# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/17 16:38:43*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006052.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_SRR1006052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006052_1.fastq.gz SRR1006052_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Apr 17 16:38:42 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1006052.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 9,966,024 |
| Mapped reads | 8,668,721 / 86.98% |
| Unmapped reads | 1,297,303 / 13.02% |
| Mapped paired reads | 8,668,721 / 86.98% |
| Mapped reads, first in pair | 4,407,650 / 44.23% |
| Mapped reads, second in pair | 4,261,071 / 42.76% |
| Mapped reads, both in pair | 7,923,736 / 79.51% |
| Mapped reads, singletons | 744,985 / 7.48% |
| Secondary alignments | 0 |
| Read min/max/mean length | 39 / 39 / 39 |
| Duplicated reads (estimated) | 868,039 / 8.71% |
| Duplication rate | 9.08% |
| Clipped reads | 748,708 / 7.51% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 87,392,357 / 26.13% |
| Number/percentage of C's | 75,725,124 / 22.64% |
| Number/percentage of T's | 90,983,157 / 27.21% |
| Number/percentage of G's | 80,315,378 / 24.02% |
| Number/percentage of N's | 15,945 / 0% |
| GC Percentage | 46.66% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.108 |
| Standard Deviation | 0.659 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.19 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 72,759.26 |
| Standard Deviation | 2,663,213.53 |
| P25/Median/P75 | 68 / 98 / 135 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.48% |
| Mismatches | 1,597,275 |
| Insertions | 11,421 |
| Mapped reads with at least one insertion | 0.13% |
| Deletions | 28,805 |
| Mapped reads with at least one deletion | 0.33% |
| Homopolymer indels | 44.26% |

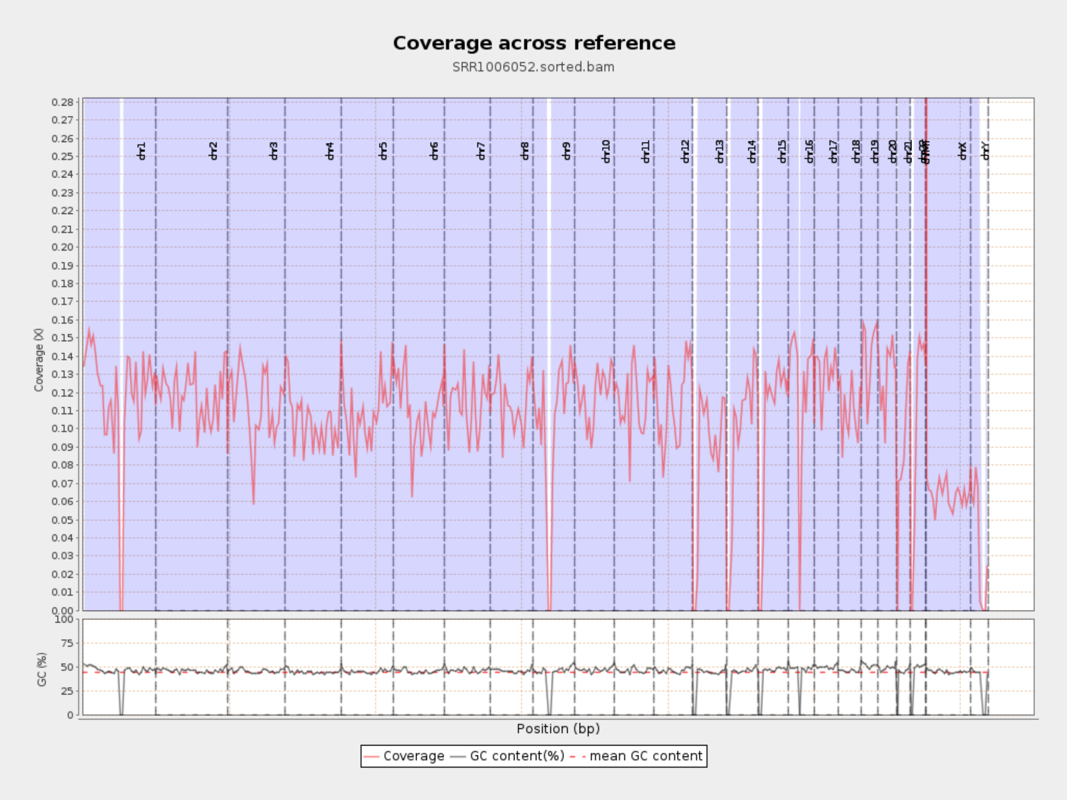
## 2.7. Chromosome stats

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

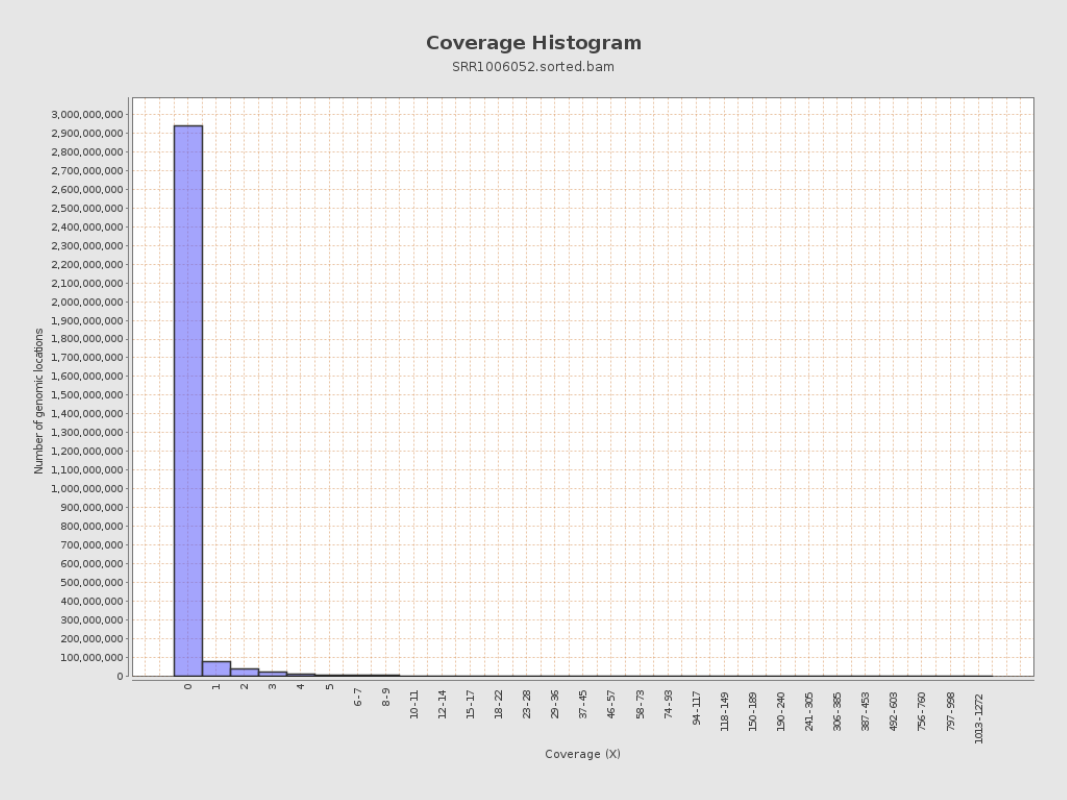
| | | | | |
|---|---|---|---|---|
| chr1 | 249250621 | 29117473 | 0.1168 | 0.6949 |
| chr2 | 243199373 | 28822411 | 0.1185 | 0.7147 |
| chr3 | 198022430 | 22323457 | 0.1127 | 0.6115 |
| chr4 | 191154276 | 19873449 | 0.104 | 0.6063 |
| chr5 | 180915260 | 19796652 | 0.1094 | 0.6015 |
| chr6 | 171115067 | 18845284 | 0.1101 | 0.664 |
| chr7 | 159138663 | 18325978 | 0.1152 | 0.7573 |
| chr8 | 146364022 | 16808761 | 0.1148 | 0.6998 |
| chr9 | 141213431 | 14387988 | 0.1019 | 0.6085 |
| chr10 | 135534747 | 16152053 | 0.1192 | 0.6523 |
| chr11 | 135006516 | 15617385 | 0.1157 | 0.9063 |
| chr12 | 133851895 | 15452644 | 0.1154 | 0.6248 |
| chr13 | 115169878 | 9906220 | 0.086 | 0.5373 |
| chr14 | 107349540 | 10296480 | 0.0959 | 0.579 |
| chr15 | 102531392 | 10365332 | 0.1011 | 0.5898 |
| chr16 | 90354753 | 10997209 | 0.1217 | 0.6929 |
| chr17 | 81195210 | 10768984 | 0.1326 | 0.713 |
| chr18 | 78077248 | 8533690 | 0.1093 | 0.6812 |
| chr19 | 59128983 | 8324499 | 0.1408 | 0.8381 |
| chr20 | 63025520 | 8147176 | 0.1293 | 0.6788 |
| chr21 | 48129895 | 4375117 | 0.0909 | 0.6193 |
| chr22 | 51304566 | 5075233 | 0.0989 | 0.6519 |
| chrMT | 16571 | 69751 | 4.2092 | 5.3738 |
| chrX | 155270560 | 9934674 | 0.064 | 0.4602 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 2150799 | 0.0362 | 0.3542 |

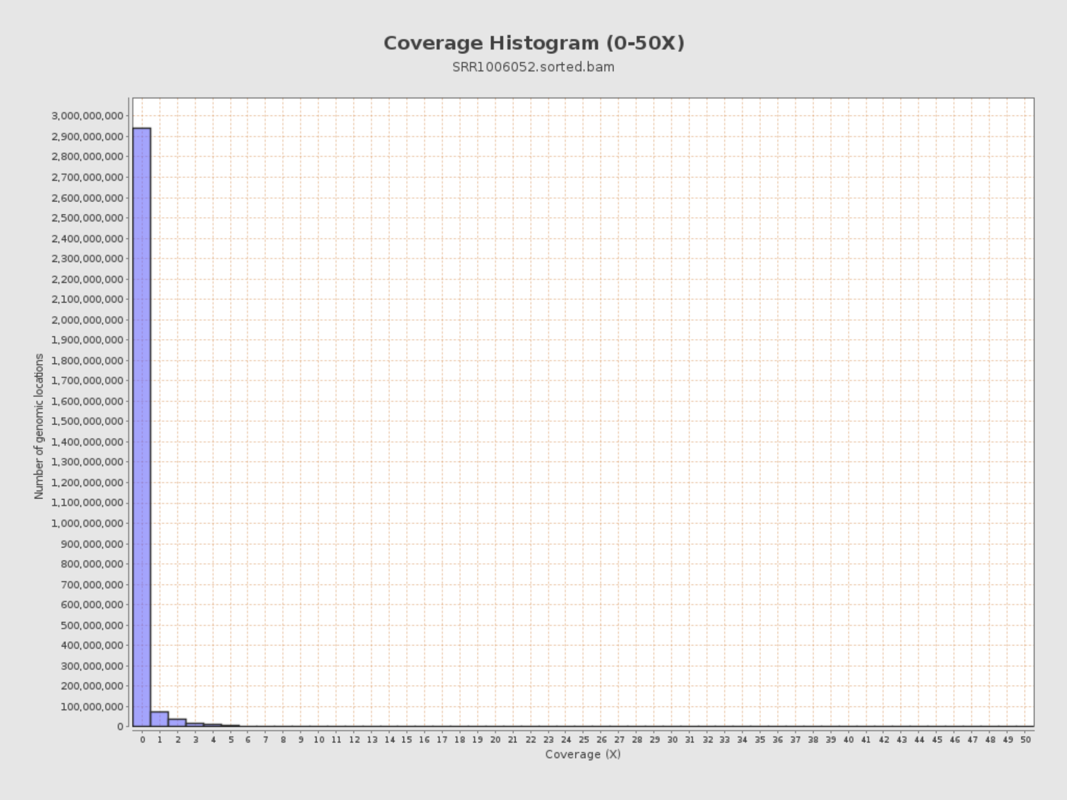
# 3. Results : Coverage across reference



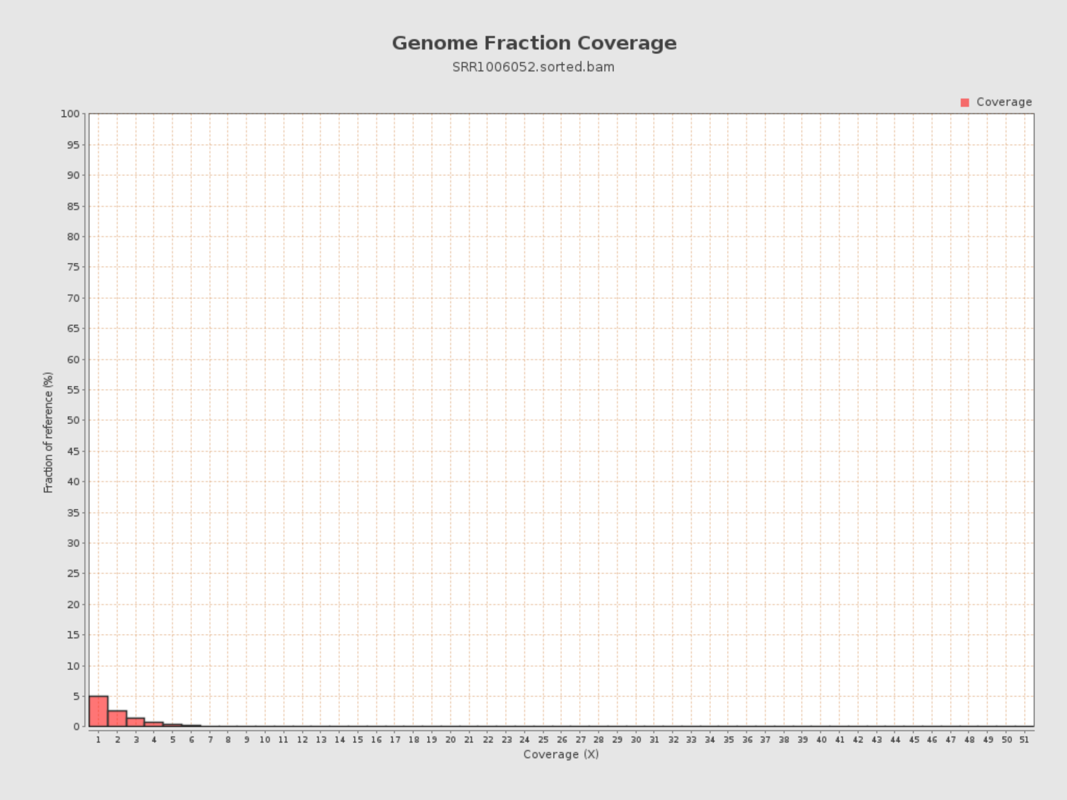
# 4. Results : Coverage Histogram



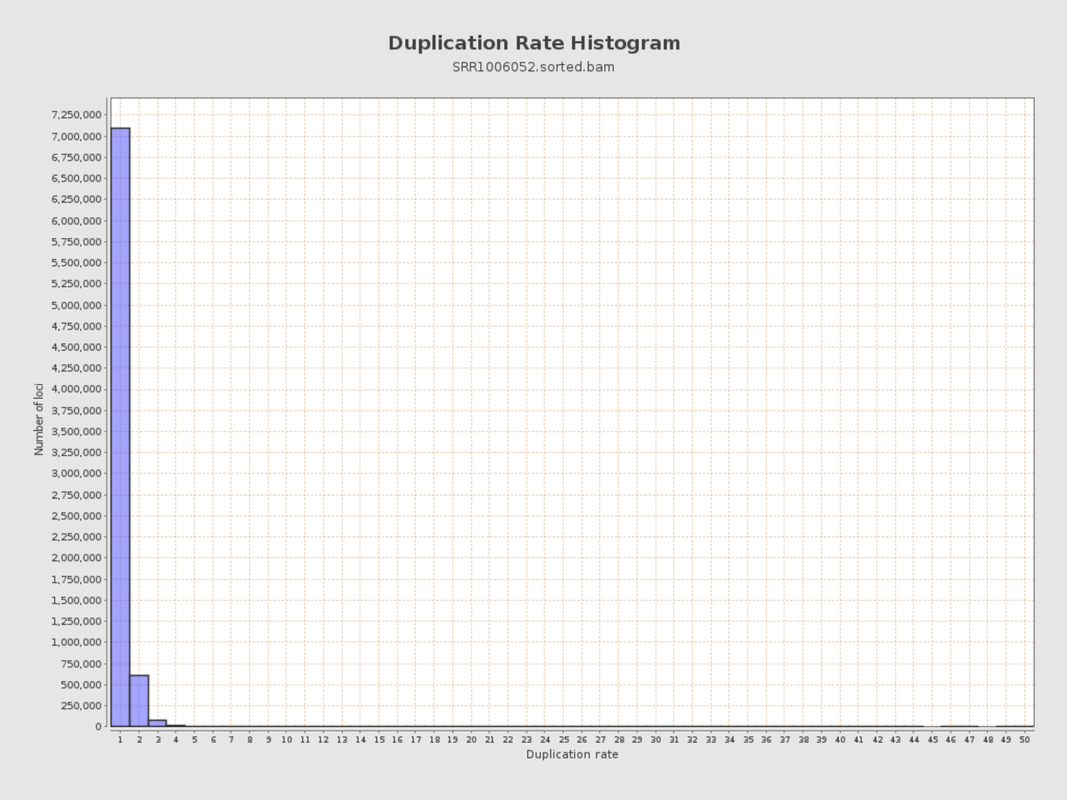
# 5. Results : Coverage Histogram (0-50X)



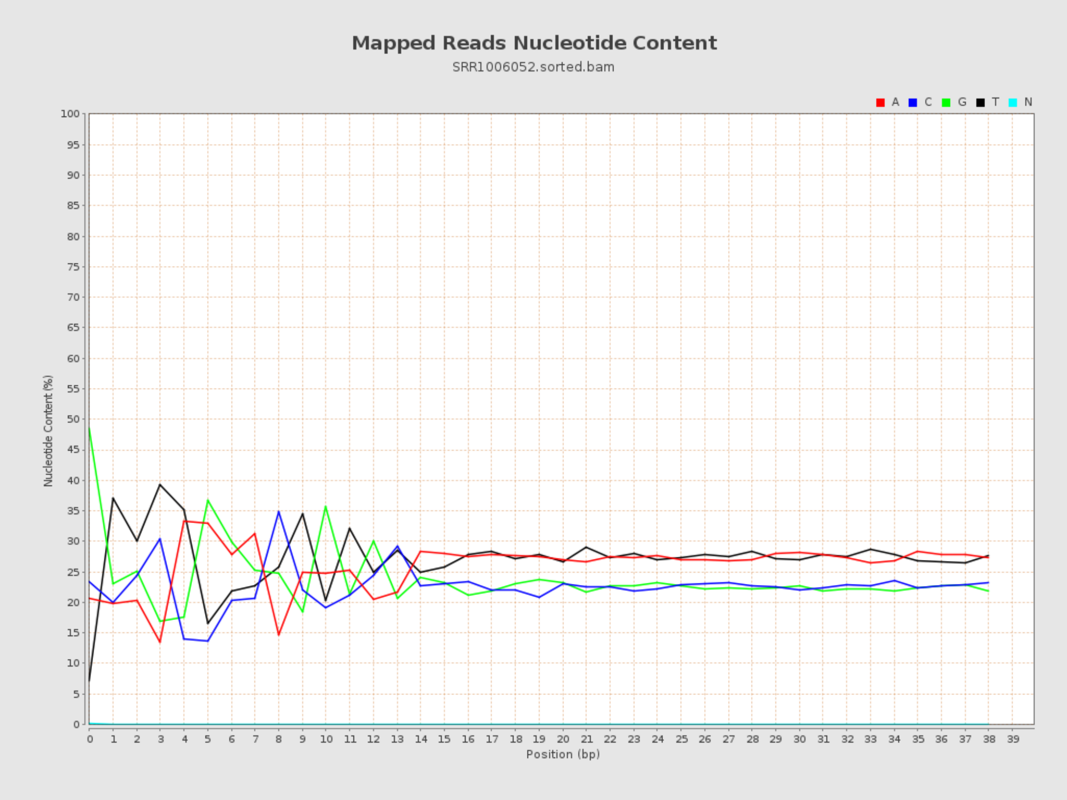
# 6. Results : Genome Fraction Coverage



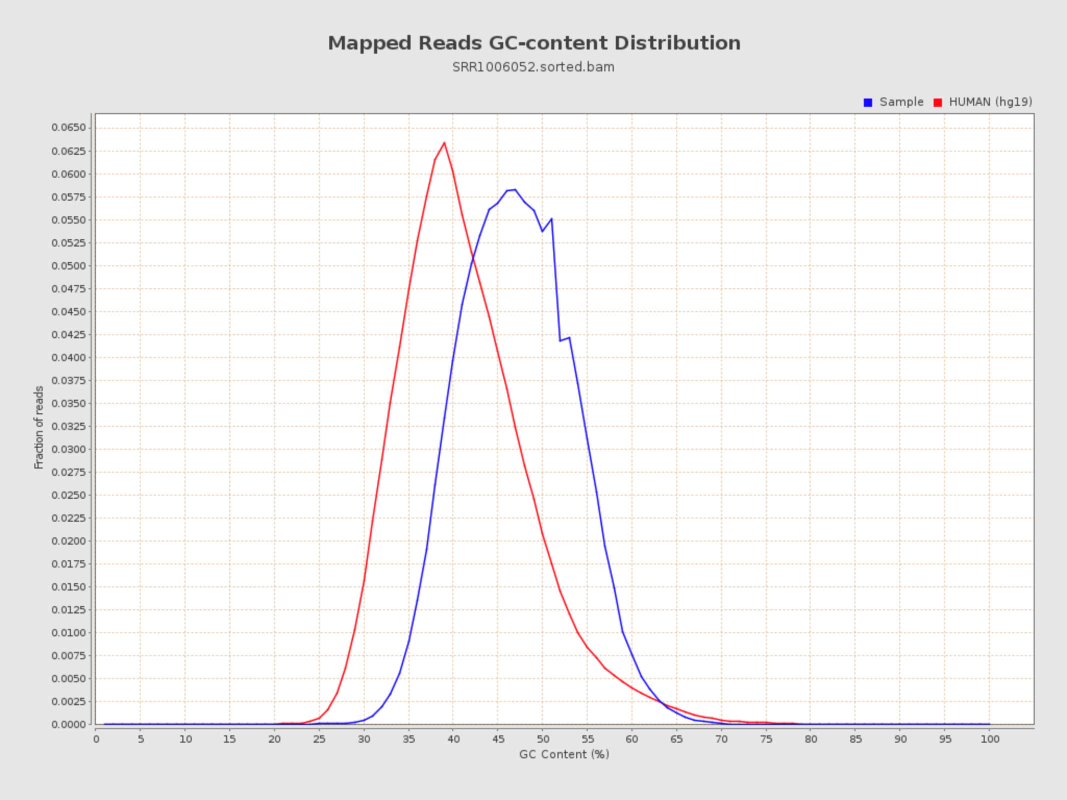
# 7. Results : Duplication Rate Histogram



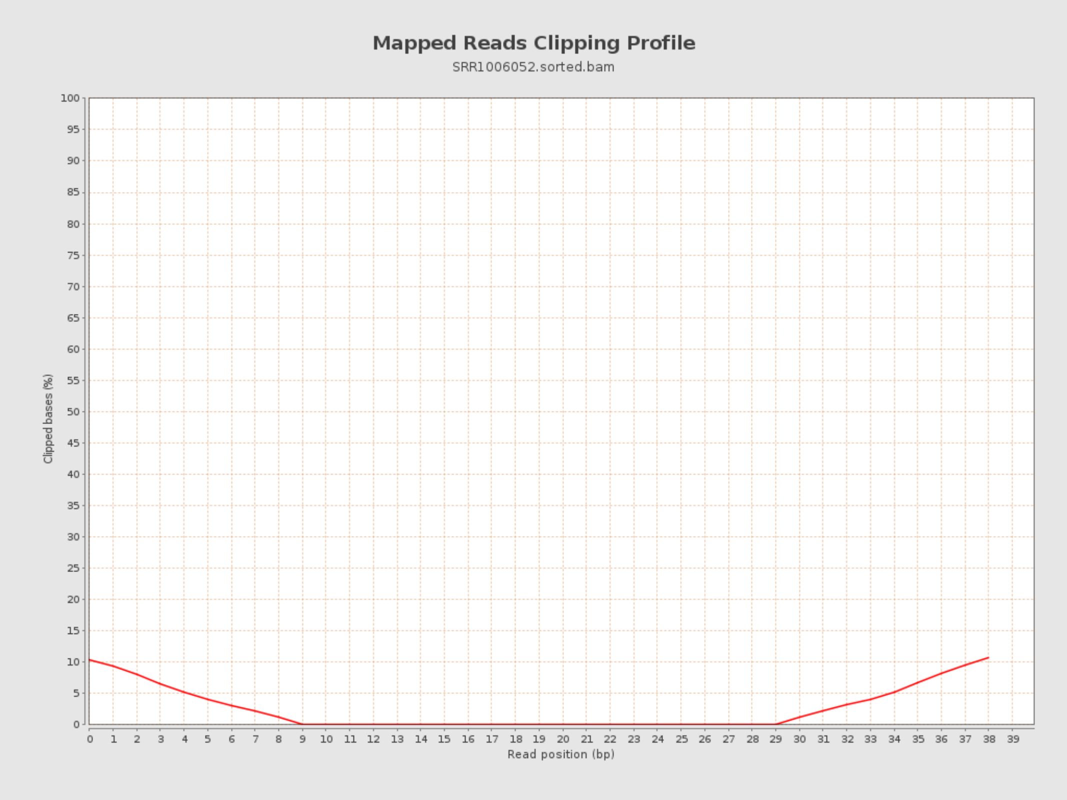
# 8. Results : Mapped Reads Nucleotide Content



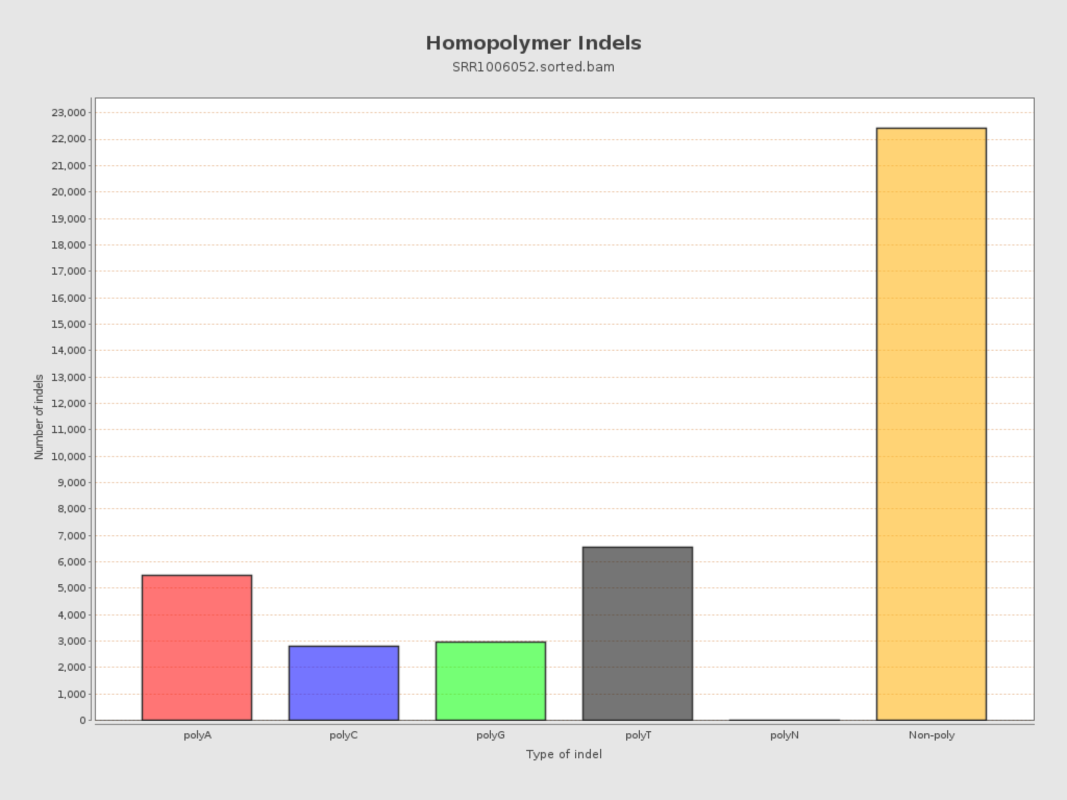
# 9. Results : Mapped Reads GC-content Distribution



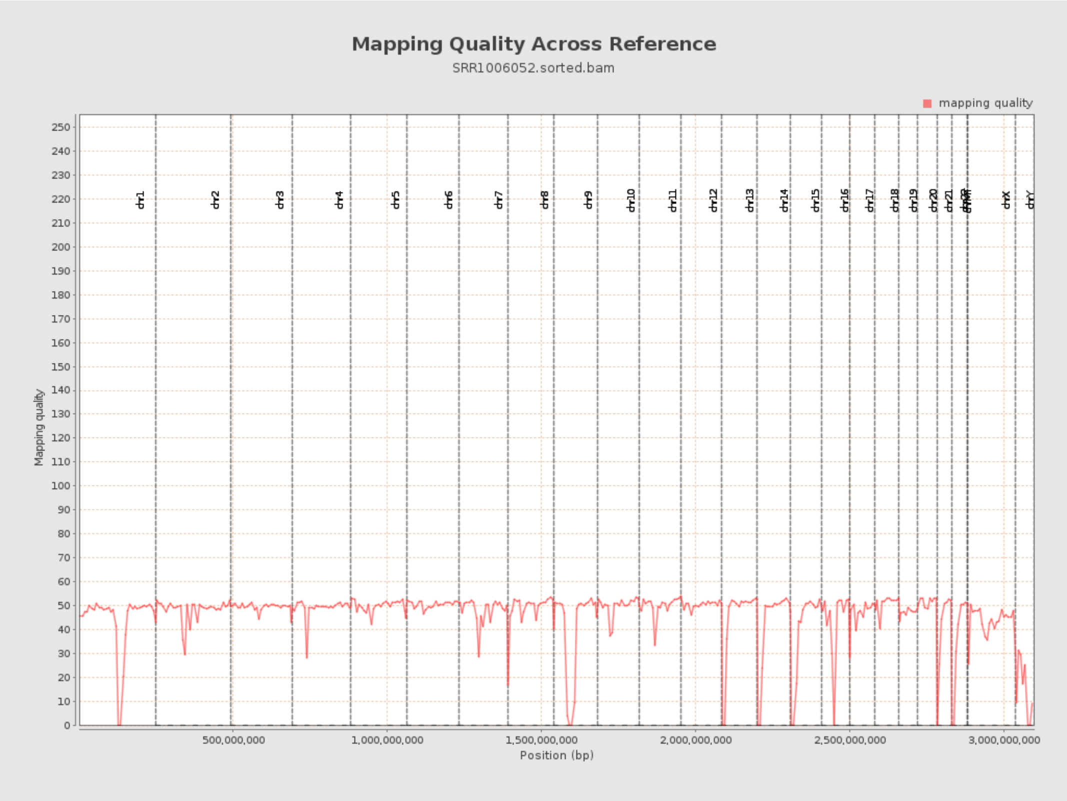
# 10. Results : Mapped Reads Clipping Profile



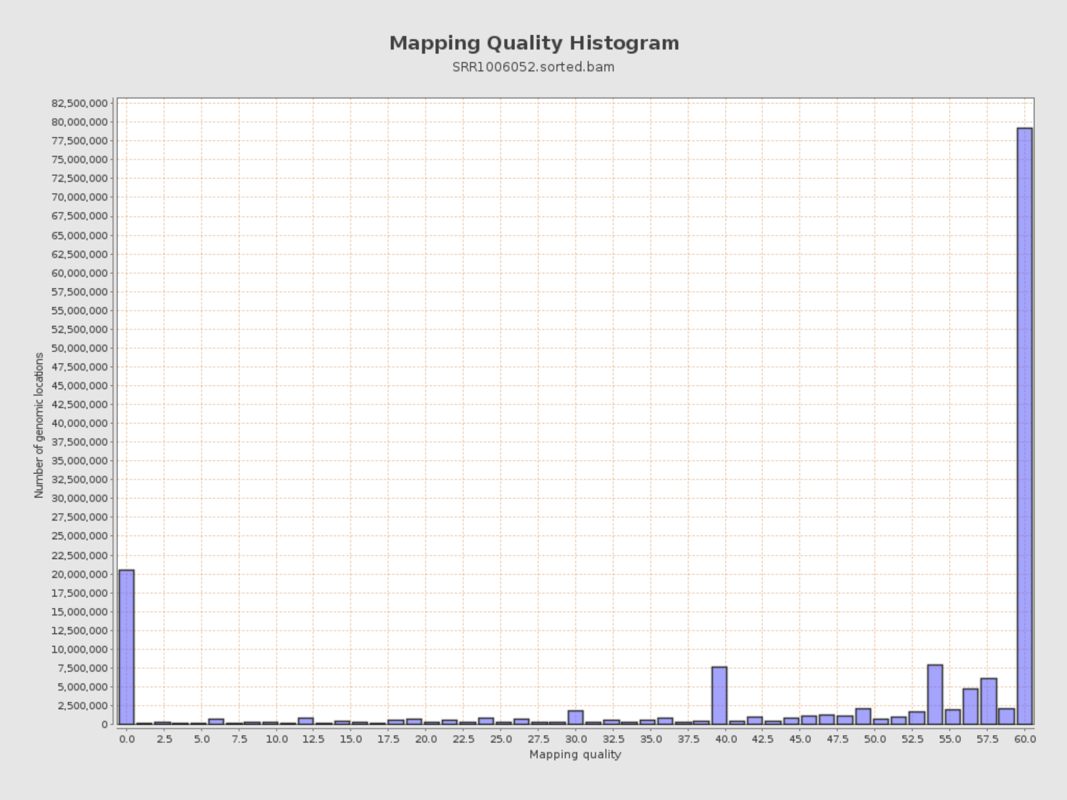
# 11. Results : Homopolymer Indels



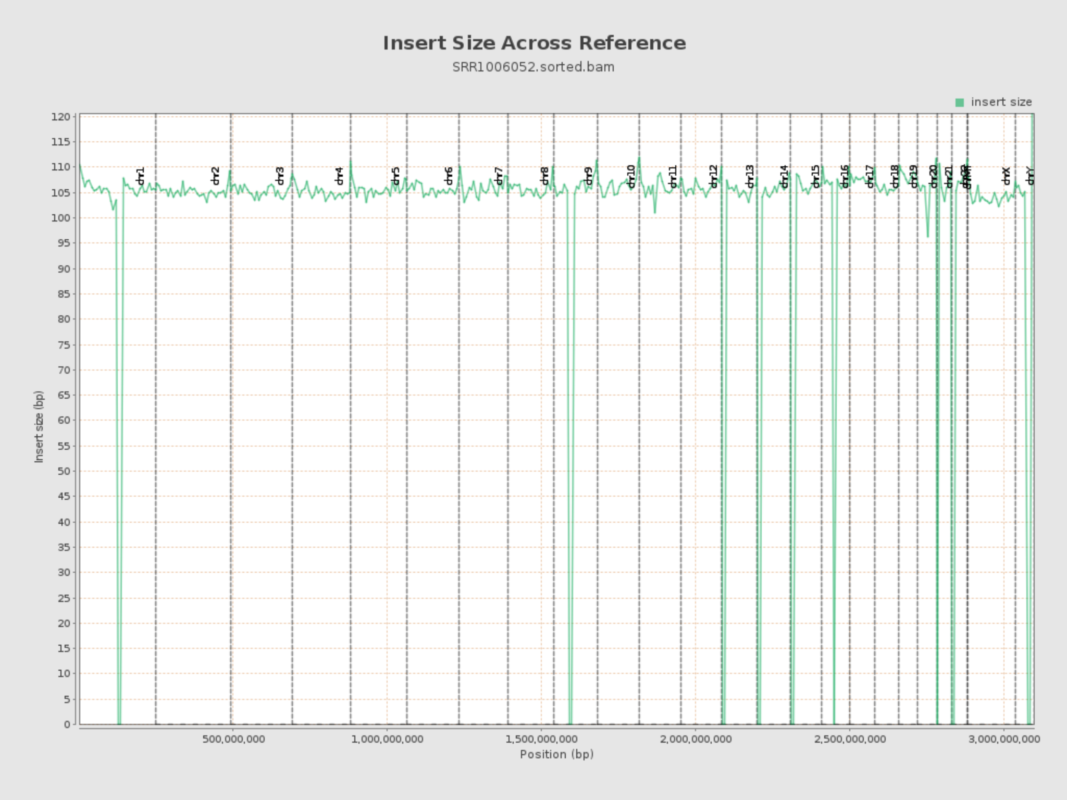
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram