# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/19 00:22:03*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR053623.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_SRR053623 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053623.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Apr 19 00:22:03 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR053623.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 12,755,729 |
| Mapped reads | 10,131,576 / 79.43% |
| Unmapped reads | 2,624,153 / 20.57% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 317 / 0% |
| Read min/max/mean length | 30 / 48 / 48 |
| Duplicated reads (estimated) | 2,331,923 / 18.28% |
| Duplication rate | 16.69% |
| Clipped reads | 786,643 / 6.17% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 141,041,627 / 29.43% |
| Number/percentage of C's | 91,350,627 / 19.06% |
| Number/percentage of T's | 144,327,502 / 30.12% |
| Number/percentage of G's | 102,250,379 / 21.34% |
| Number/percentage of N's | 199,427 / 0.04% |
| GC Percentage | 40.4% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1548 |
| | |

| | |
|---|---|
| Standard Deviation | 1.0176 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.16 |

## 2.5. Mismatches and indels

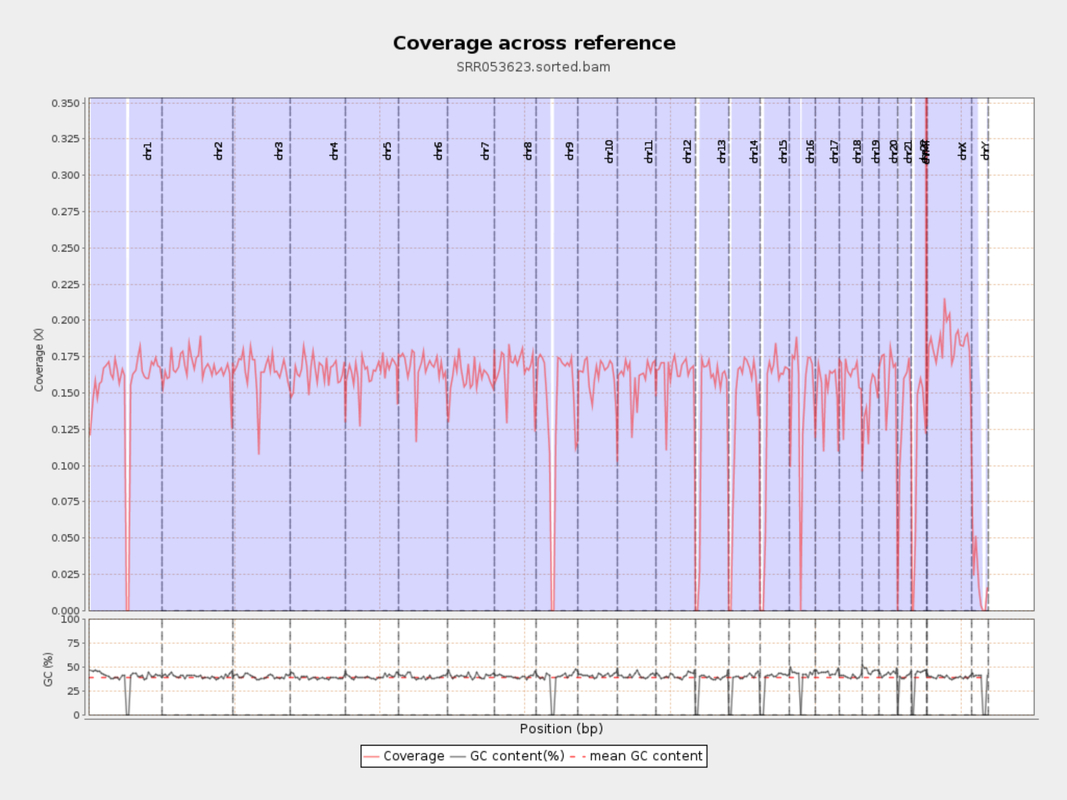
| | |
|---|---|
| General error rate | 0.55% |
| Mismatches | 2,618,747 |
| Insertions | 20,816 |
| Mapped reads with at least one insertion | 0.21% |
| Deletions | 62,336 |
| Mapped reads with at least one deletion | 0.61% |
| Homopolymer indels | 48.75% |

## 2.6. Chromosome stats

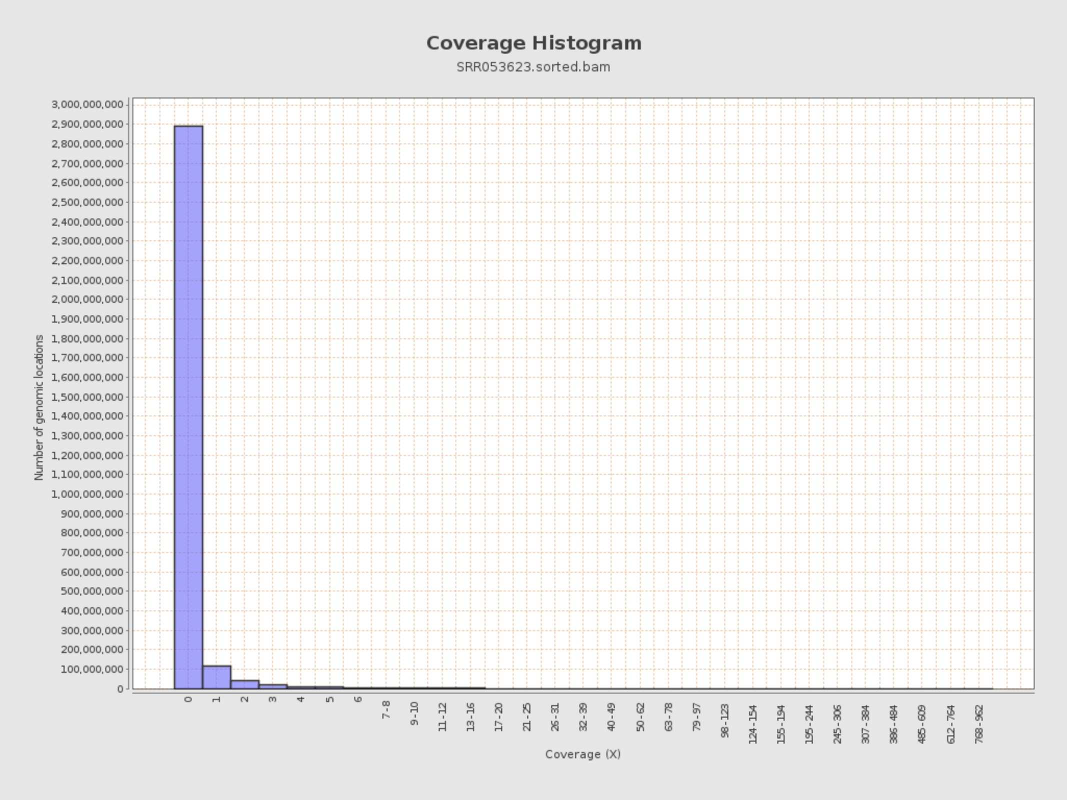
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 38041828 | 0.1526 | 1.071 |
| chr2 | 243199373 | 40803938 | 0.1678 | 1.2821 |
| chr3 | 198022430 | 32764534 | 0.1655 | 0.9458 |
| chr4 | 191154276 | 31475211 | 0.1647 | 0.9979 |
| chr5 | 180915260 | 29760938 | 0.1645 | 0.9261 |
| chr6 | 171115067 | 28613319 | 0.1672 | 1.0056 |
| chr7 | 159138663 | 25734540 | 0.1617 | 1.1915 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 24385195 | 0.1666 | 1.0322 |
| chr9 | 141213431 | 19929567 | 0.1411 | 0.9938 |
| chr10 | 135534747 | 22198974 | 0.1638 | 1.0345 |
| chr11 | 135006516 | 21610325 | 0.1601 | 1.0607 |
| chr12 | 133851895 | 21907251 | 0.1637 | 0.9386 |
| chr13 | 115169878 | 15676042 | 0.1361 | 0.8483 |
| chr14 | 107349540 | 14585165 | 0.1359 | 0.9863 |
| chr15 | 102531392 | 13803275 | 0.1346 | 0.8285 |
| chr16 | 90354753 | 13270555 | 0.1469 | 0.9211 |
| chr17 | 81195210 | 12282964 | 0.1513 | 0.8807 |
| chr18 | 78077248 | 12562008 | 0.1609 | 1.0916 |
| chr19 | 59128983 | 8473592 | 0.1433 | 1.0093 |
| chr20 | 63025520 | 10141401 | 0.1609 | 0.9635 |
| chr21 | 48129895 | 6277011 | 0.1304 | 0.9447 |
| chr22 | 51304566 | 5232449 | 0.102 | 0.7171 |
| chrMT | 16571 | 91747 | 5.5366 | 12.5589 |
| chrX | 155270560 | 28480672 | 0.1834 | 1.1243 |
| chrY | 59373566 | 1159410 | 0.0195 | 0.3744 |

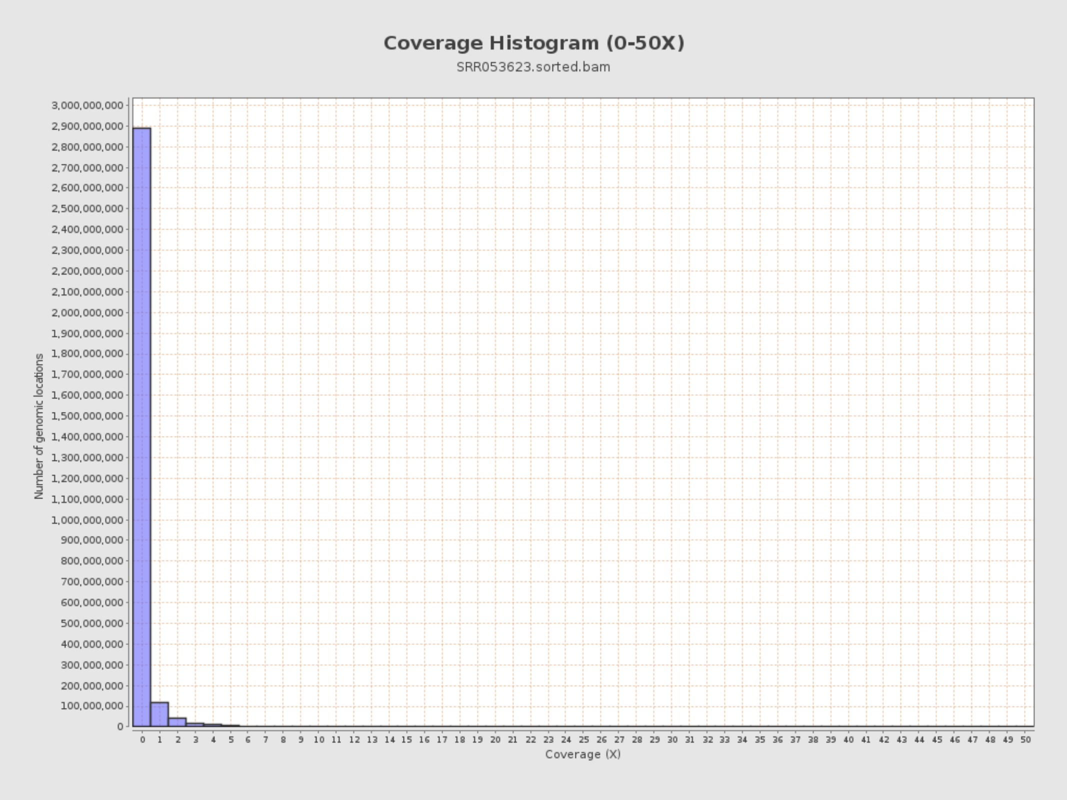
# 3. Results : Coverage across reference



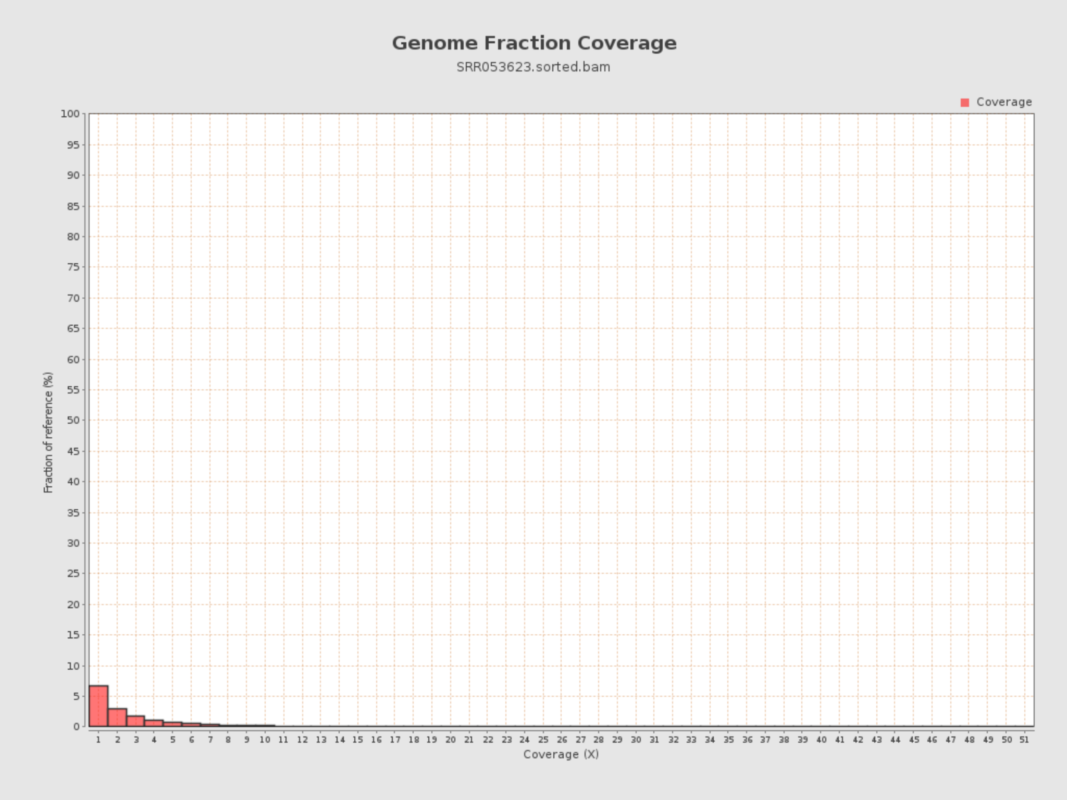
# 4. Results : Coverage Histogram



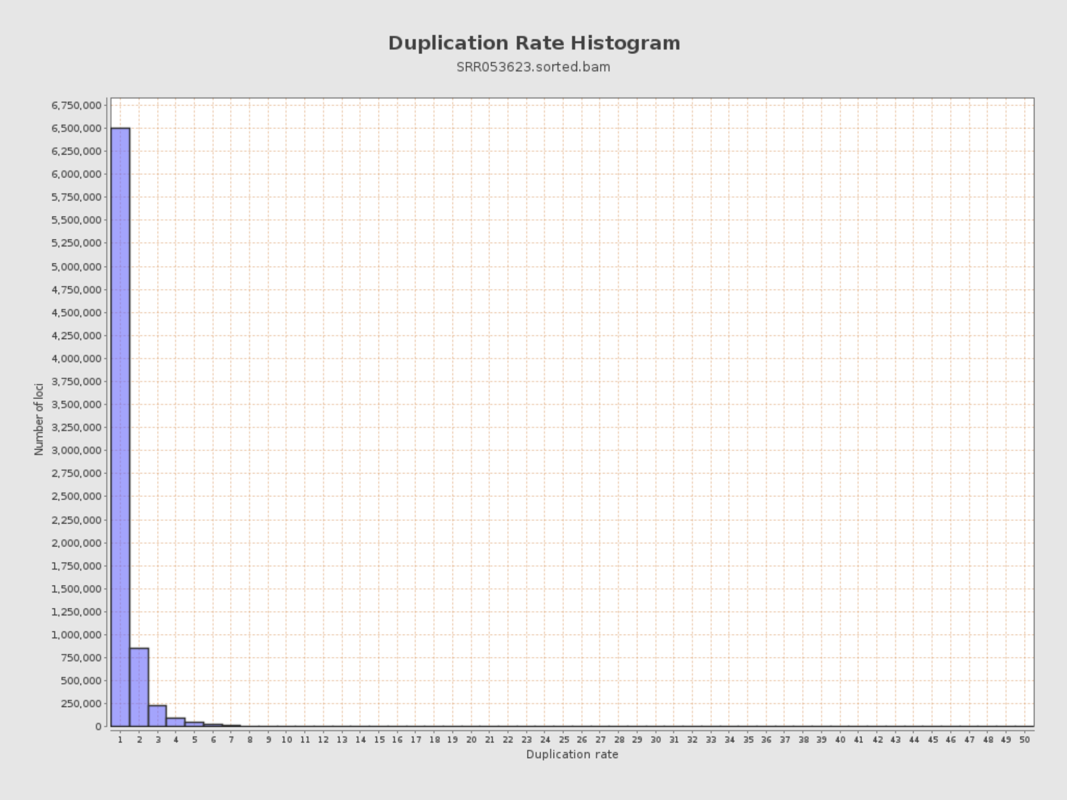
# 5. Results : Coverage Histogram (0-50X)



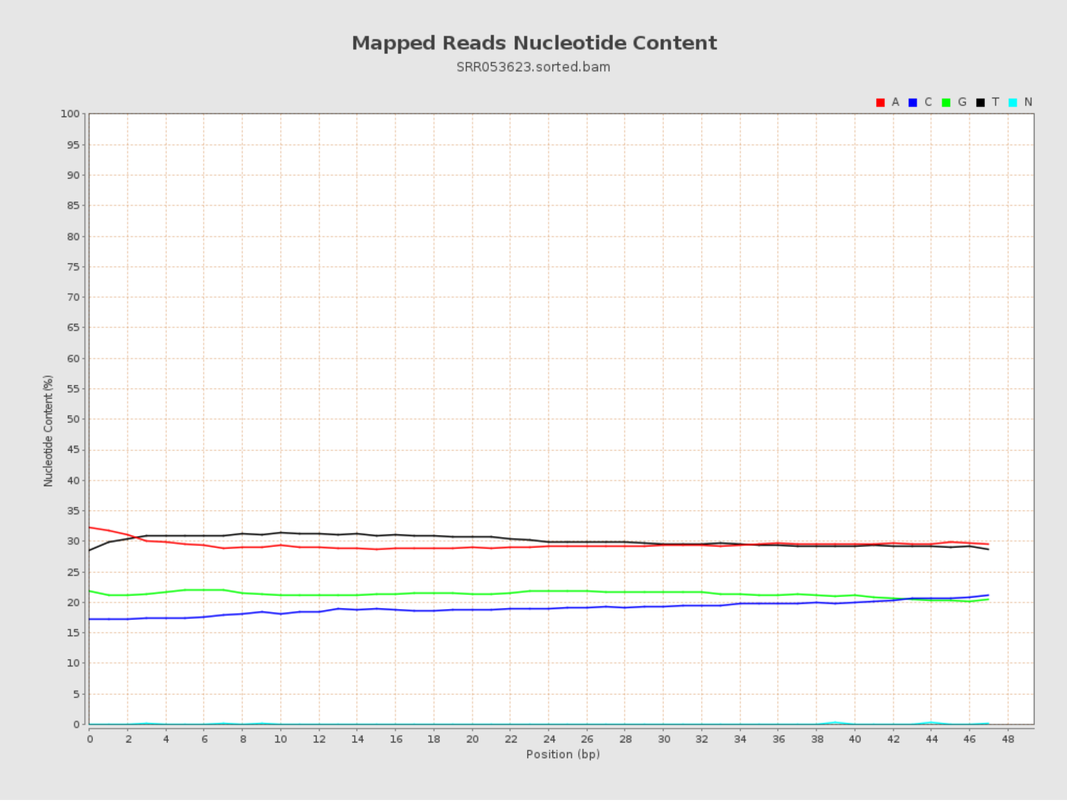
# 6. Results : Genome Fraction Coverage



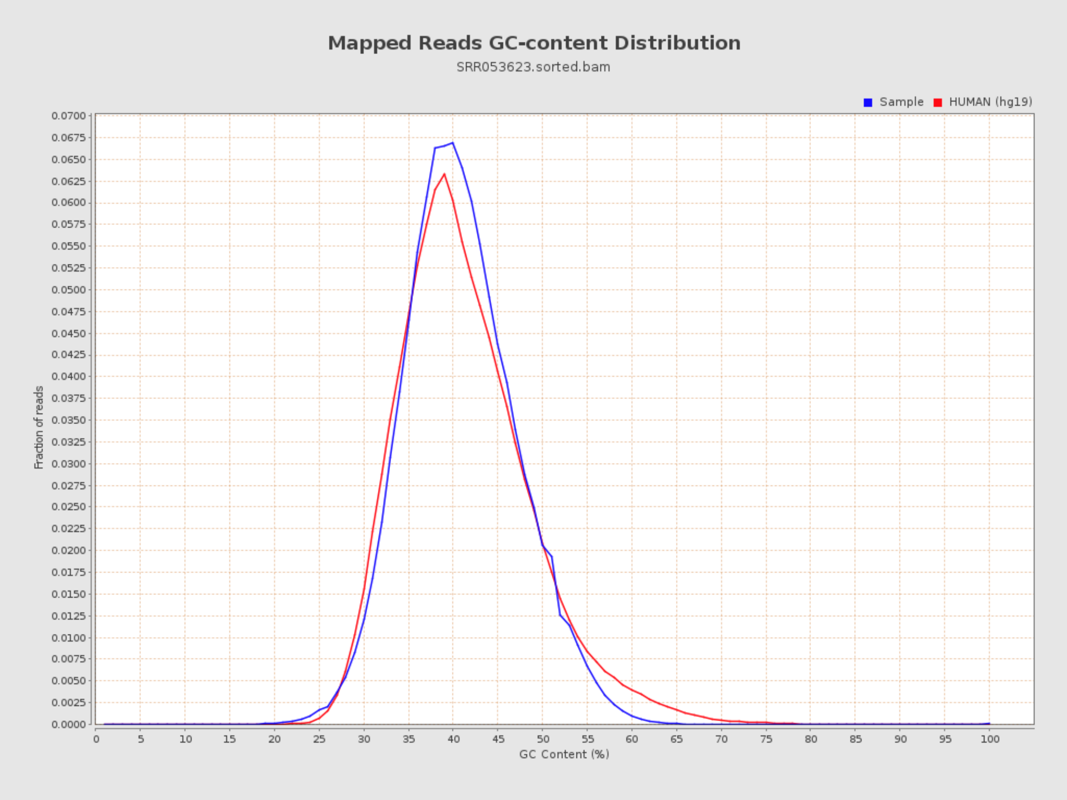
# 7. Results : Duplication Rate Histogram



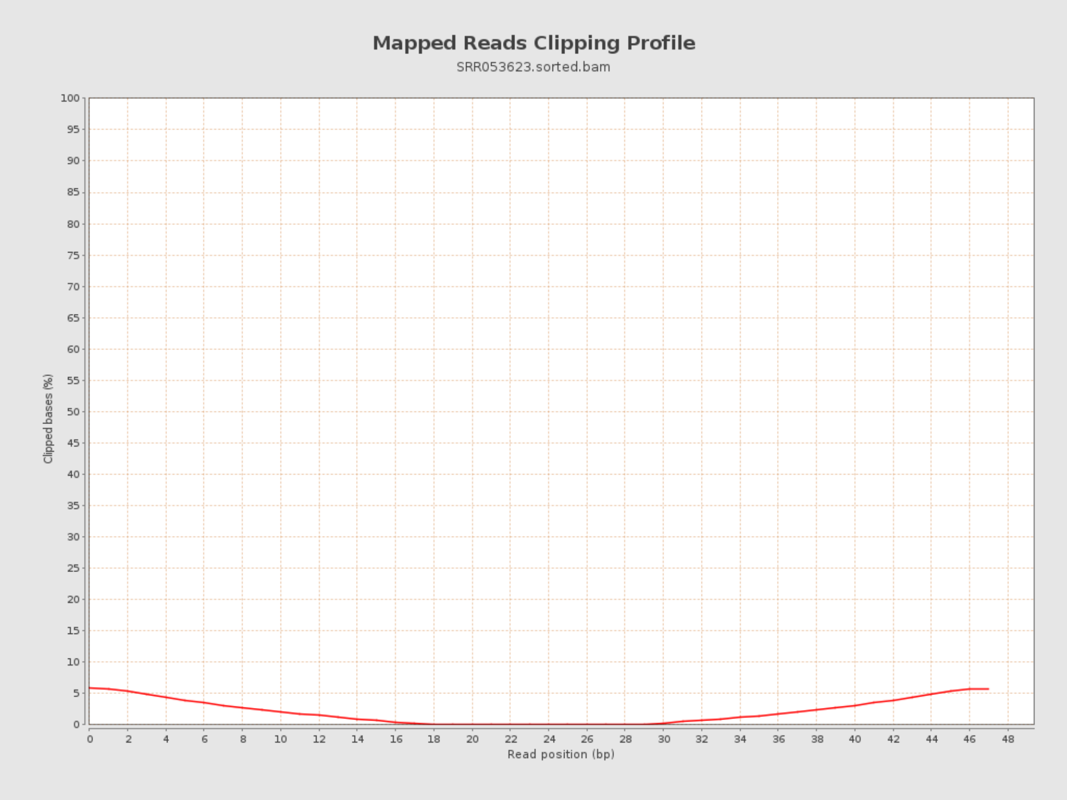
# 8. Results : Mapped Reads Nucleotide Content



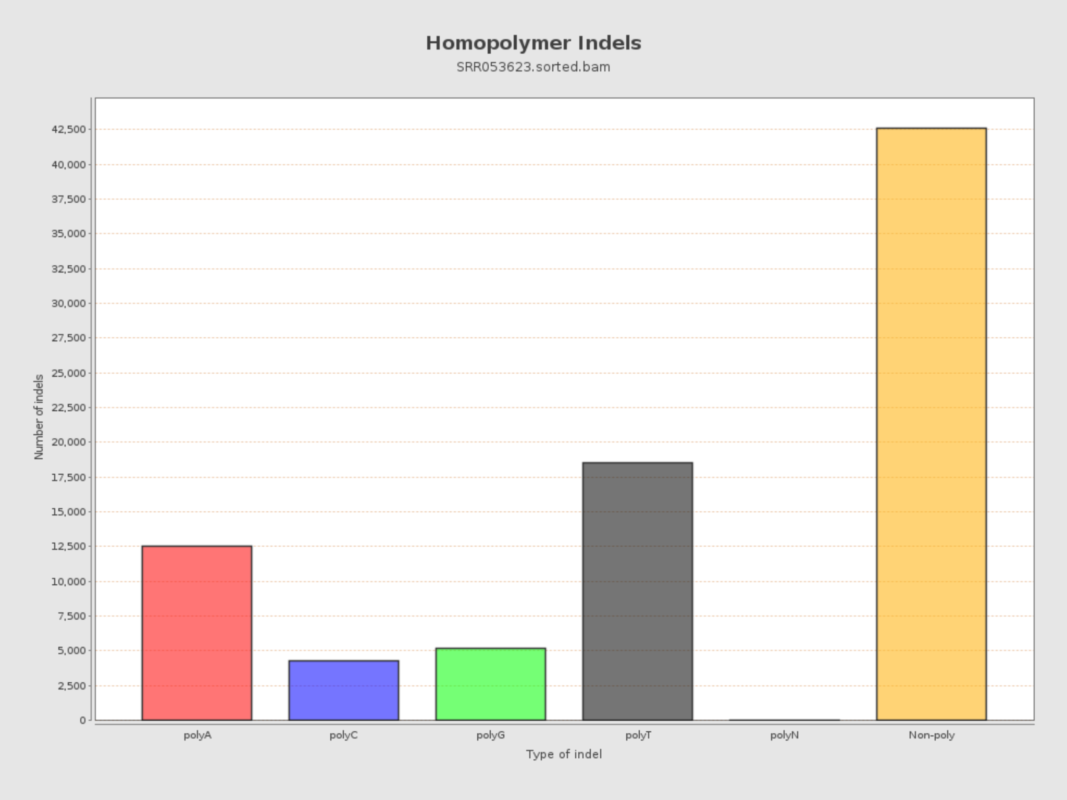
# 9. Results : Mapped Reads GC-content Distribution



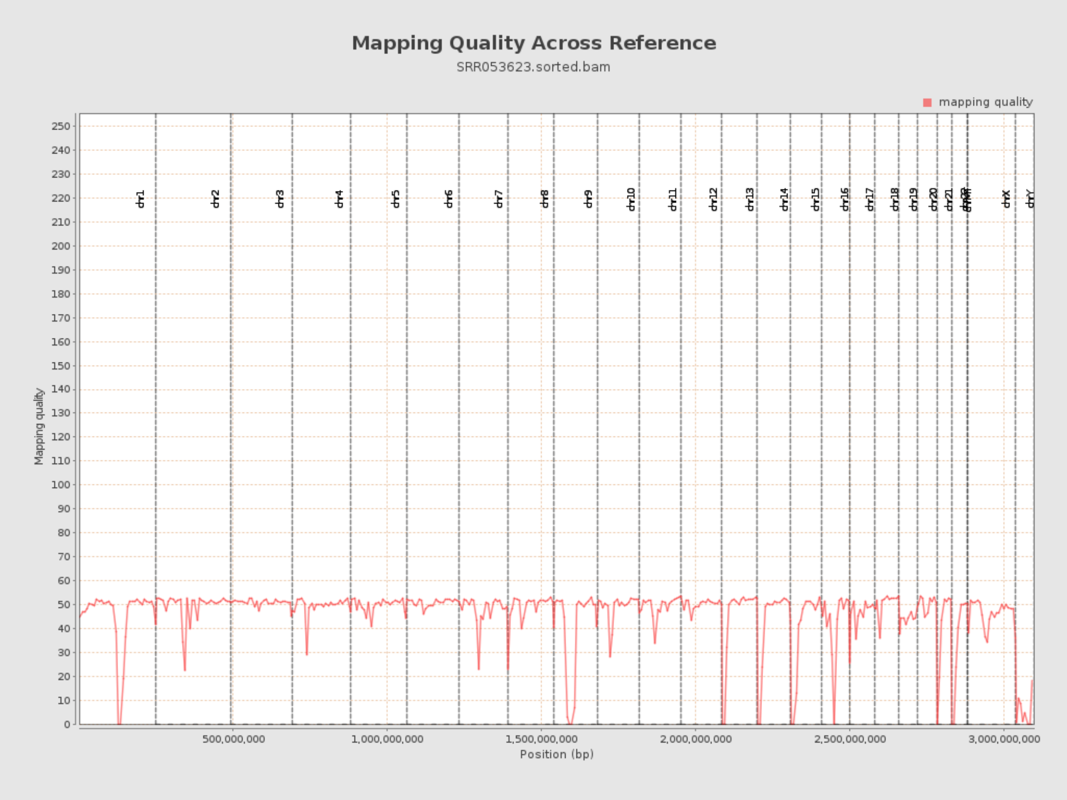
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram