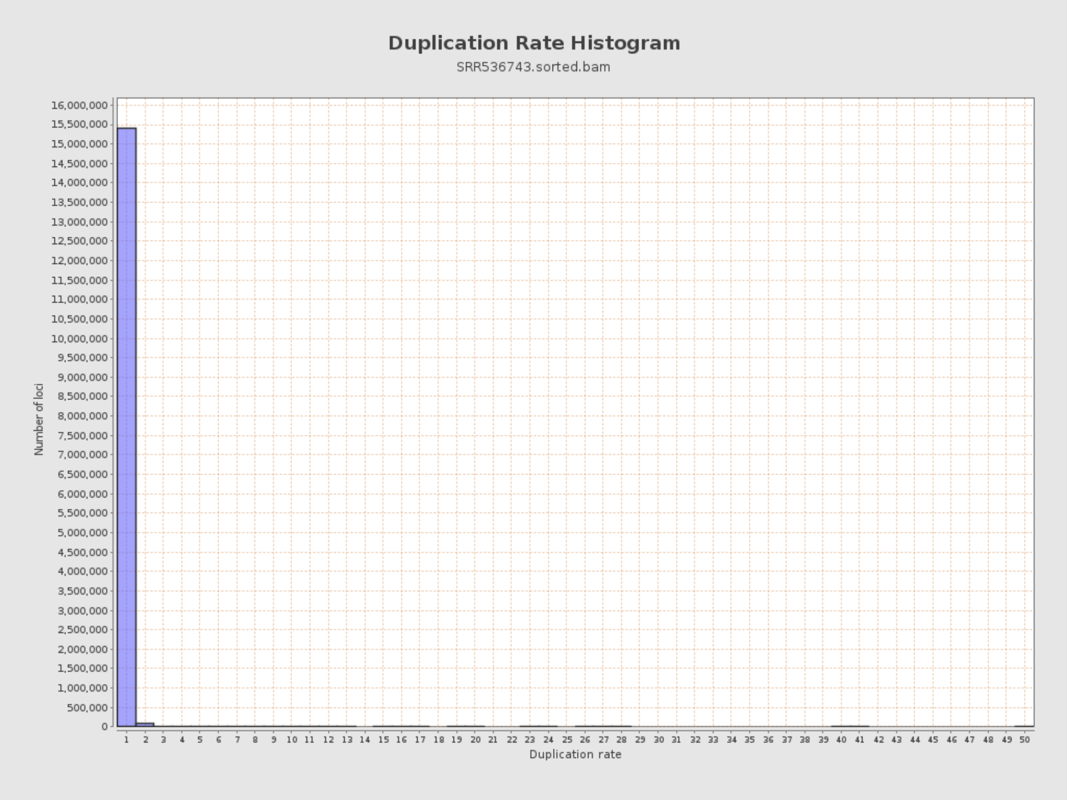
# 5. Results : Coverage Histogram (0-50X)



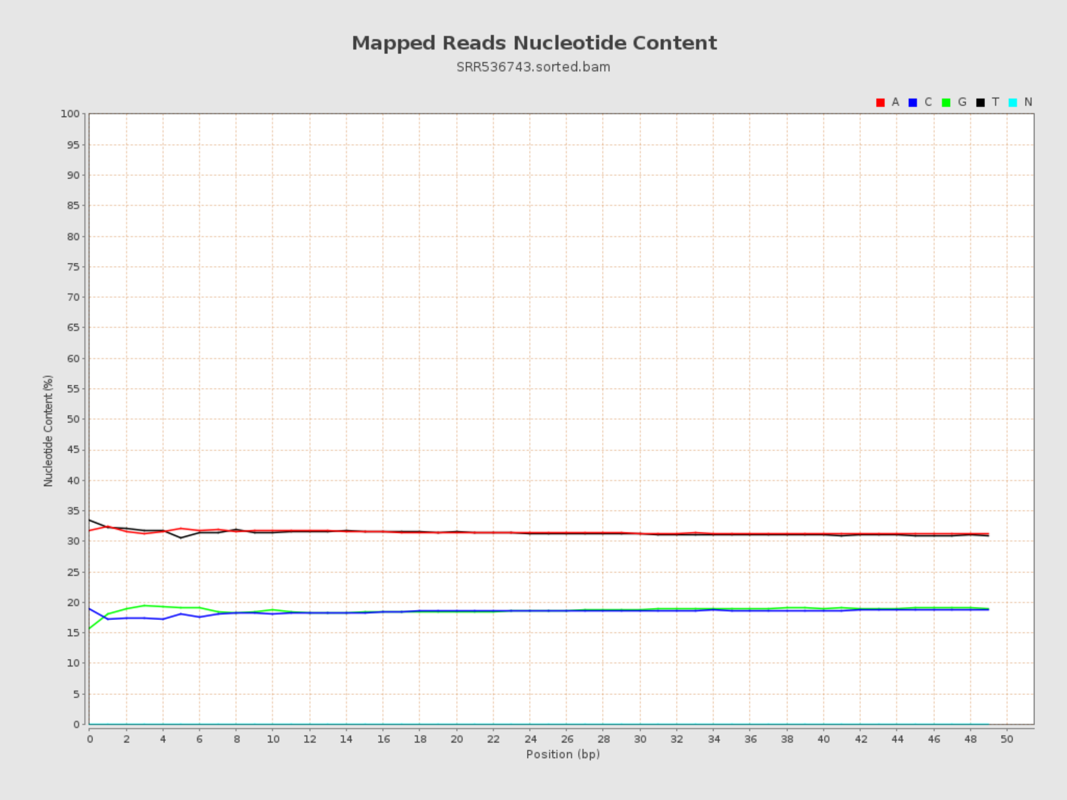
# 6. Results : Genome Fraction Coverage



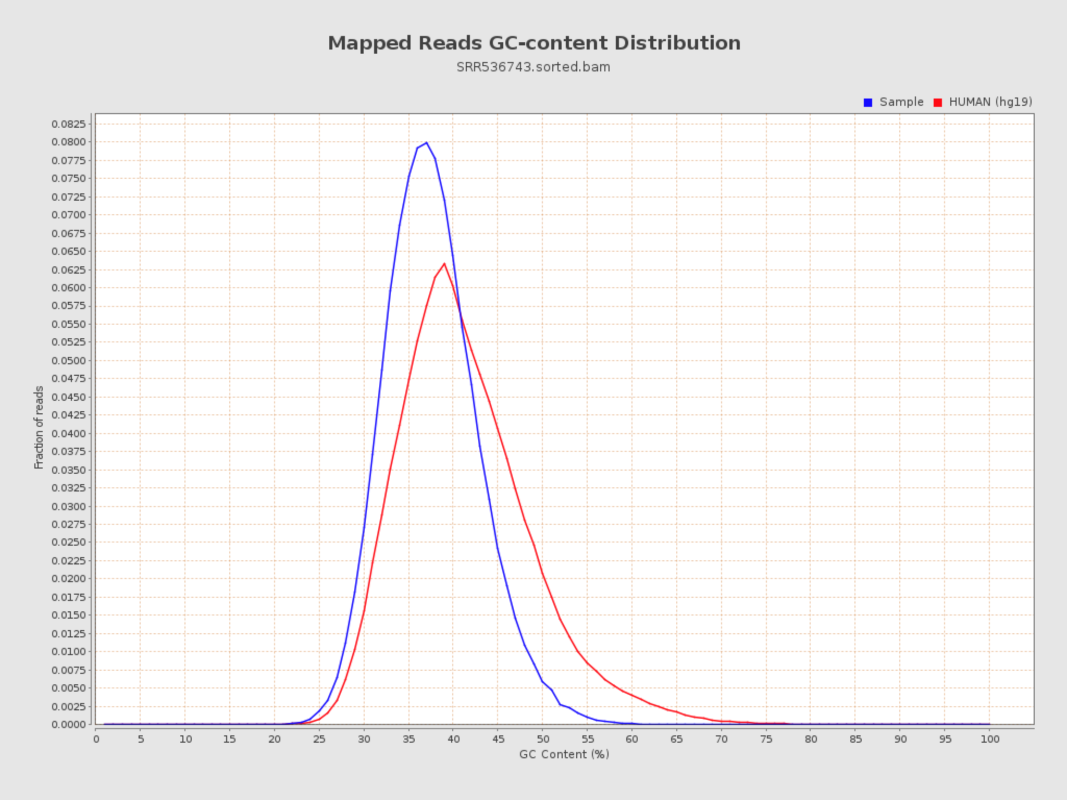
# 7. Results : Duplication Rate Histogram



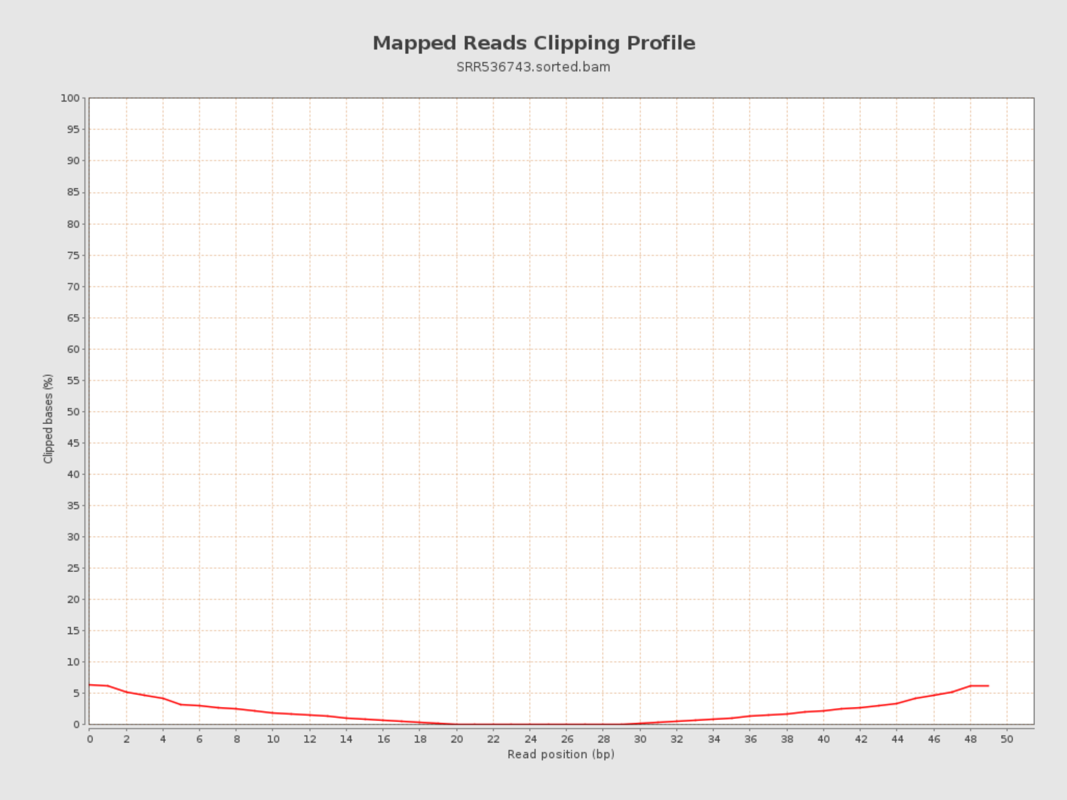
# 8. Results : Mapped Reads Nucleotide Content



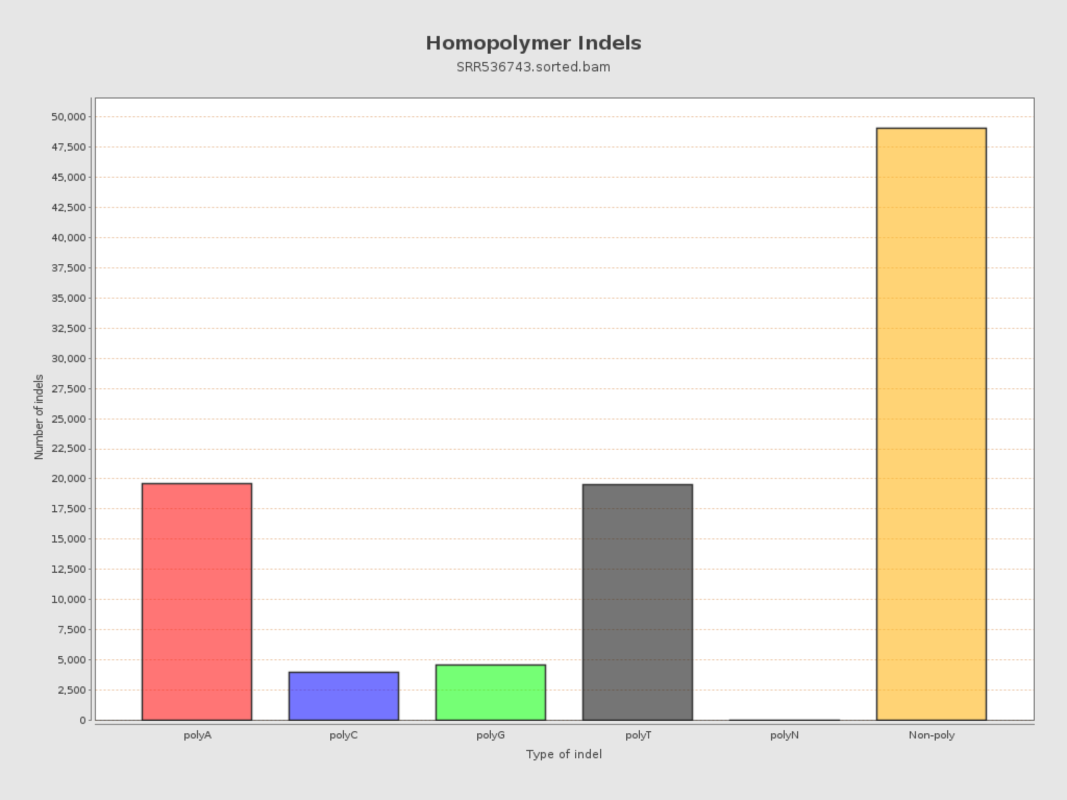
# 9. Results : Mapped Reads GC-content Distribution



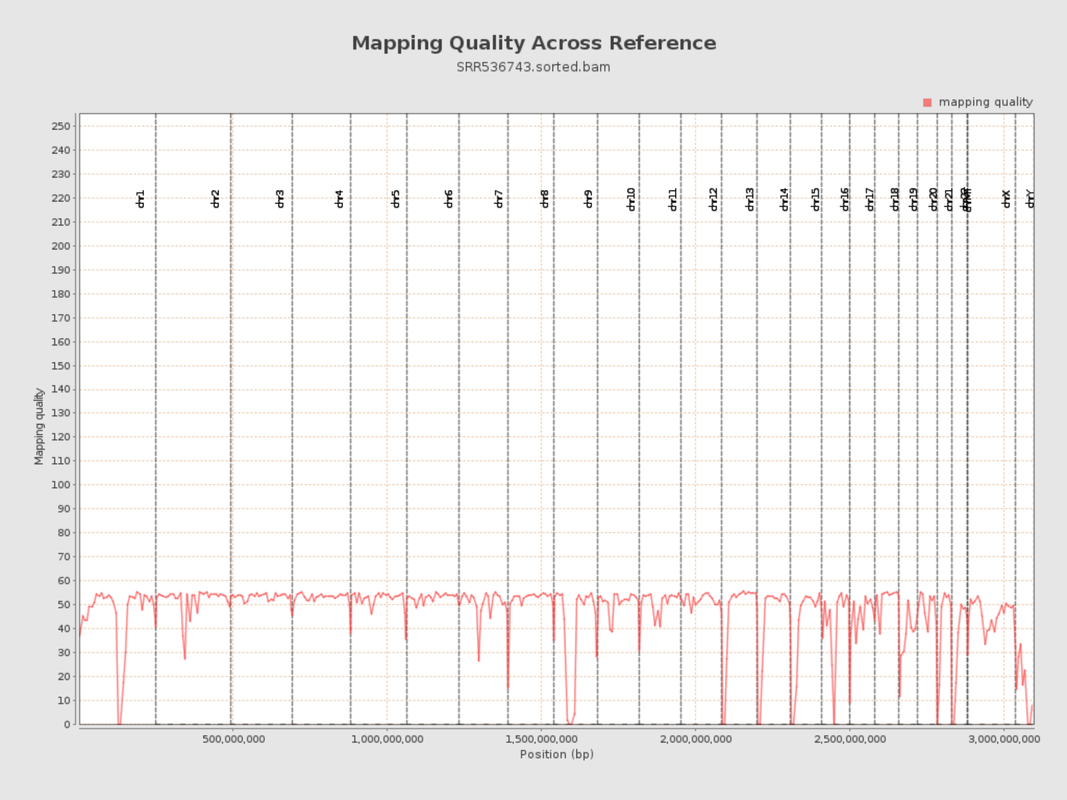
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram