# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/20 07:42:15*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR090142.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_SRR090142 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090142.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Apr 20 07:42:14 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR090142.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 25,129,587 |
| Mapped reads | 22,441,111 / 89.3% |
| Unmapped reads | 2,688,476 / 10.7% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 146,464 / 0.58% |
| Read min/max/mean length | 30 / 76 / 76.2 |
| Duplicated reads (estimated) | 3,269,146 / 13.01% |
| Duplication rate | 9.99% |
| Clipped reads | 11,728,520 / 46.67% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 396,044,840 / 27.14% |
| Number/percentage of C's | 268,041,143 / 18.37% |
| Number/percentage of T's | 457,888,327 / 31.38% |
| Number/percentage of G's | 336,693,207 / 23.07% |
| Number/percentage of N's | 479,040 / 0.03% |
| GC Percentage | 41.44% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.4715 |
| | |

| | |
|---|---|
| Standard Deviation | 4.0385 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.9 |

## 2.5. Mismatches and indels

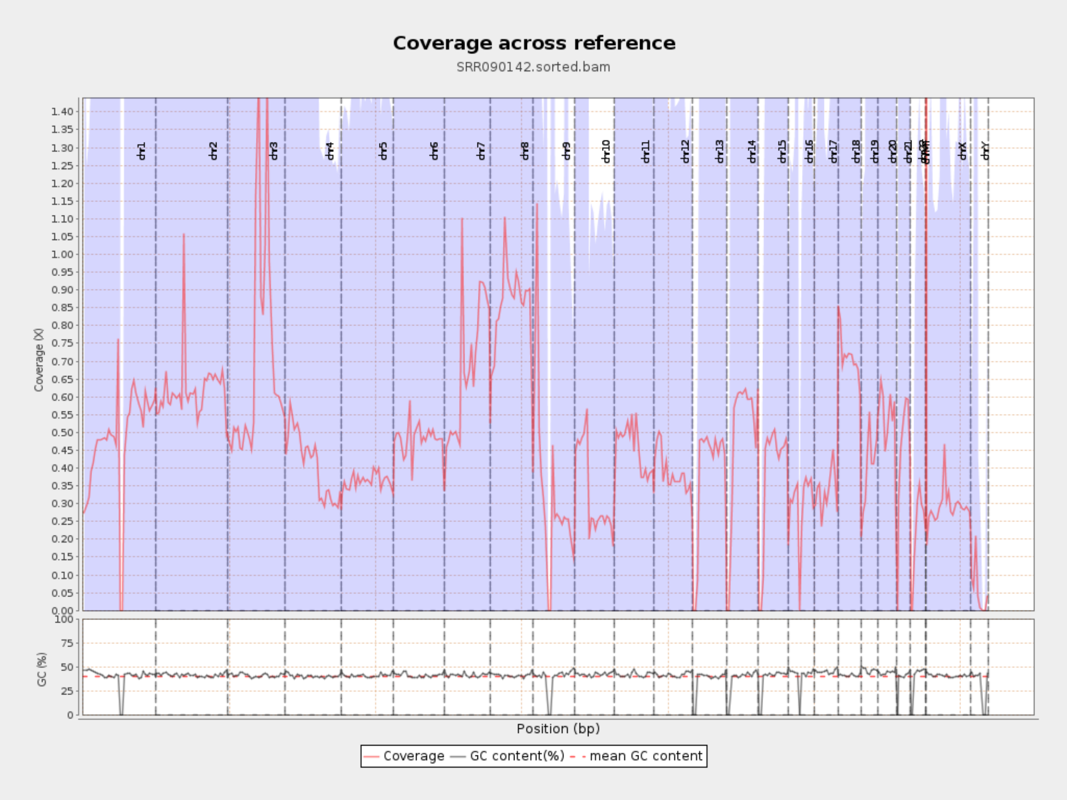
| | |
|---|---|
| General error rate | 0.78% |
| Mismatches | 11,181,878 |
| Insertions | 103,295 |
| Mapped reads with at least one insertion | 0.46% |
| Deletions | 315,501 |
| Mapped reads with at least one deletion | 1.39% |
| Homopolymer indels | 46.51% |

## 2.6. Chromosome stats

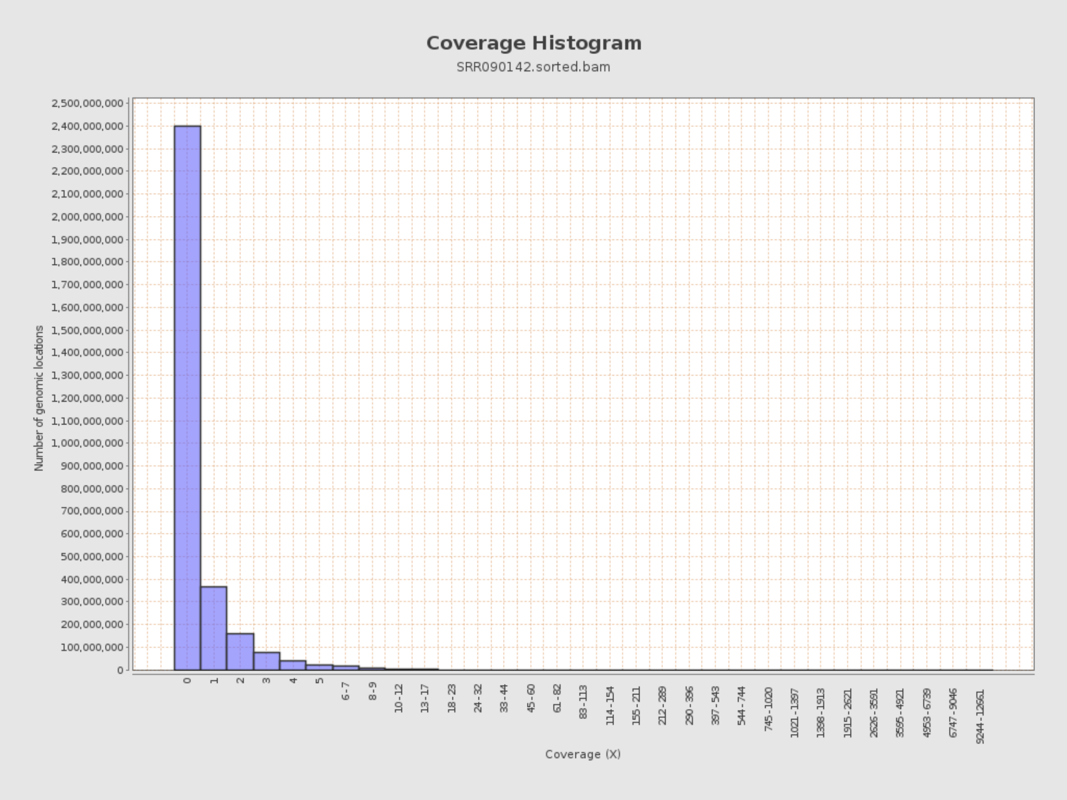
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 119256344 | 0.4785 | 7.0103 |
| chr2 | 243199373 | 151311682 | 0.6222 | 5.5356 |
| chr3 | 198022430 | 137214698 | 0.6929 | 1.6117 |
| chr4 | 191154276 | 78382292 | 0.41 | 1.524 |
| chr5 | 180915260 | 65674817 | 0.363 | 1.1534 |
| chr6 | 171115067 | 82841120 | 0.4841 | 1.8517 |
| chr7 | 159138663 | 108190428 | 0.6799 | 8.2484 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 125898261 | 0.8602 | 7.8361 |
| chr9 | 141213431 | 46621424 | 0.3301 | 3.4378 |
| chr10 | 135534747 | 44415938 | 0.3277 | 2.6916 |
| chr11 | 135006516 | 61188734 | 0.4532 | 2.9669 |
| chr12 | 133851895 | 51934531 | 0.388 | 1.2452 |
| chr13 | 115169878 | 44476269 | 0.3862 | 1.0916 |
| chr14 | 107349540 | 52342055 | 0.4876 | 1.5192 |
| chr15 | 102531392 | 38336638 | 0.3739 | 1.1858 |
| chr16 | 90354753 | 26388808 | 0.2921 | 1.1686 |
| chr17 | 81195210 | 27639973 | 0.3404 | 1.5688 |
| chr18 | 78077248 | 55790178 | 0.7146 | 5.1555 |
| chr19 | 59128983 | 24131887 | 0.4081 | 3.8783 |
| chr20 | 63025520 | 34536707 | 0.548 | 1.5395 |
| chr21 | 48129895 | 21506167 | 0.4468 | 1.465 |
| chr22 | 51304566 | 11208372 | 0.2185 | 0.8003 |
| chrMT | 16571 | 2007112 | 121.122 | 63.7052 |
| chrX | 155270560 | 45098469 | 0.2905 | 1.6233 |
| chrY | 59373566 | 3286495 | 0.0554 | 2.0011 |

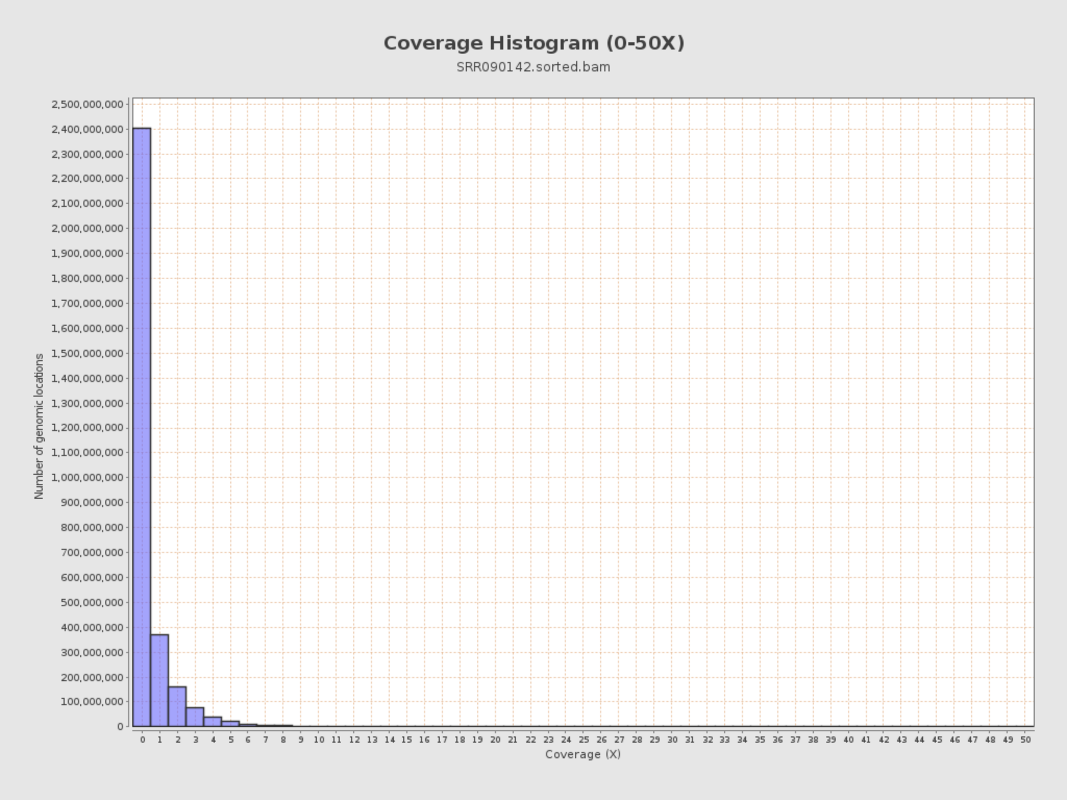
# 3. Results : Coverage across reference



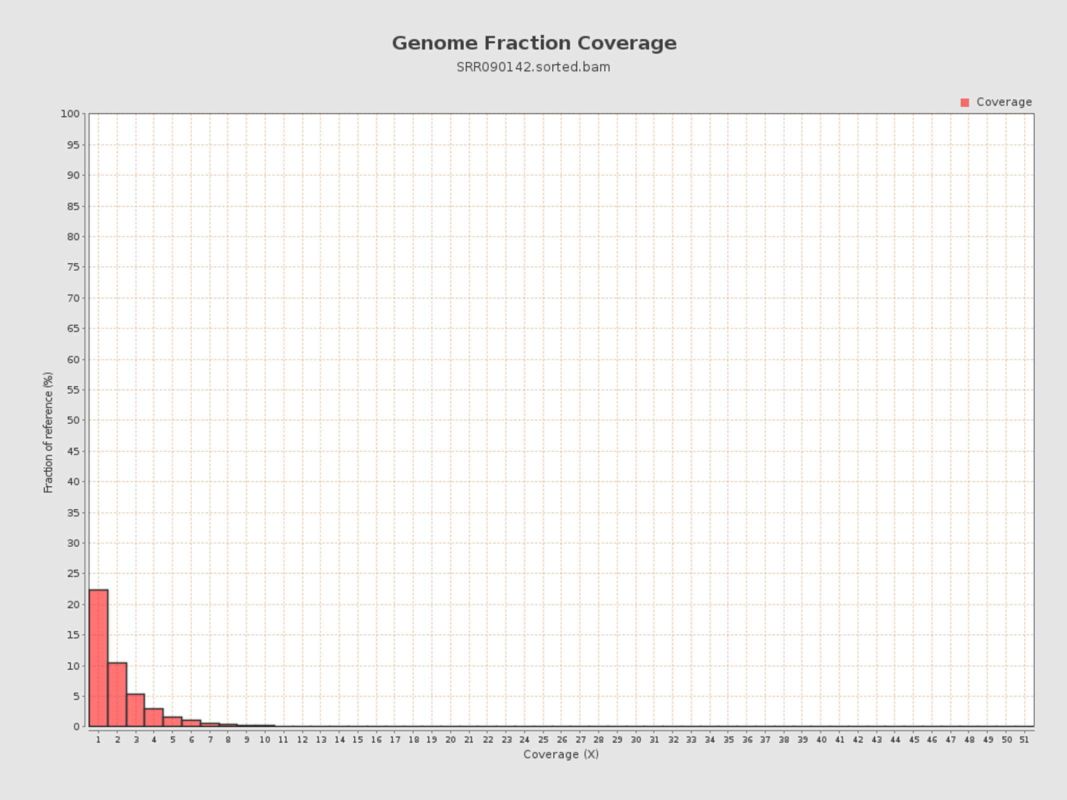
# 4. Results : Coverage Histogram



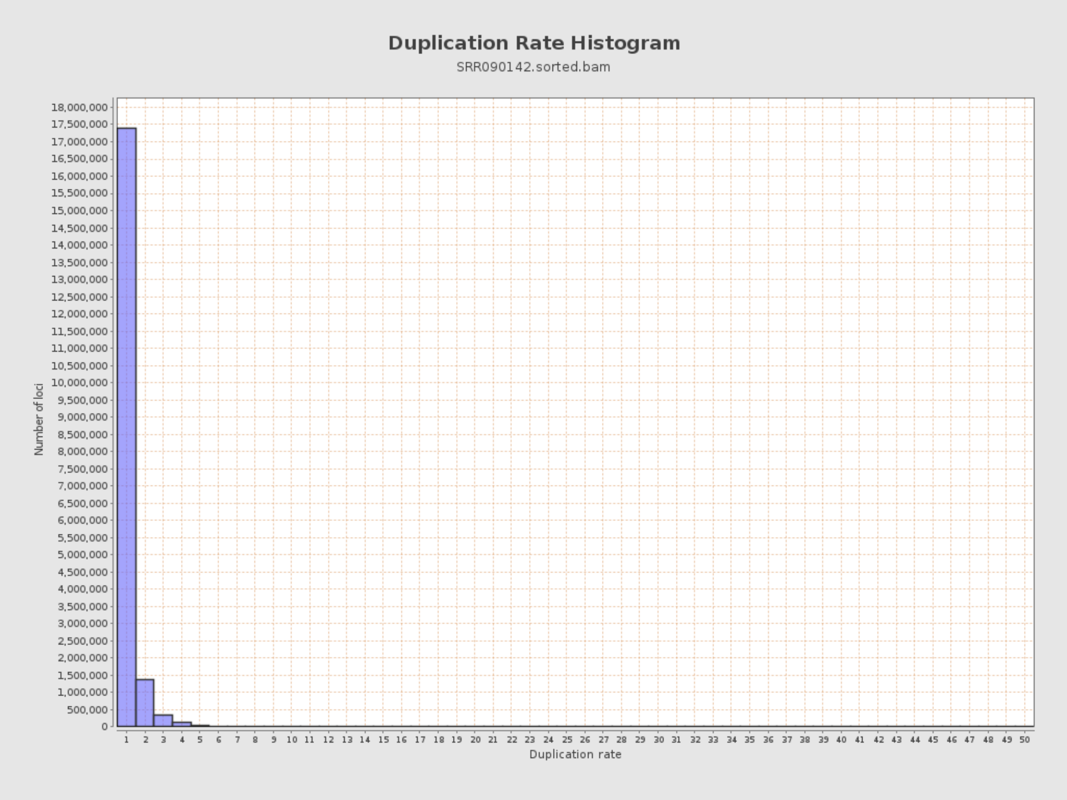
# 5. Results : Coverage Histogram (0-50X)



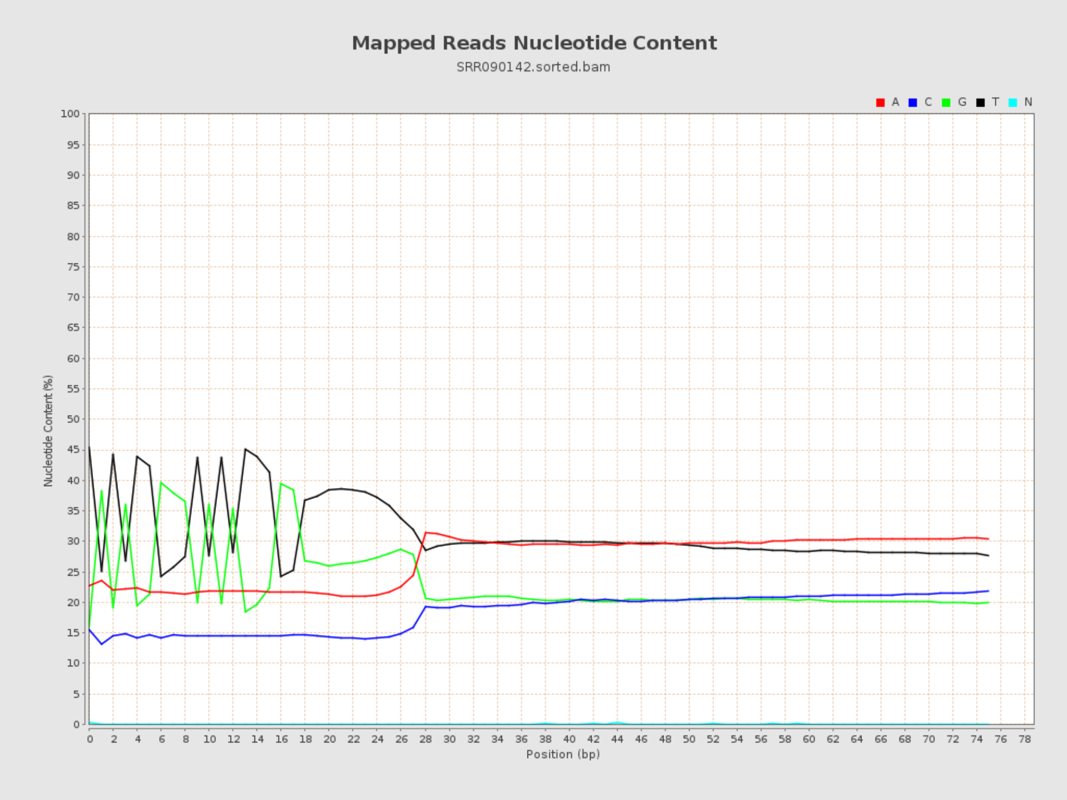
# 6. Results : Genome Fraction Coverage



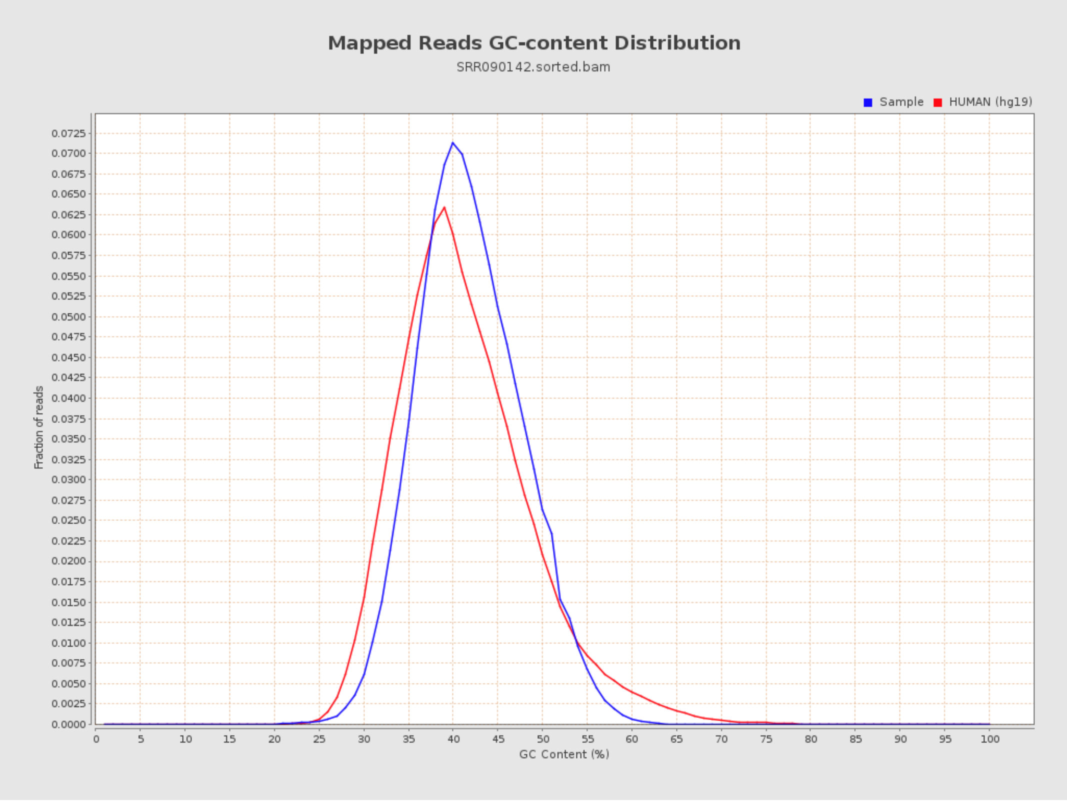
# 7. Results : Duplication Rate Histogram



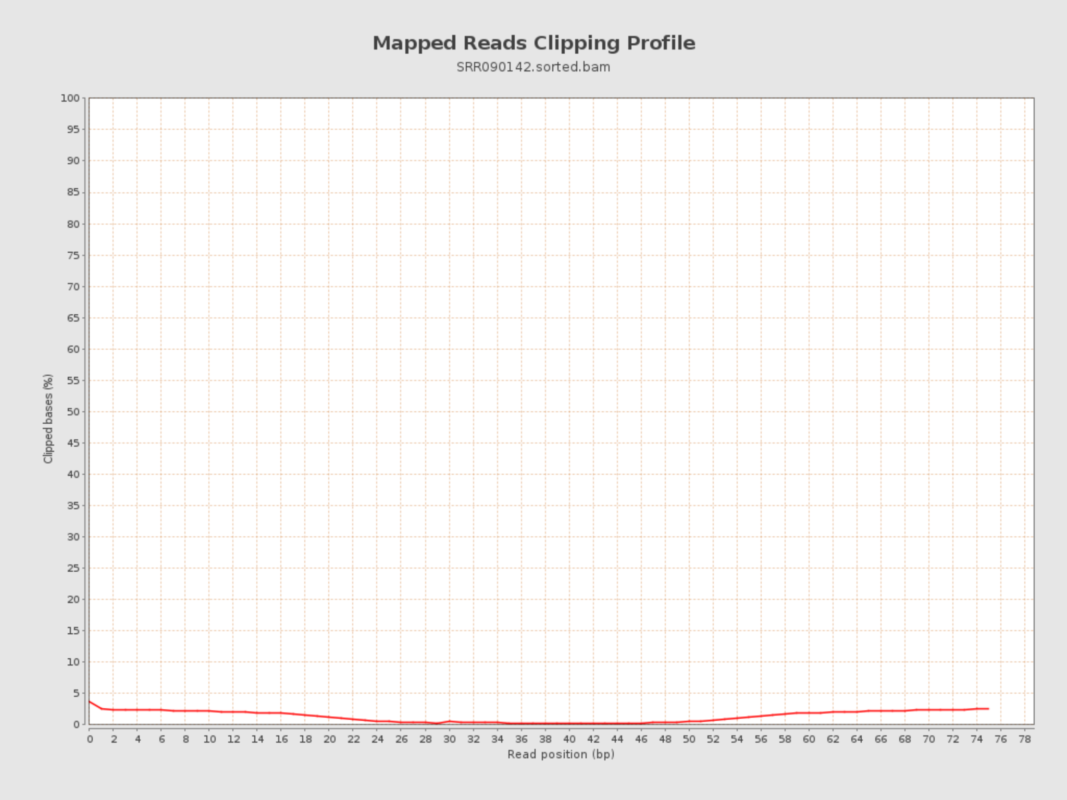
# 8. Results : Mapped Reads Nucleotide Content



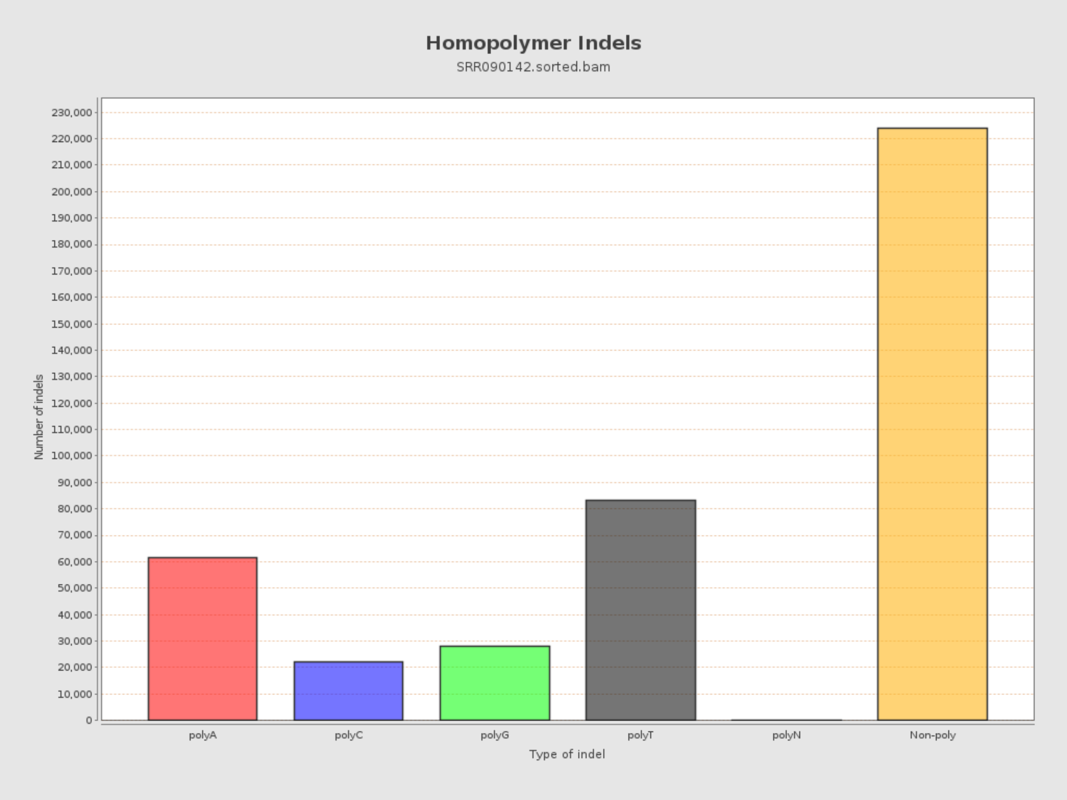
# 9. Results : Mapped Reads GC-content Distribution



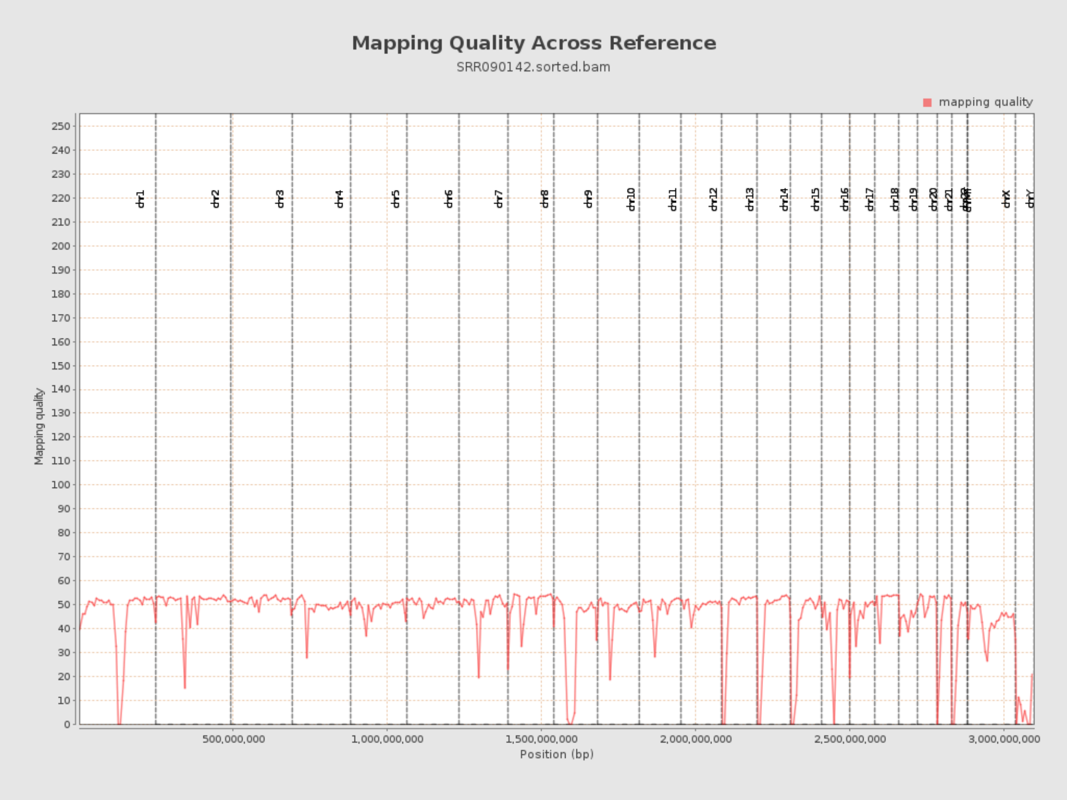
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram