# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/03/18 21:49:26*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR536754.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_SRR536754 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536754.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Mar 18 21:49:25 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR536754.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 21,888,688 |
| Mapped reads | 21,117,546 / 96.48% |
| Unmapped reads | 771,142 / 3.52% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 500 / 0% |
| Read min/max/mean length | 30 / 50 / 50 |
| Duplicated reads (estimated) | 173,214 / 0.79% |
| Duplication rate | 0.81% |
| Clipped reads | 339,929 / 1.55% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 324,037,479 / 30.77% |
| Number/percentage of C's | 200,652,487 / 19.05% |
| Number/percentage of T's | 324,232,506 / 30.79% |
| Number/percentage of G's | 203,690,678 / 19.34% |
| Number/percentage of N's | 423,190 / 0.04% |
| GC Percentage | 38.4% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.3402 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6446 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.39 |

## 2.5. Mismatches and indels

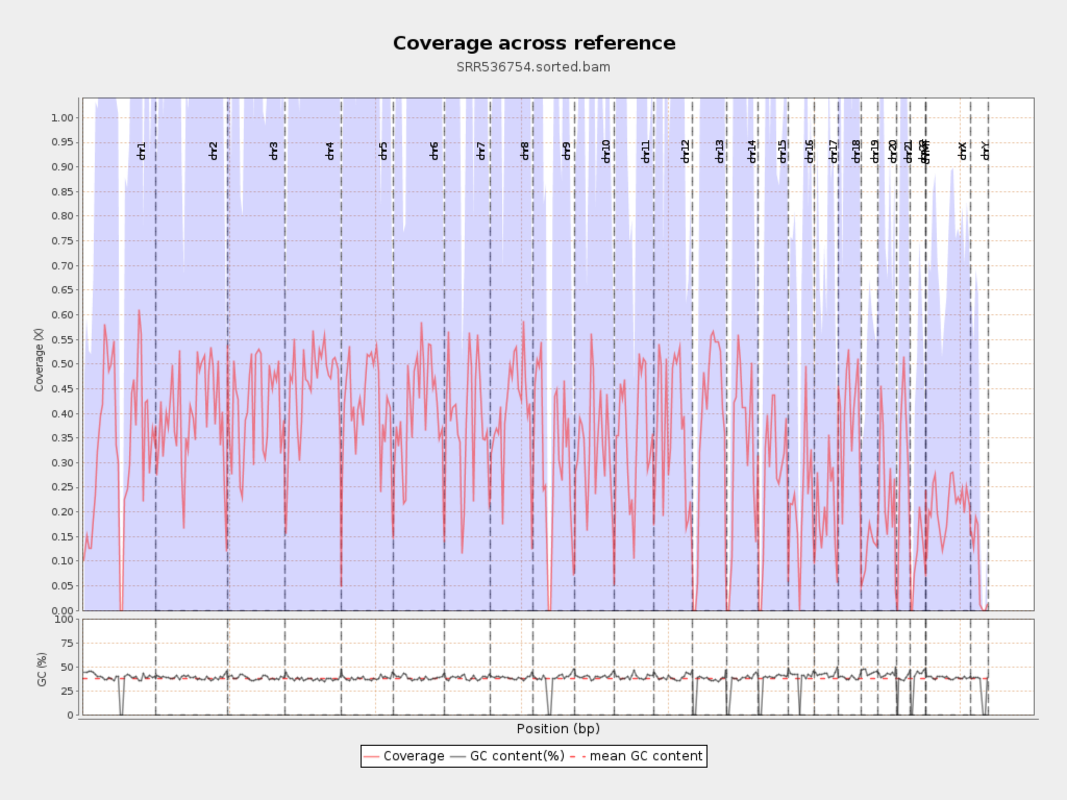
| | |
|---|---|
| General error rate | 0.36% |
| Mismatches | 3,686,796 |
| Insertions | 55,842 |
| Mapped reads with at least one insertion | 0.26% |
| Deletions | 53,335 |
| Mapped reads with at least one deletion | 0.25% |
| Homopolymer indels | 48.19% |

## 2.6. Chromosome stats

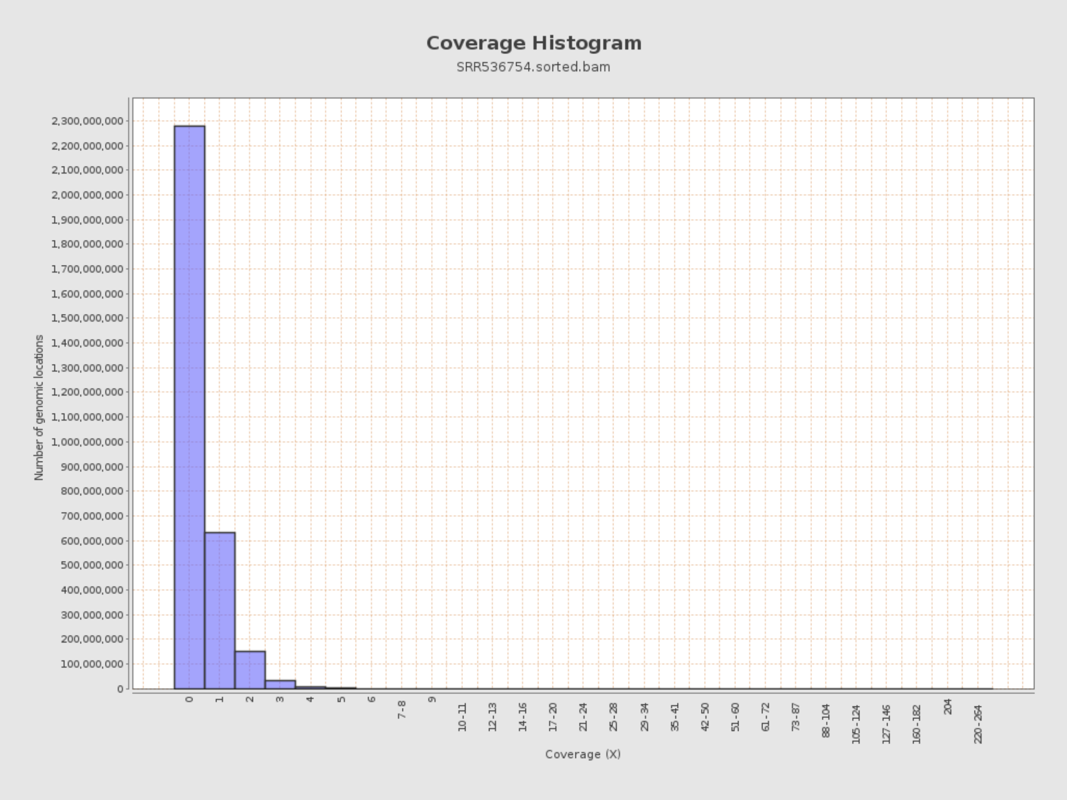
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 82958728 | 0.3328 | 0.6534 |
| chr2 | 243199373 | 95501265 | 0.3927 | 0.6788 |
| chr3 | 198022430 | 81408355 | 0.4111 | 0.6909 |
| chr4 | 191154276 | 87384898 | 0.4571 | 0.7273 |
| chr5 | 180915260 | 74261679 | 0.4105 | 0.6903 |
| chr6 | 171115067 | 70715982 | 0.4133 | 0.6959 |
| chr7 | 159138663 | 59854395 | 0.3761 | 0.6735 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 59647829 | 0.4075 | 0.6912 |
| chr9 | 141213431 | 43909037 | 0.3109 | 0.6222 |
| chr10 | 135534747 | 46010732 | 0.3395 | 0.6319 |
| chr11 | 135006516 | 47853422 | 0.3545 | 0.6591 |
| chr12 | 133851895 | 49031811 | 0.3663 | 0.6678 |
| chr13 | 115169878 | 43993266 | 0.382 | 0.6841 |
| chr14 | 107349540 | 34470461 | 0.3211 | 0.6365 |
| chr15 | 102531392 | 27970811 | 0.2728 | 0.5851 |
| chr16 | 90354753 | 19655103 | 0.2175 | 0.5176 |
| chr17 | 81195210 | 16521179 | 0.2035 | 0.501 |
| chr18 | 78077248 | 31469057 | 0.4031 | 0.6889 |
| chr19 | 59128983 | 7378214 | 0.1248 | 0.3828 |
| chr20 | 63025520 | 16181118 | 0.2567 | 0.5616 |
| chr21 | 48129895 | 13851856 | 0.2878 | 0.6209 |
| chr22 | 51304566 | 5548384 | 0.1081 | 0.3645 |
| chrMT | 16571 | 4049 | 0.2443 | 0.4962 |
| chrX | 155270560 | 32735034 | 0.2108 | 0.4818 |
| chrY | 59373566 | 4808239 | 0.081 | 0.3178 |

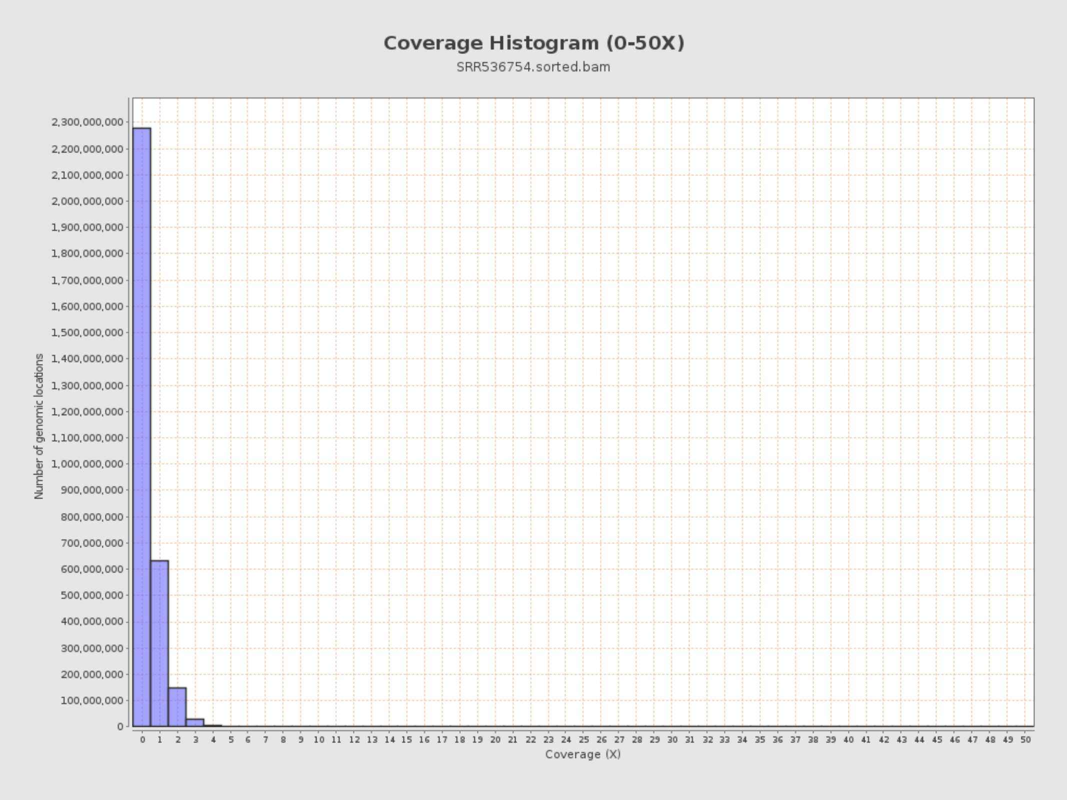
# 3. Results : Coverage across reference



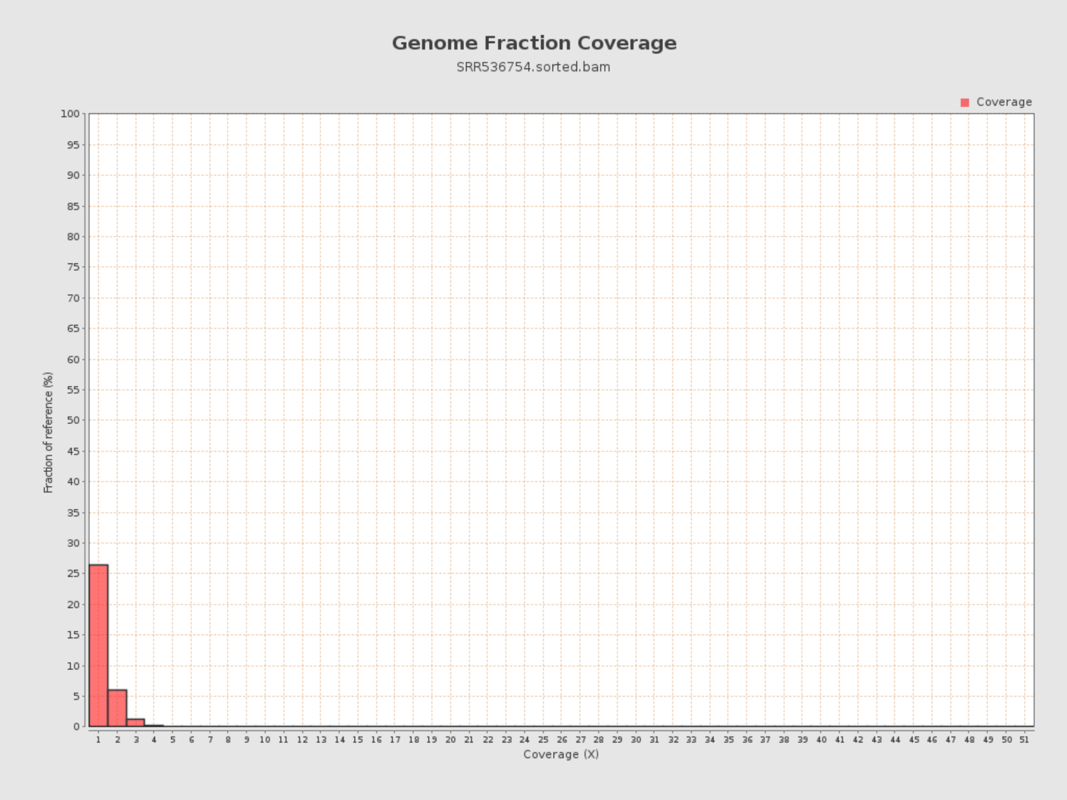
# 4. Results : Coverage Histogram



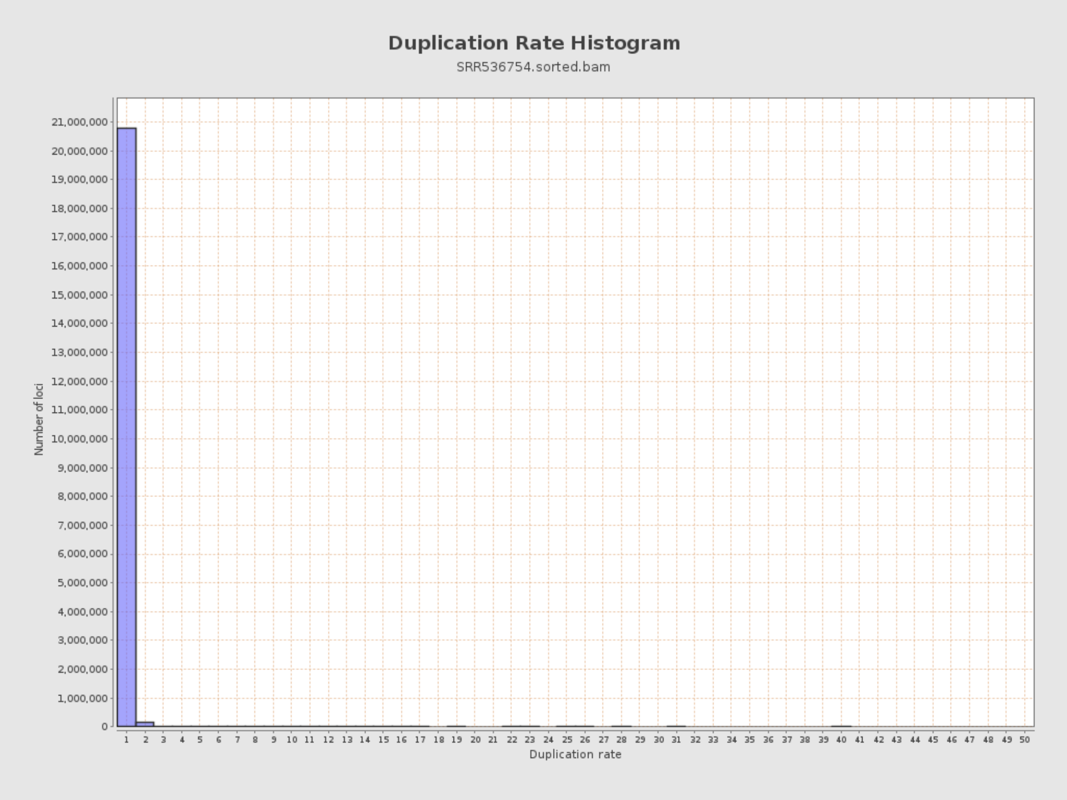
# 5. Results : Coverage Histogram (0-50X)



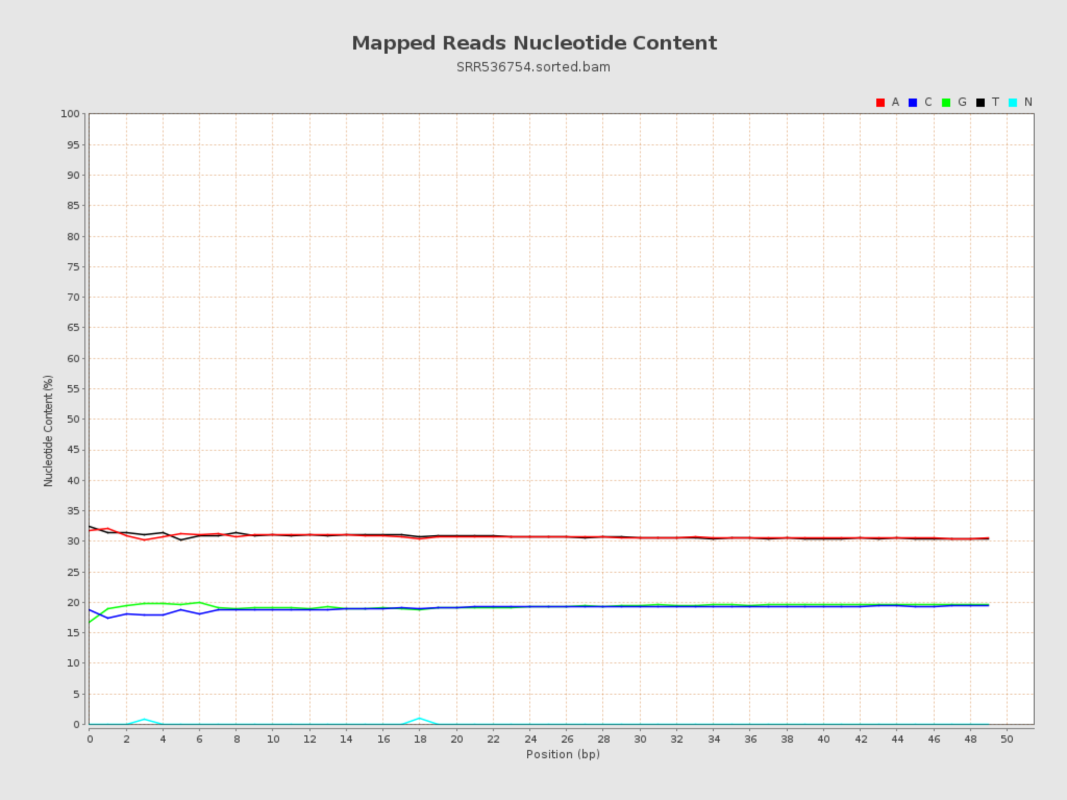
# 6. Results : Genome Fraction Coverage



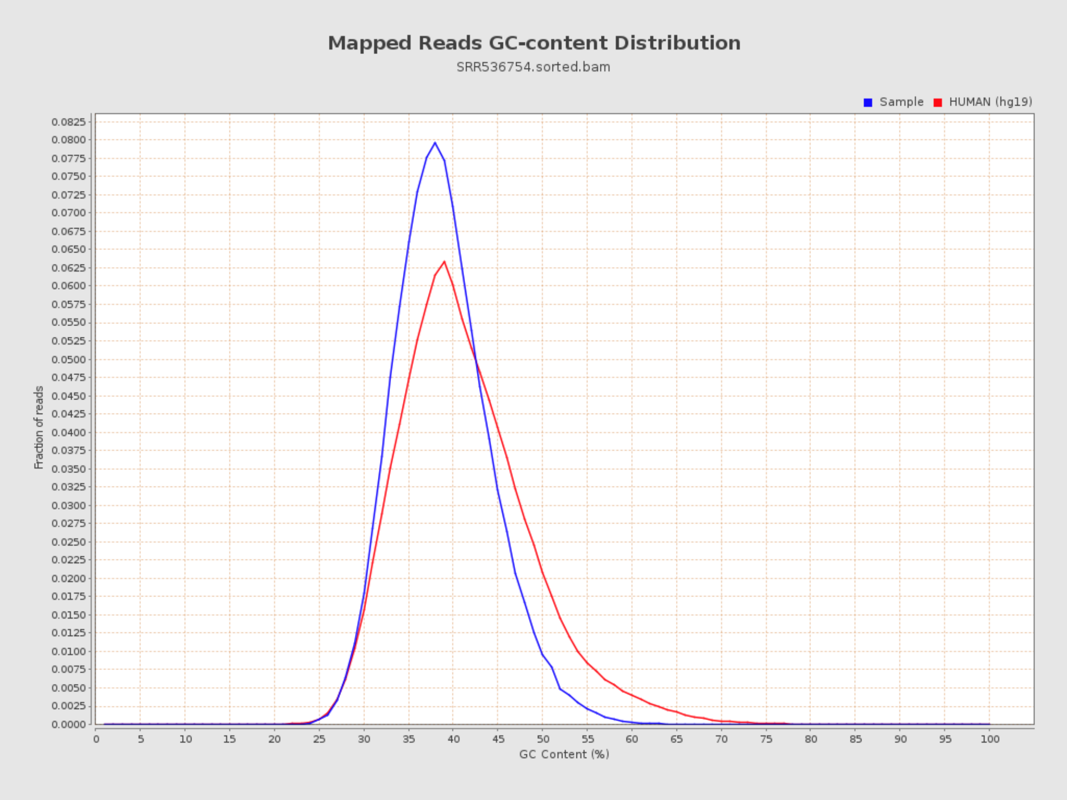
# 7. Results : Duplication Rate Histogram



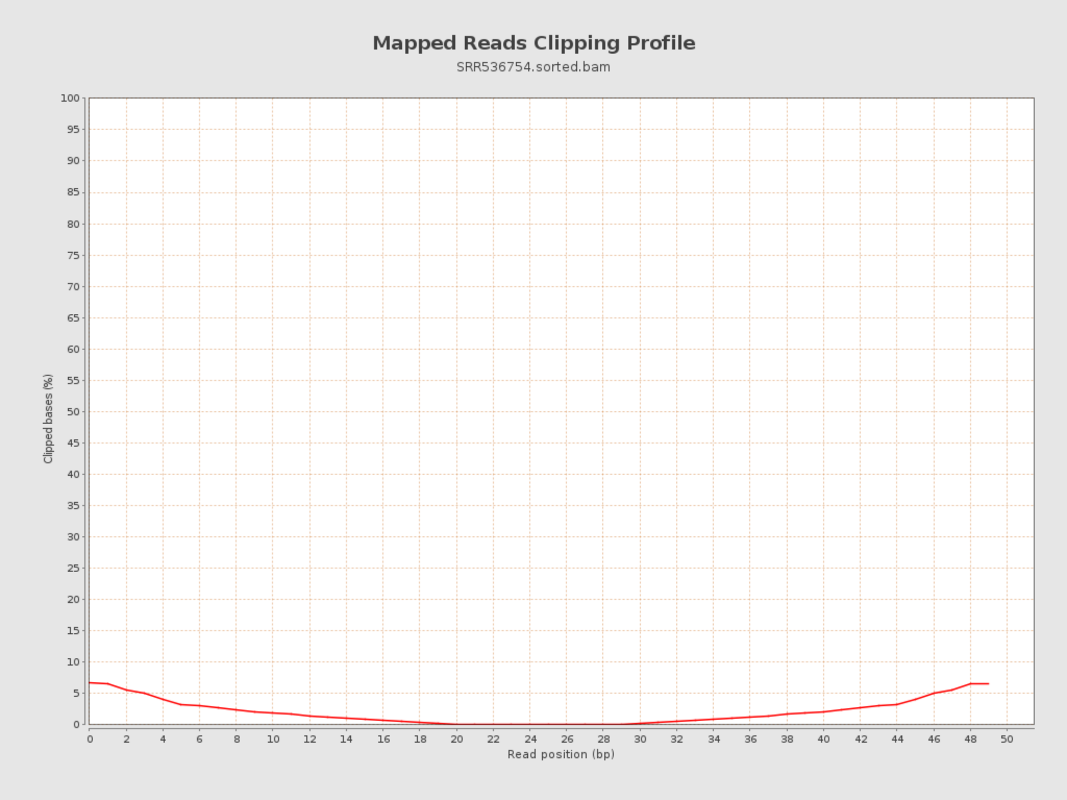
# 8. Results : Mapped Reads Nucleotide Content



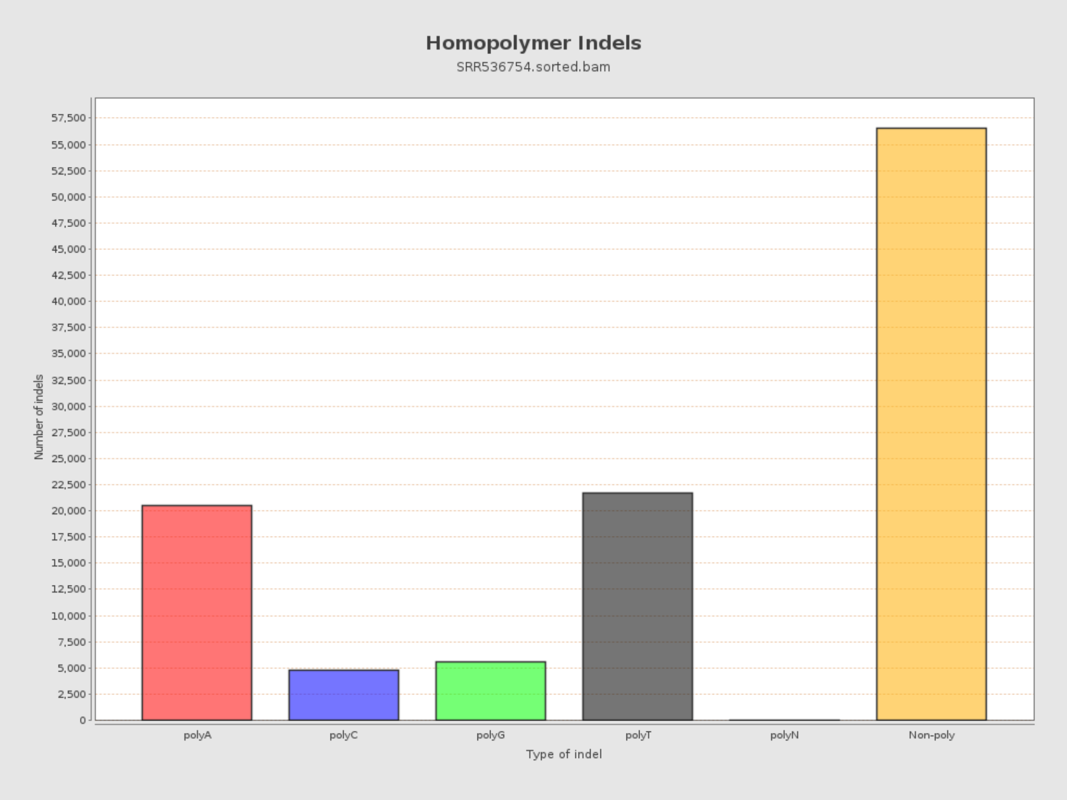
# 9. Results : Mapped Reads GC-content Distribution



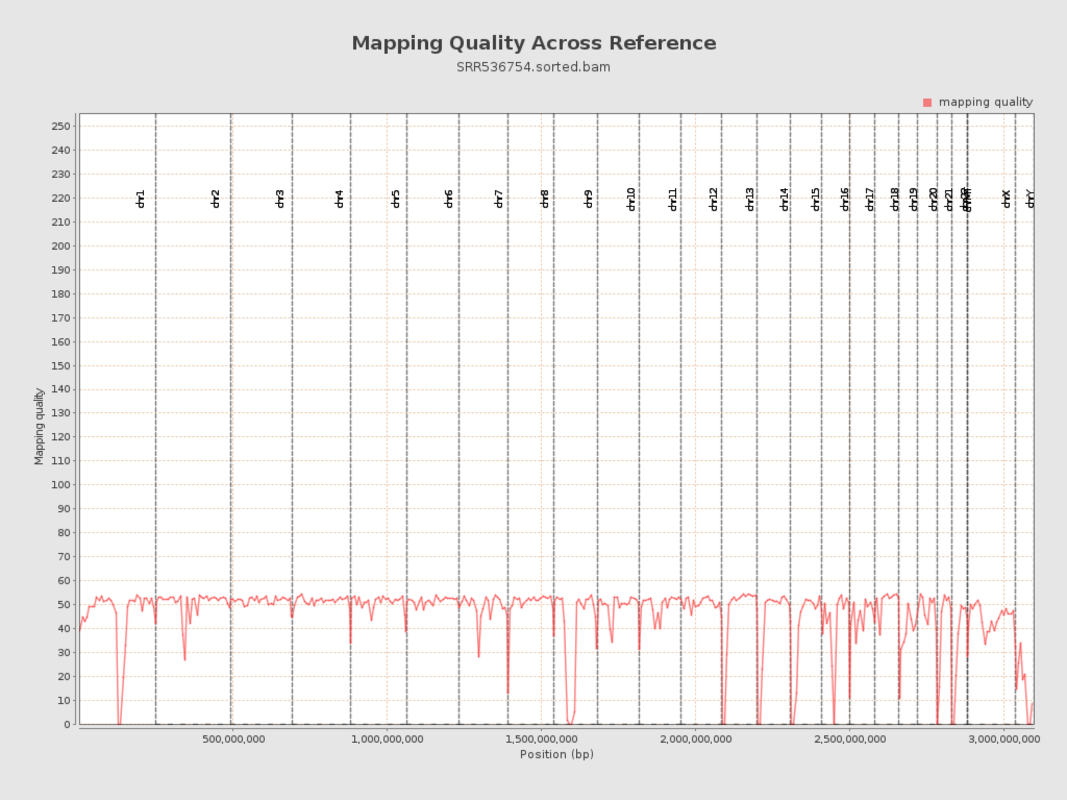
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram