# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/17 14:51:03*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006028.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_SRR1006028 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006028_1.fastq.gz SRR1006028_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Apr 17 14:51:02 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1006028.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 13,103,140 |
| Mapped reads | 8,188,168 / 62.49% |
| Unmapped reads | 4,914,972 / 37.51% |
| Mapped paired reads | 8,188,168 / 62.49% |
| Mapped reads, first in pair | 4,156,065 / 31.72% |
| Mapped reads,  second in pair | 4,032,103 / 30.77% |
| Mapped reads, both in pair | 6,983,796 / 53.3% |
| Mapped reads, singletons | 1,204,372 / 9.19% |
| Secondary alignments | 0 |
| Read min/max/mean length | 39 / 39 / 39 |
| Duplicated reads (estimated) | 271,784 / 2.07% |
| Duplication rate | 2.67% |
| Clipped reads | 732,088 / 5.59% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 94,650,643 / 29.96% |
| Number/percentage of C's | 63,859,598 / 20.21% |
| Number/percentage of T's | 92,717,626 / 29.34% |
| Number/percentage of G's | 64,614,342 / 20.45% |
| Number/percentage of N's | 117,402 / 0.04% |
| GC Percentage | 40.66% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1021 |
| Standard Deviation | 0.568 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.78 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 72,498.96 |
| Standard Deviation | 2,596,181.95 |
| P25/Median/P75 | 73 / 103 / 147 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.77% |
| Mismatches | 2,430,699 |
| Insertions | 9,257 |
| Mapped reads with at least one insertion | 0.11% |
| Deletions | 27,446 |
| Mapped reads with at least one deletion | 0.34% |
| Homopolymer indels | 45.39% |

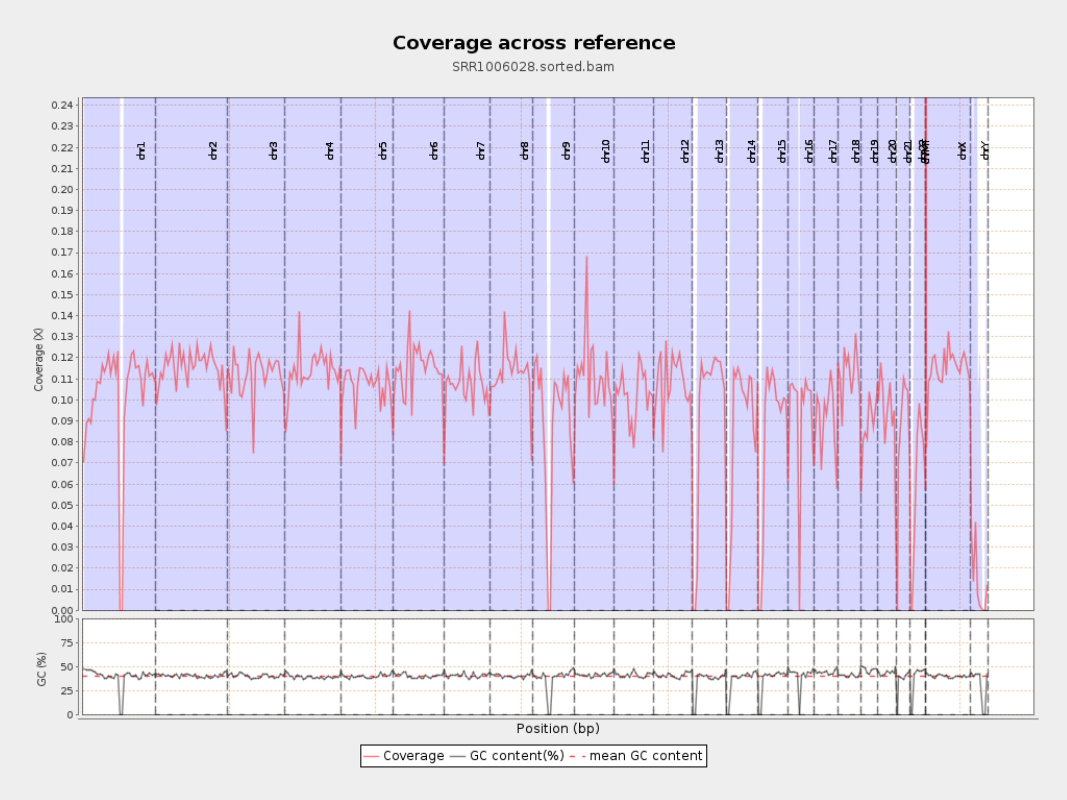
## 2.7. Chromosome stats

| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| | | | | |

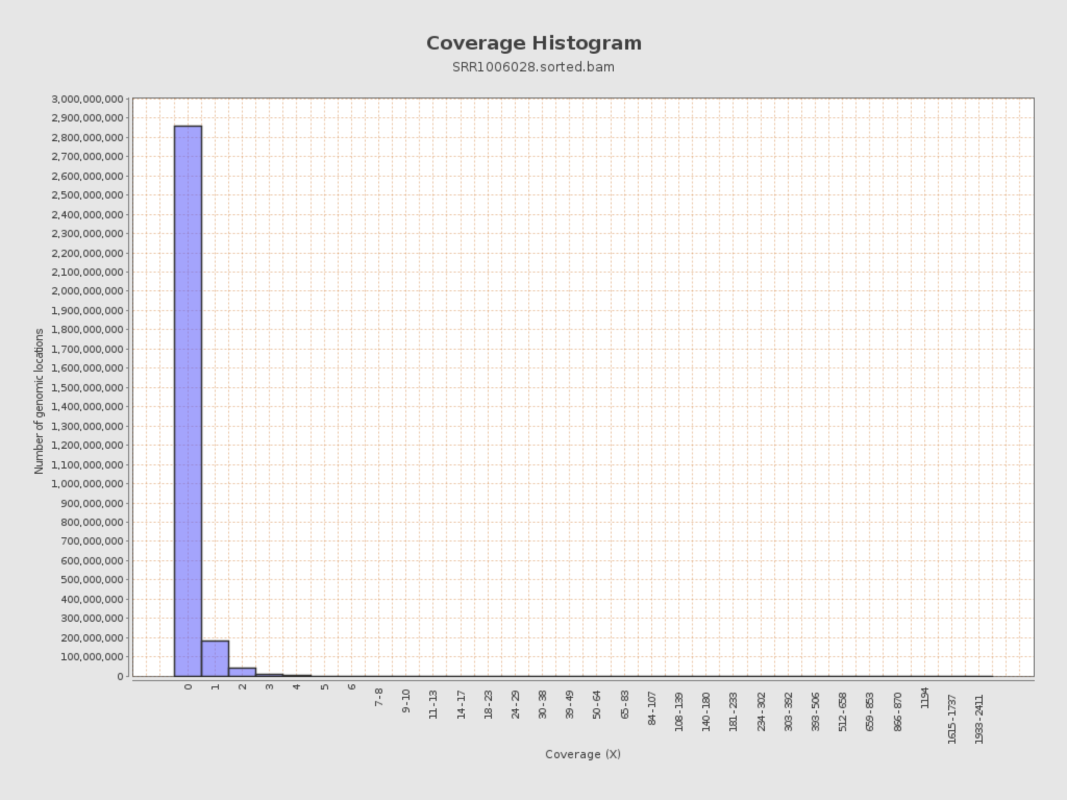
| | | | | |
|---|---|---|---|---|
| chr1 | 249250621 | 25408118 | 0.1019 | 0.755 |
| chr2 | 243199373 | 28062273 | 0.1154 | 0.5452 |
| chr3 | 198022430 | 22189051 | 0.1121 | 0.4201 |
| chr4 | 191154276 | 21782853 | 0.114 | 0.4705 |
| chr5 | 180915260 | 19254494 | 0.1064 | 0.4093 |
| chr6 | 171115067 | 19798125 | 0.1157 | 0.5236 |
| chr7 | 159138663 | 17042595 | 0.1071 | 0.6119 |
| chr8 | 146364022 | 16496744 | 0.1127 | 1.2557 |
| chr9 | 141213431 | 12463447 | 0.0883 | 0.4486 |
| chr10 | 135534747 | 15124396 | 0.1116 | 0.6637 |
| chr11 | 135006516 | 13707163 | 0.1015 | 0.4638 |
| chr12 | 133851895 | 14469653 | 0.1081 | 0.4162 |
| chr13 | 115169878 | 10778131 | 0.0936 | 0.3841 |
| chr14 | 107349540 | 9215173 | 0.0858 | 0.3942 |
| chr15 | 102531392 | 8500302 | 0.0829 | 0.3619 |
| chr16 | 90354753 | 8240449 | 0.0912 | 0.459 |
| chr17 | 81195210 | 7476515 | 0.0921 | 0.4017 |
| chr18 | 78077248 | 8841309 | 0.1132 | 0.6805 |
| chr19 | 59128983 | 5296748 | 0.0896 | 0.5939 |
| chr20 | 63025520 | 6033698 | 0.0957 | 0.4051 |
| chr21 | 48129895 | 4038031 | 0.0839 | 0.4143 |
| chr22 | 51304566 | 3051602 | 0.0595 | 0.3077 |
| chrMT | 16571 | 79844 | 4.8183 | 3.9299 |
| chrX | 155270560 | 17852721 | 0.115 | 0.4642 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 791086 | 0.0133 | 0.2716 |

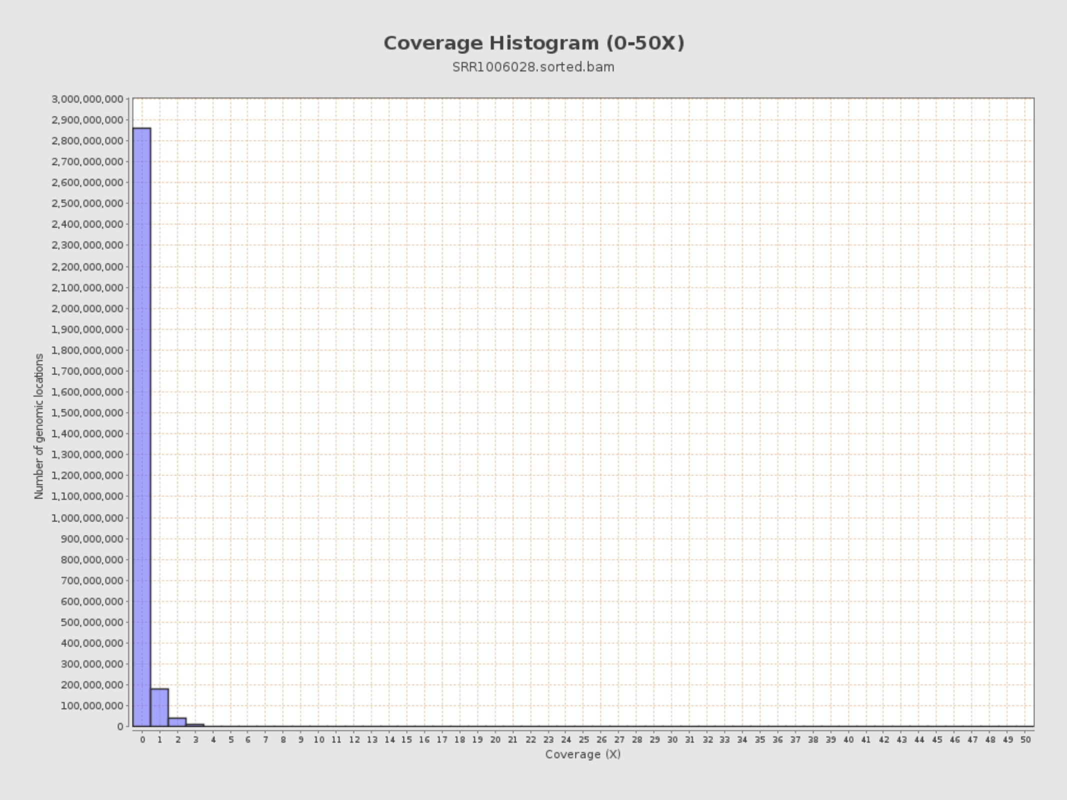
# 3. Results : Coverage across reference



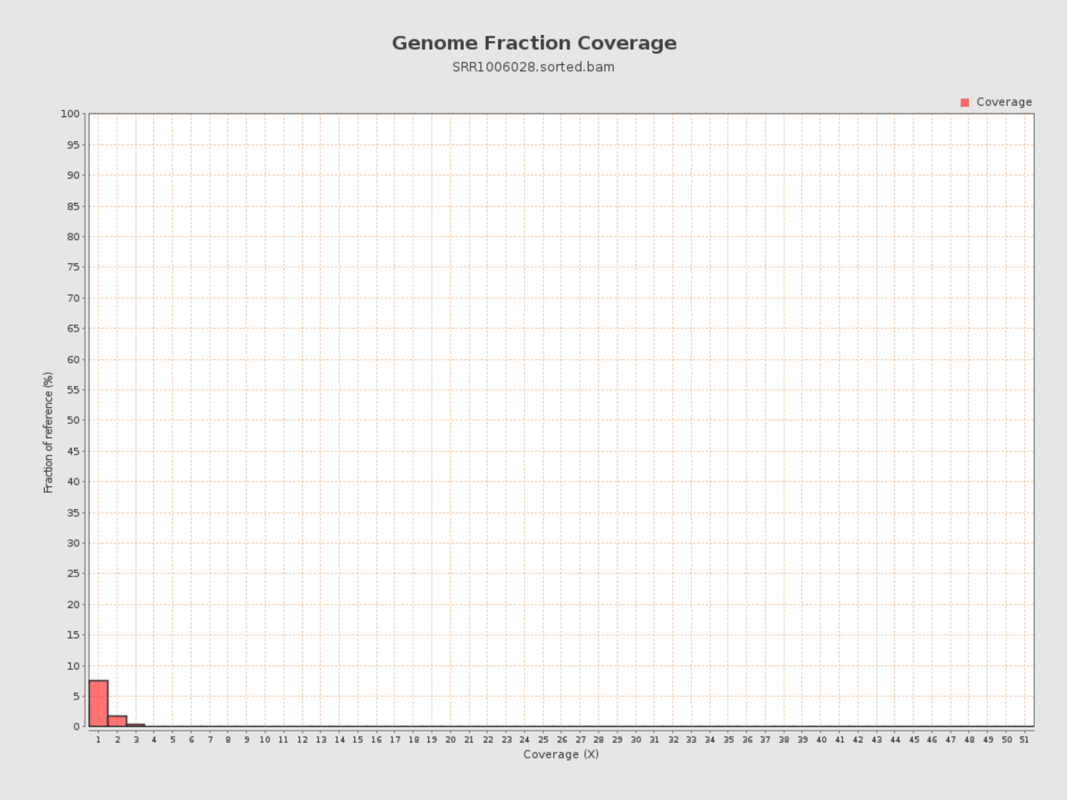
# 4. Results : Coverage Histogram



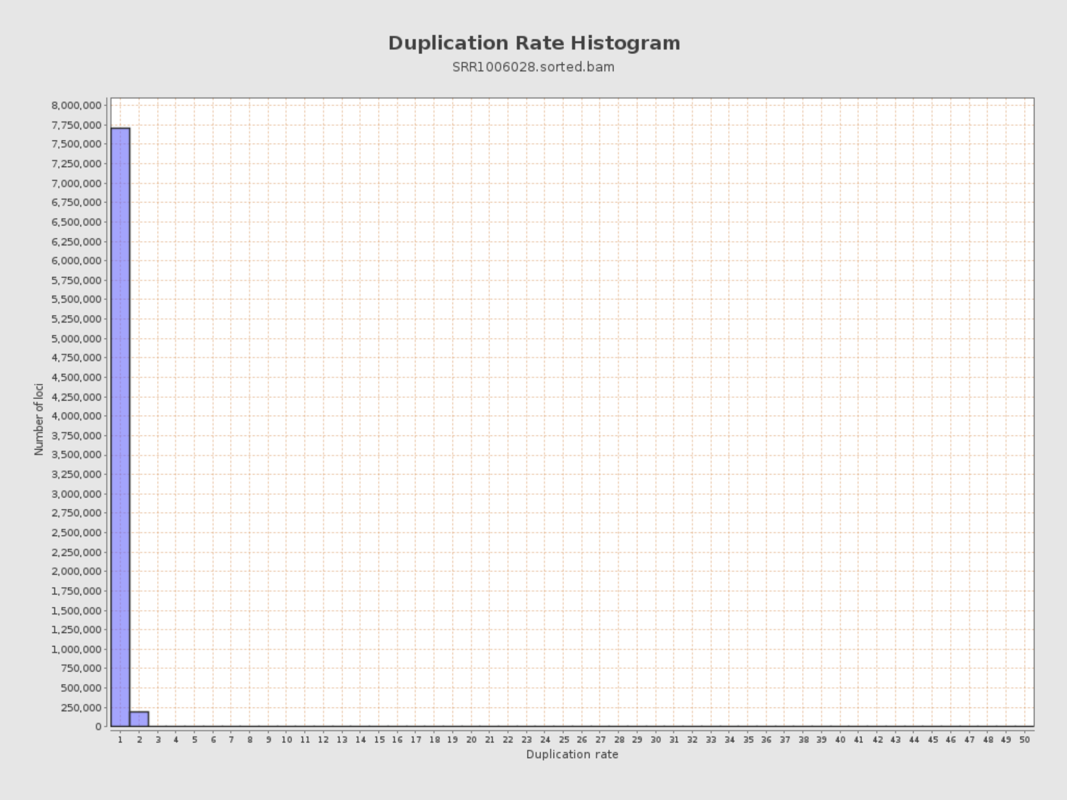
# 5. Results : Coverage Histogram (0-50X)



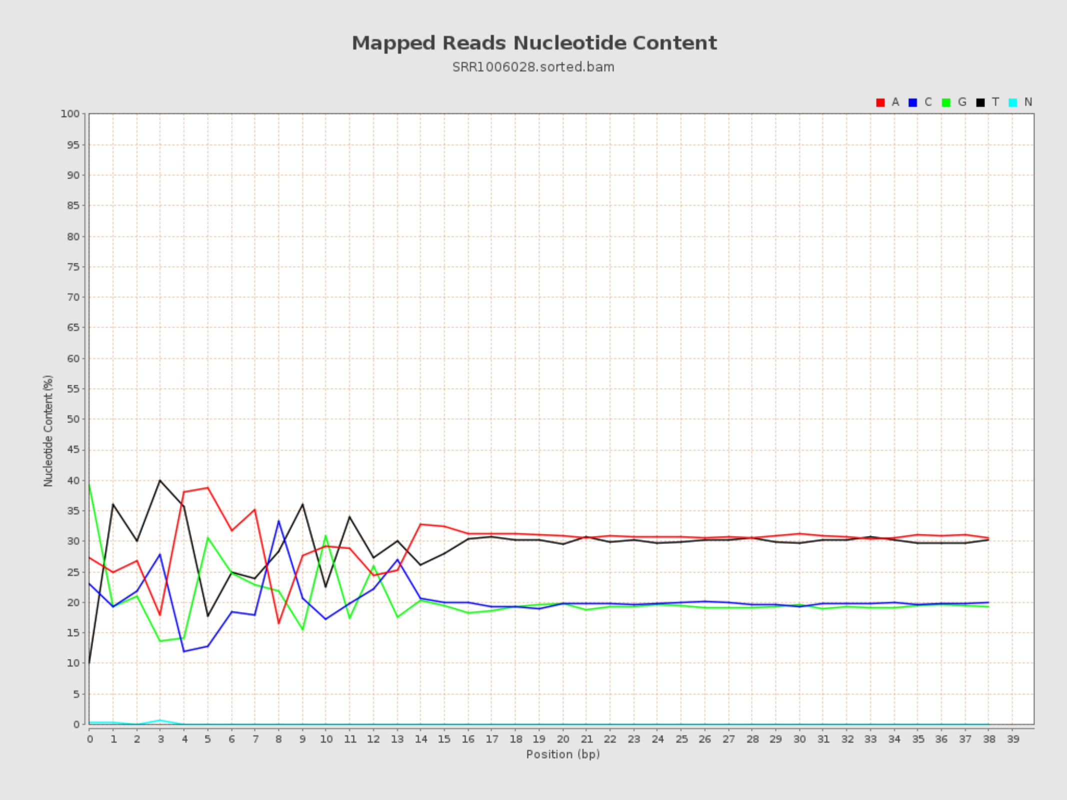
# 6. Results : Genome Fraction Coverage



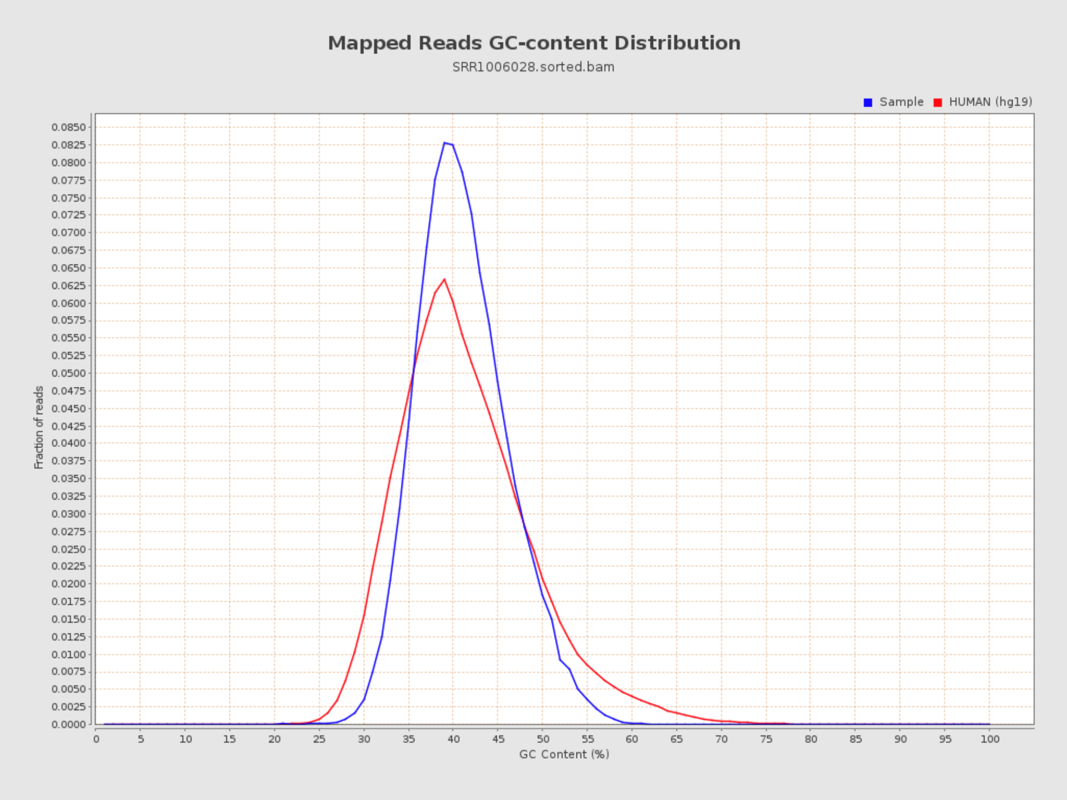
# 7. Results : Duplication Rate Histogram



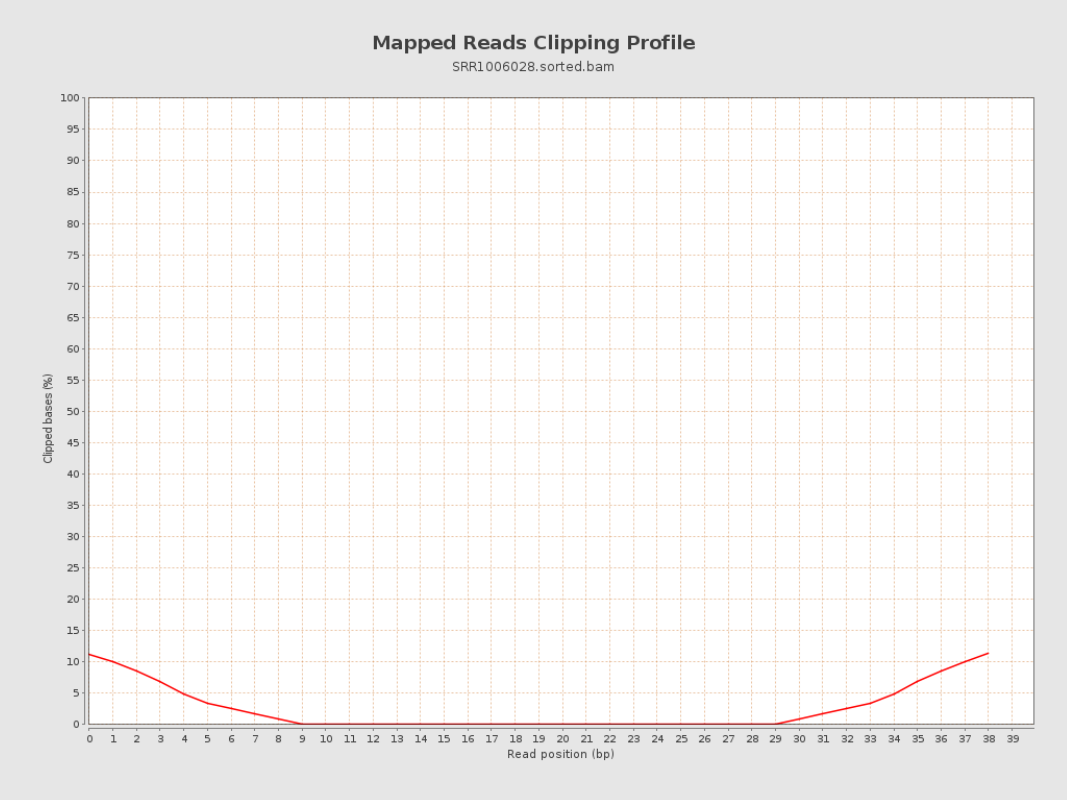
# 8. Results : Mapped Reads Nucleotide Content



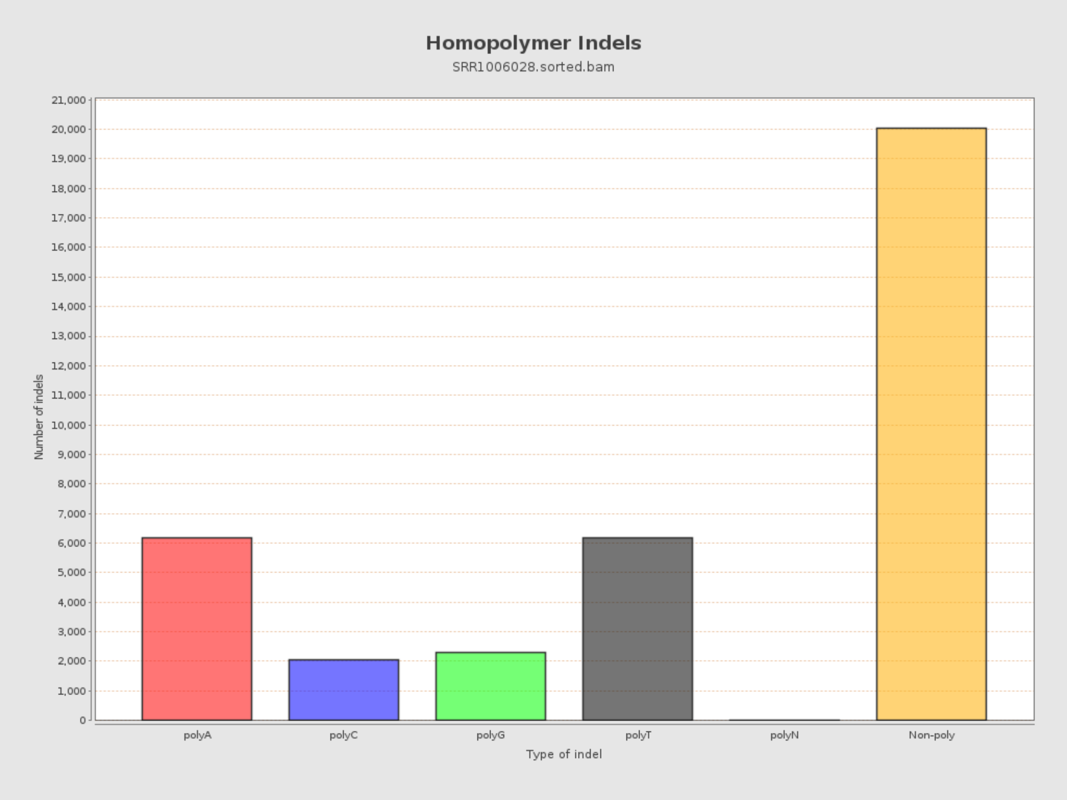
# 9. Results : Mapped Reads GC-content Distribution



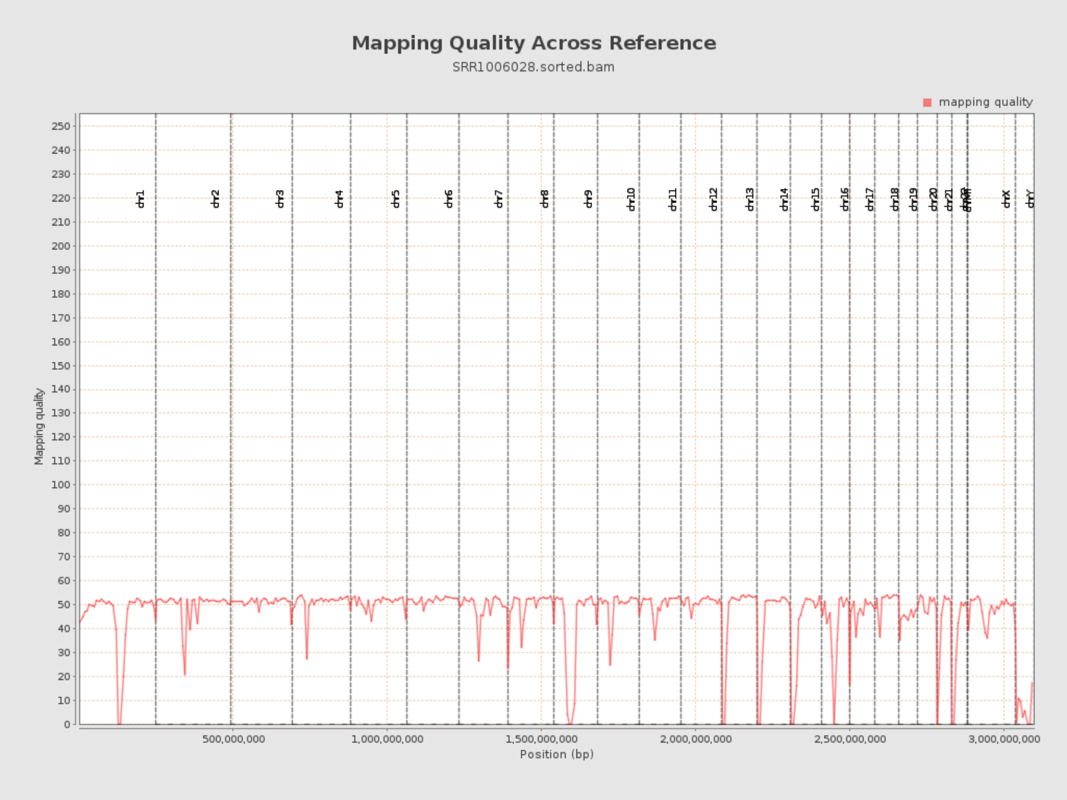
# 10. Results : Mapped Reads Clipping Profile



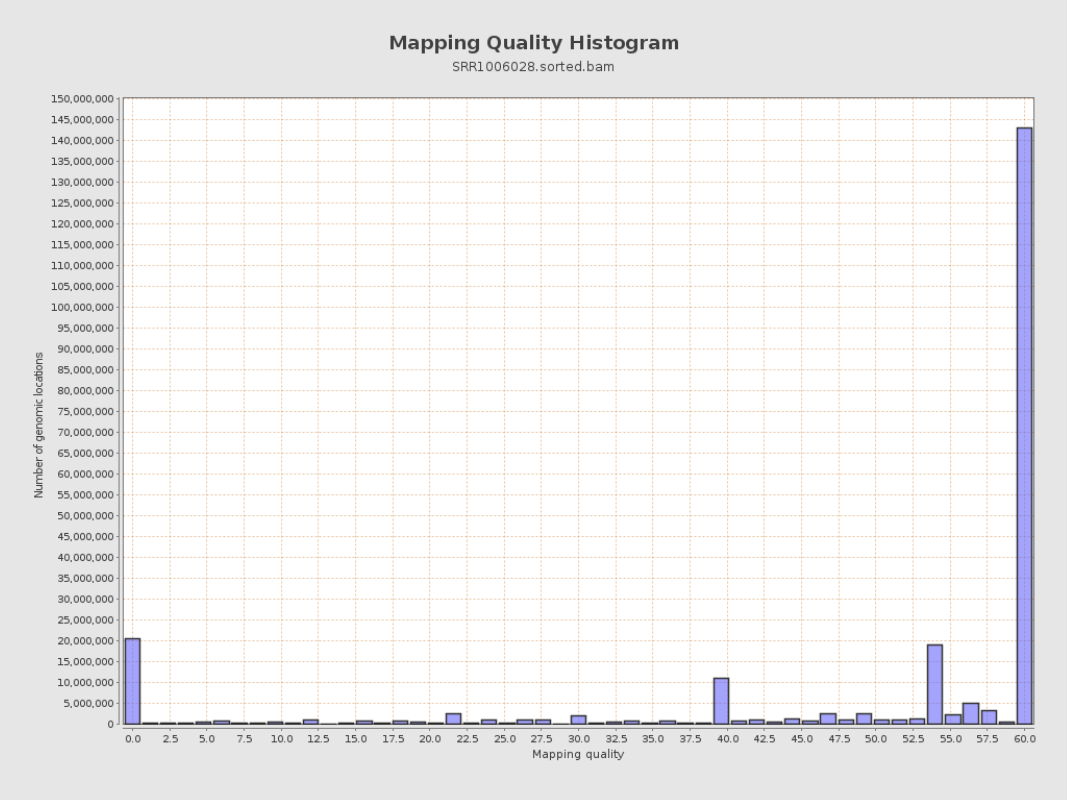
# 11. Results : Homopolymer Indels



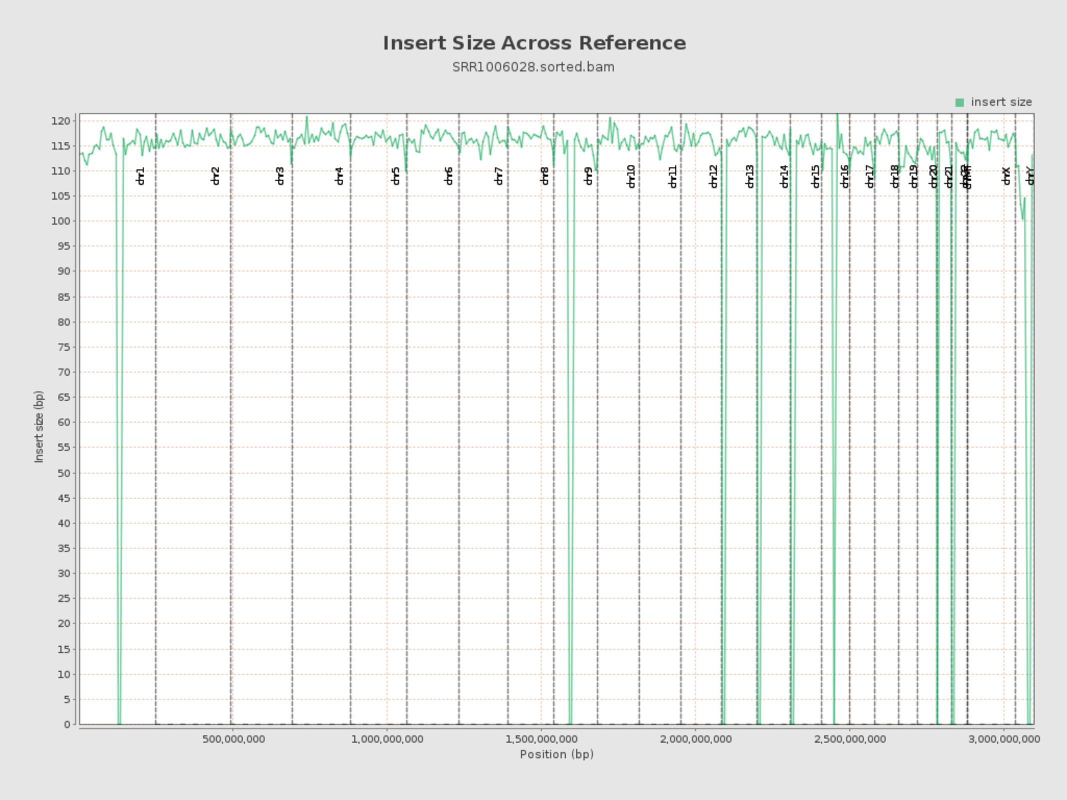
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram