# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/19 00:40:04*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR053629.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_SRR053629 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053629.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Apr 19 00:40:04 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR053629.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 11,997,232 |
| Mapped reads | 9,003,753 / 75.05% |
| Unmapped reads | 2,993,479 / 24.95% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 259 / 0% |
| Read min/max/mean length | 30 / 48 / 48 |
| Duplicated reads (estimated) | 2,548,307 / 21.24% |
| Duplication rate | 19.18% |
| Clipped reads | 769,752 / 6.42% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 125,967,407 / 29.62% |
| Number/percentage of C's | 81,672,135 / 19.21% |
| Number/percentage of T's | 127,636,734 / 30.02% |
| Number/percentage of G's | 89,734,038 / 21.1% |
| Number/percentage of N's | 198,619 / 0.05% |
| GC Percentage | 40.31% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1374 |
| | |

| | |
|---|---|
| Standard Deviation | 1.1197 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.57 |

## 2.5. Mismatches and indels

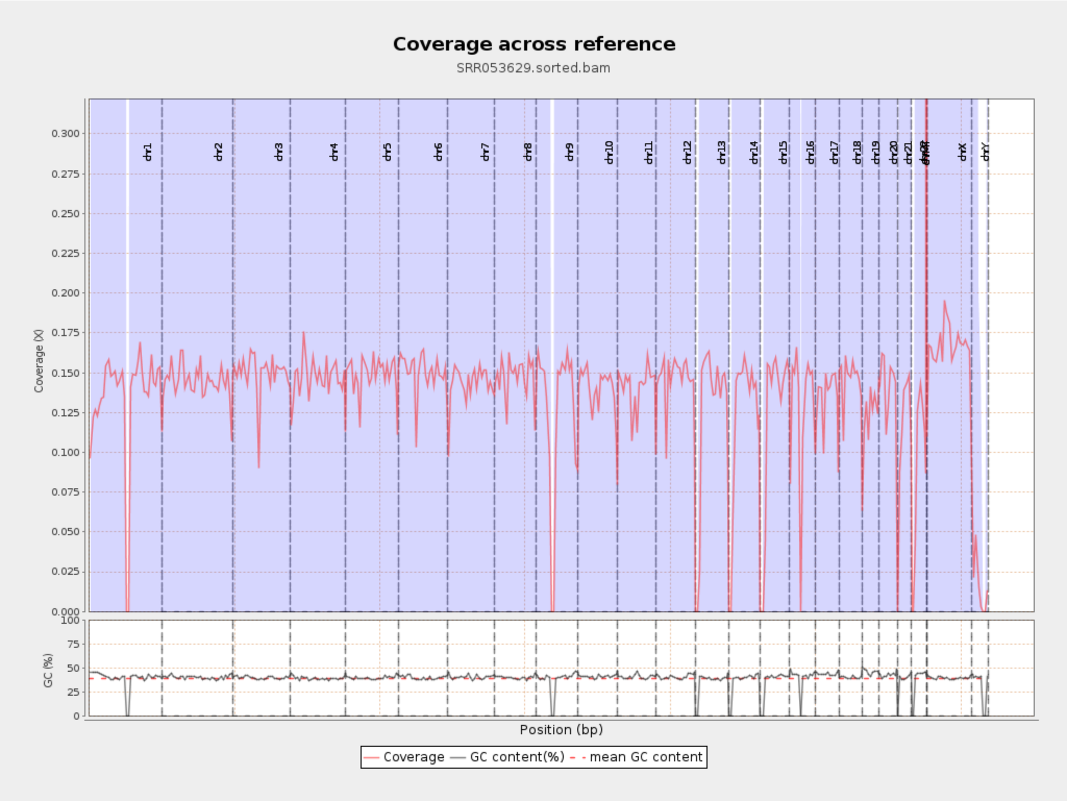
| | |
|---|---|
| General error rate | 0.6% |
| Mismatches | 2,535,712 |
| Insertions | 18,075 |
| Mapped reads with at least one insertion | 0.2% |
| Deletions | 54,918 |
| Mapped reads with at least one deletion | 0.61% |
| Homopolymer indels | 47.31% |

## 2.6. Chromosome stats

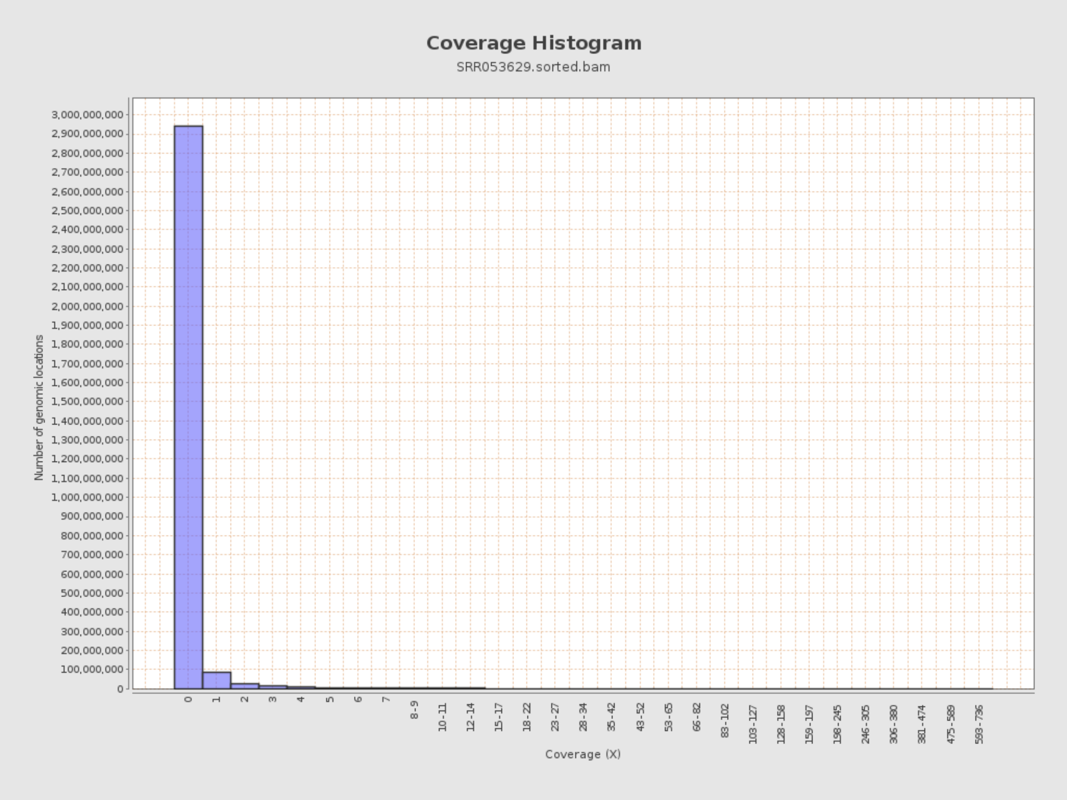
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 33296567 | 0.1336 | 1.1515 |
| chr2 | 243199373 | 35327877 | 0.1453 | 1.2825 |
| chr3 | 198022430 | 29642997 | 0.1497 | 1.1189 |
| chr4 | 191154276 | 28096489 | 0.147 | 1.1516 |
| chr5 | 180915260 | 26991141 | 0.1492 | 1.1001 |
| chr6 | 171115067 | 25712921 | 0.1503 | 1.1848 |
| chr7 | 159138663 | 22930192 | 0.1441 | 1.1571 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 21590941 | 0.1475 | 1.1628 |
| chr9 | 141213431 | 17712089 | 0.1254 | 1.0292 |
| chr10 | 135534747 | 19186585 | 0.1416 | 1.1612 |
| chr11 | 135006516 | 18923766 | 0.1402 | 1.1493 |
| chr12 | 133851895 | 19612734 | 0.1465 | 1.0855 |
| chr13 | 115169878 | 14122005 | 0.1226 | 0.9992 |
| chr14 | 107349540 | 12951322 | 0.1206 | 1.0485 |
| chr15 | 102531392 | 12341897 | 0.1204 | 0.9745 |
| chr16 | 90354753 | 11583756 | 0.1282 | 1.0361 |
| chr17 | 81195210 | 10876095 | 0.1339 | 1.0206 |
| chr18 | 78077248 | 11433578 | 0.1464 | 1.1975 |
| chr19 | 59128983 | 7329434 | 0.124 | 1.1489 |
| chr20 | 63025520 | 8860479 | 0.1406 | 1.0758 |
| chr21 | 48129895 | 5385673 | 0.1119 | 1.023 |
| chr22 | 51304566 | 4469114 | 0.0871 | 0.8004 |
| chrMT | 16571 | 52235 | 3.1522 | 6.9106 |
| chrX | 155270560 | 25789624 | 0.1661 | 1.2467 |
| chrY | 59373566 | 1069836 | 0.018 | 0.3844 |

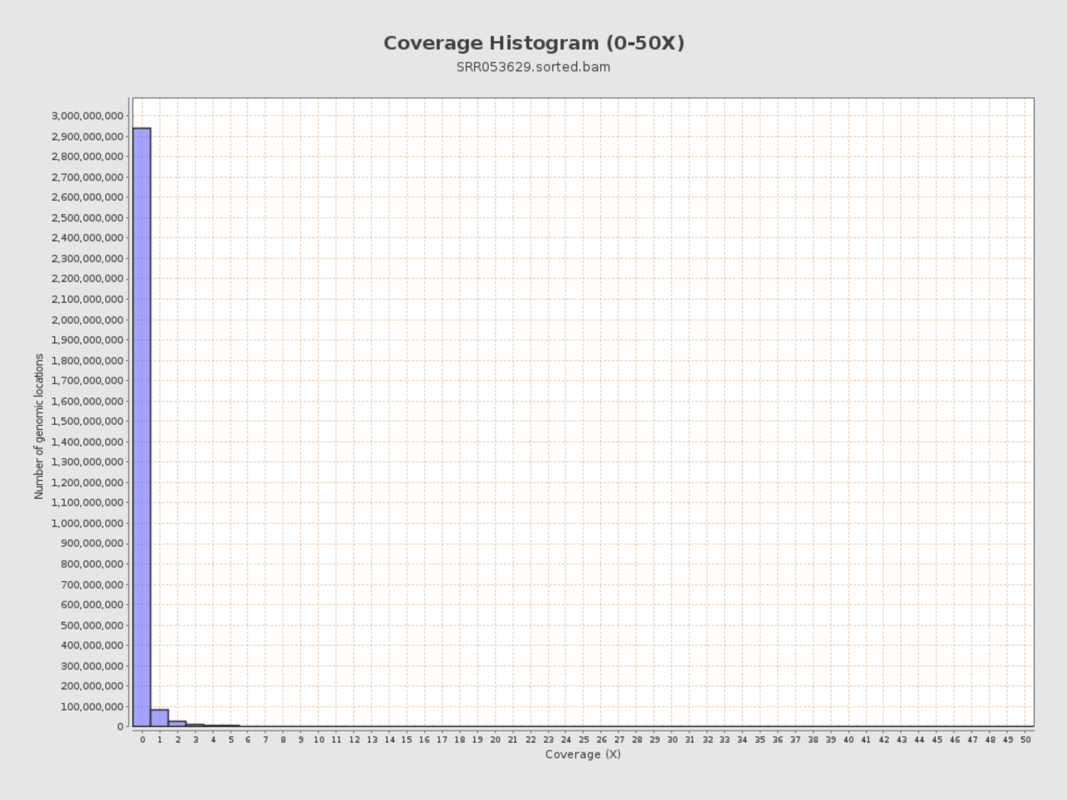
# 3. Results : Coverage across reference



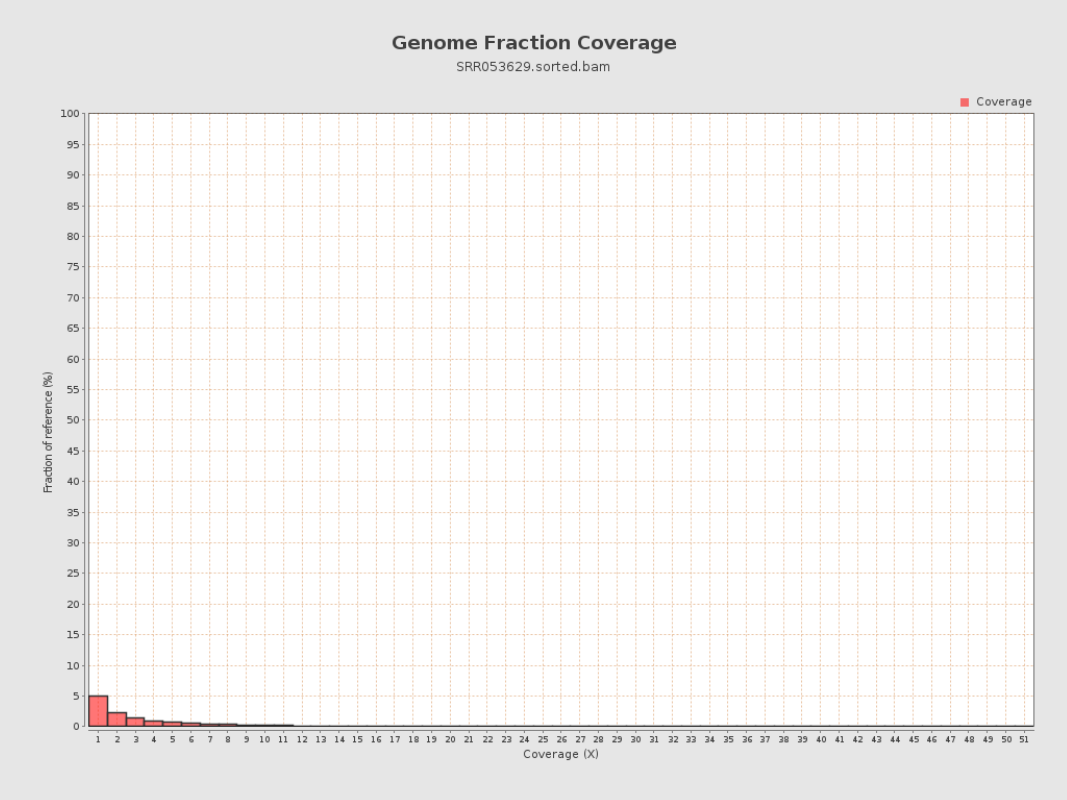
# 4. Results : Coverage Histogram



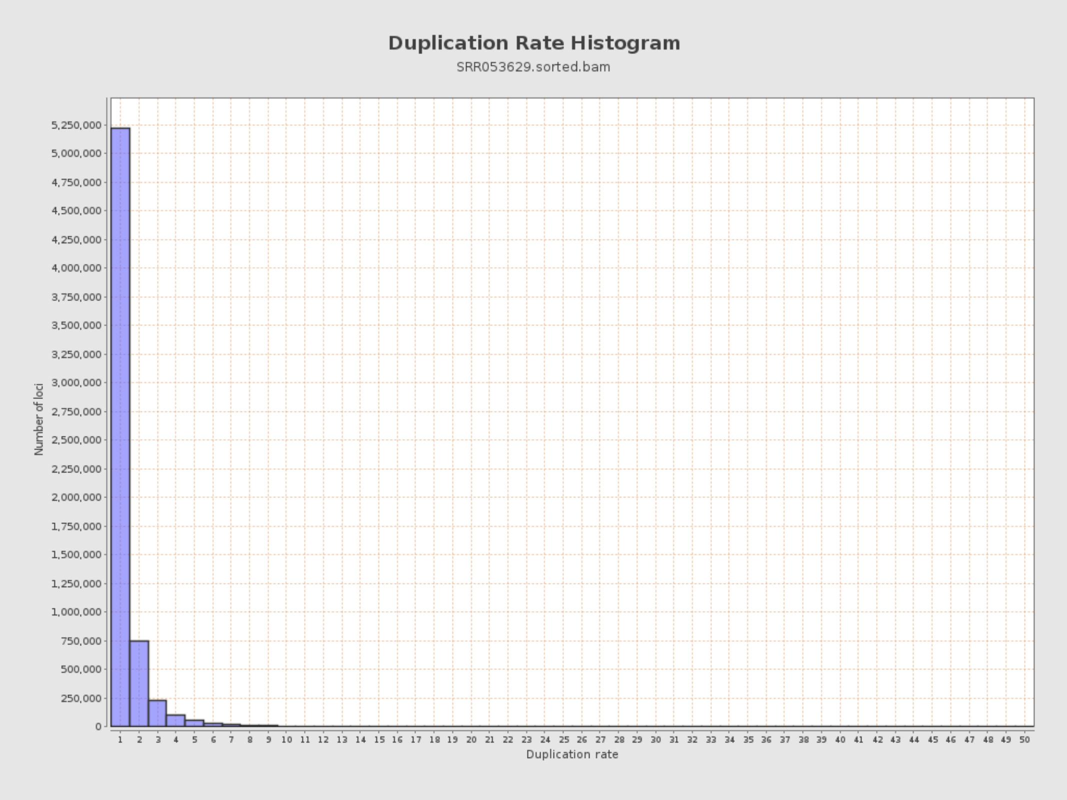
# 5. Results : Coverage Histogram (0-50X)



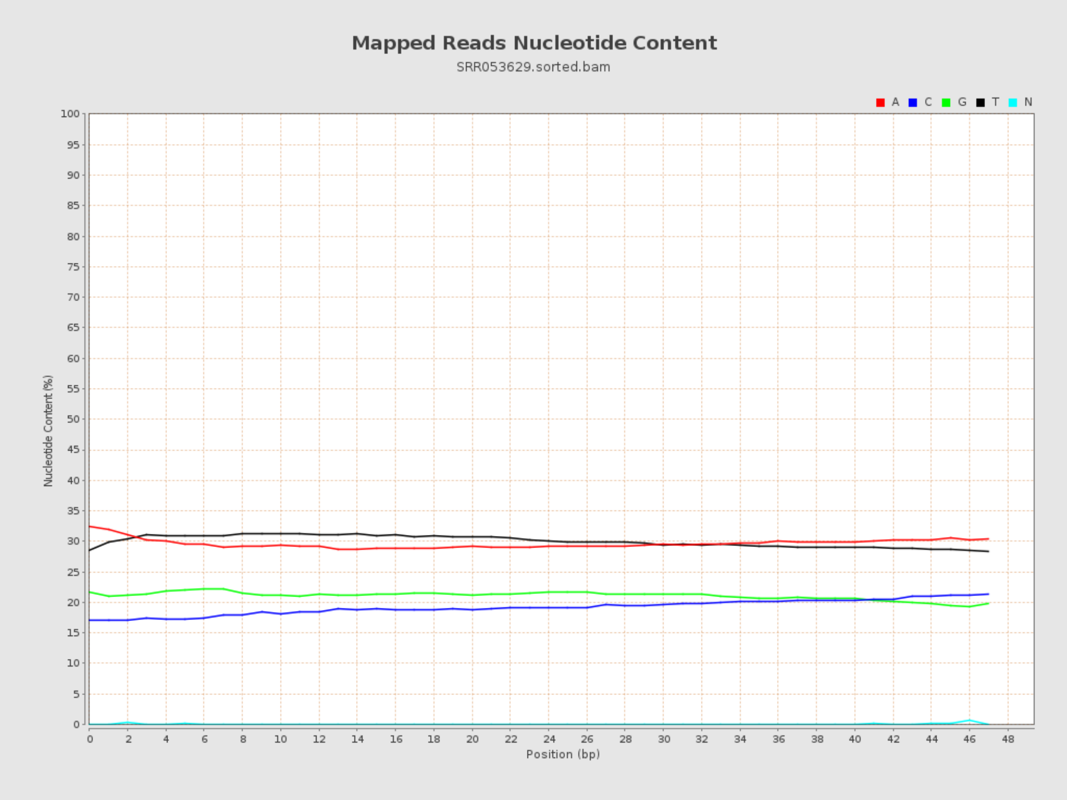
# 6. Results : Genome Fraction Coverage



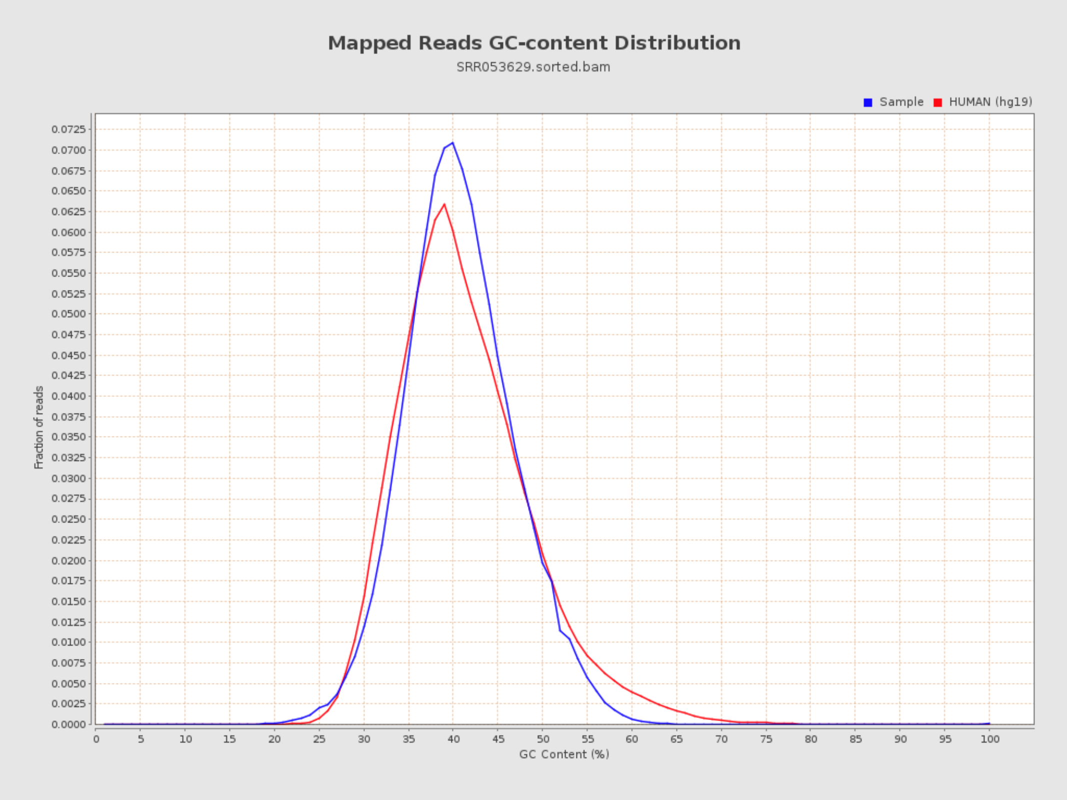
# 7. Results : Duplication Rate Histogram



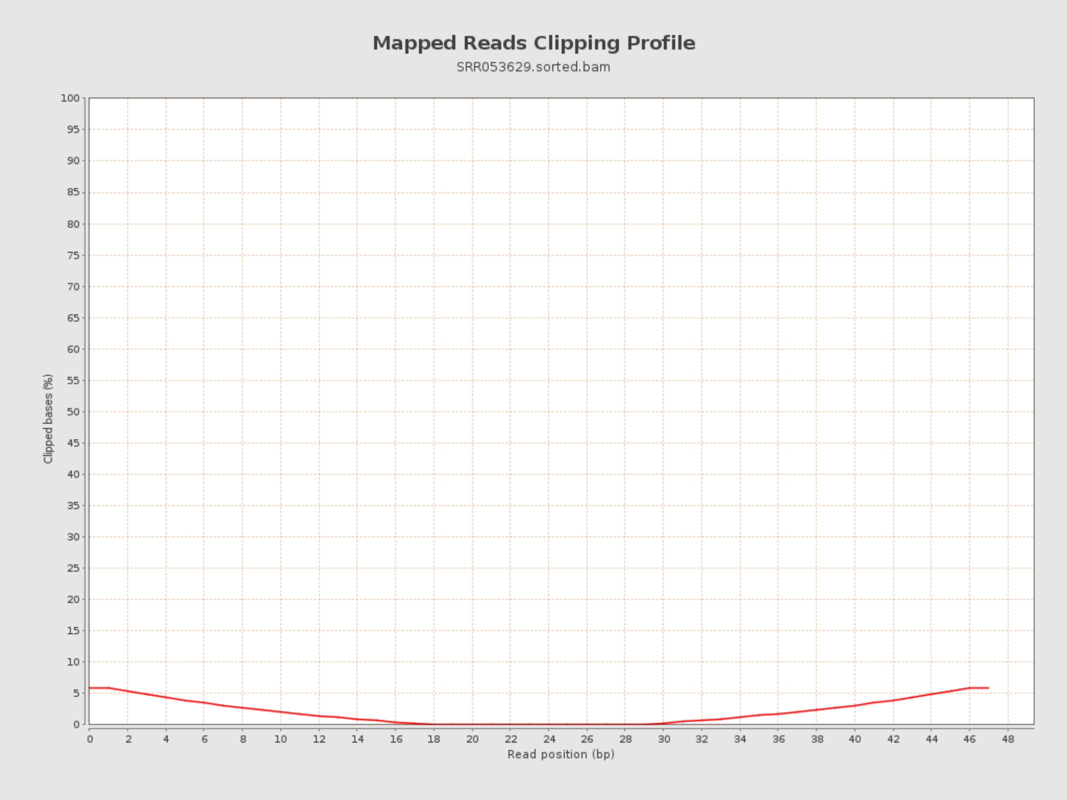
# 8. Results : Mapped Reads Nucleotide Content



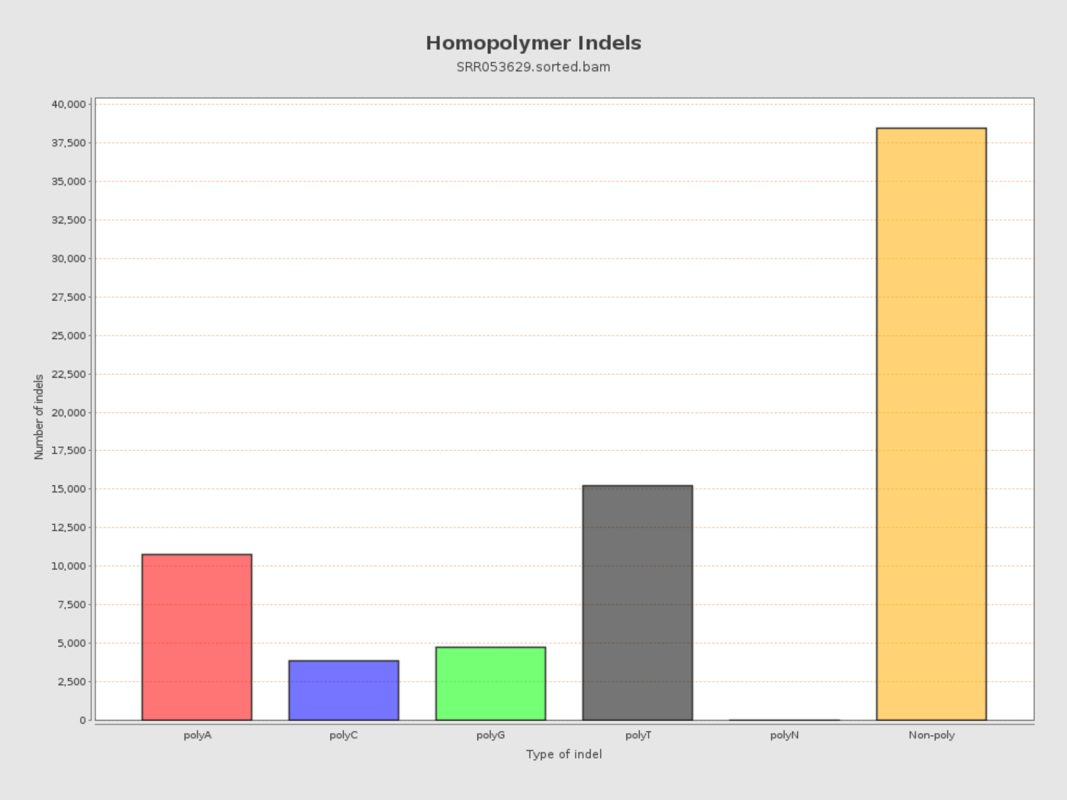
# 9. Results : Mapped Reads GC-content Distribution



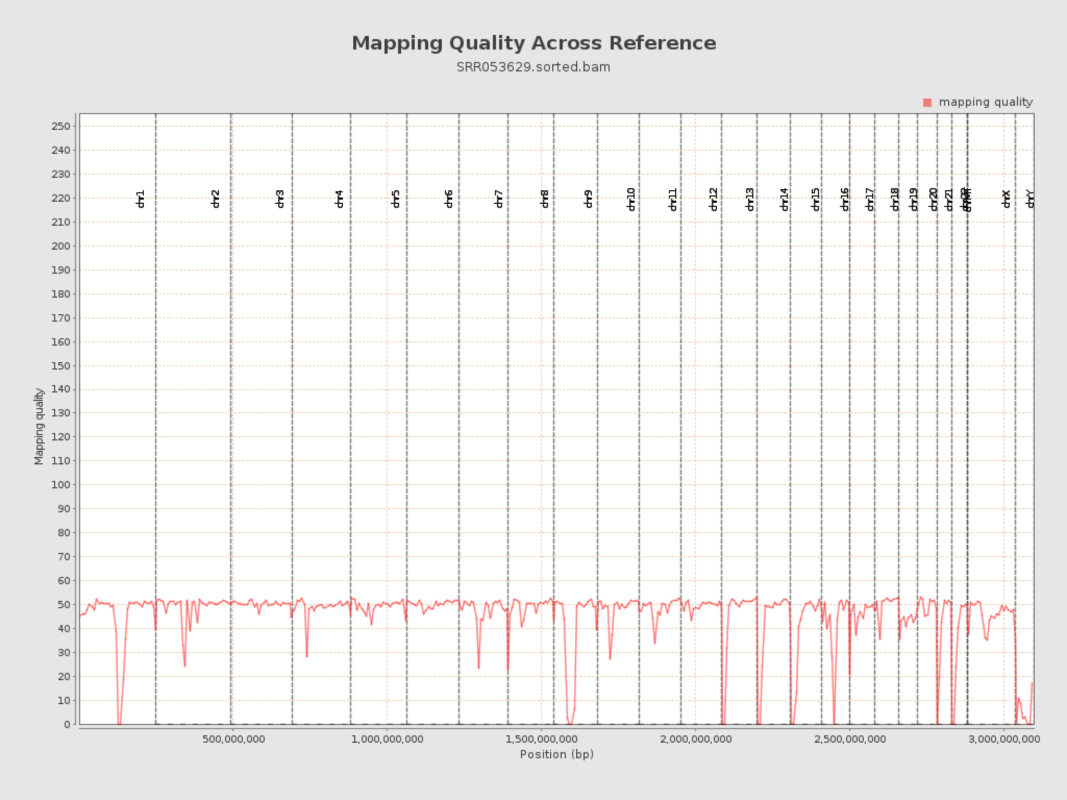
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram