# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/19 18:20:36*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR089610.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_SRR089610 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089610.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Apr 19 18:20:35 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR089610.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 16,682,719 |
| Mapped reads | 13,798,085 / 82.71% |
| Unmapped reads | 2,884,634 / 17.29% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 597 / 0% |
| Read min/max/mean length | 30 / 48 / 48 |
| Duplicated reads (estimated) | 3,232,847 / 19.38% |
| Duplication rate | 15.27% |
| Clipped reads | 1,186,620 / 7.11% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 188,497,691 / 28.95% |
| Number/percentage of C's | 137,144,809 / 21.06% |
| Number/percentage of T's | 186,301,957 / 28.61% |
| Number/percentage of G's | 139,263,196 / 21.39% |
| Number/percentage of N's | 11,042 / 0% |
| GC Percentage | 42.44% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.2104 |
| | |

| | |
|---|---|
| Standard Deviation | 1.4167 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.71 |

## 2.5. Mismatches and indels

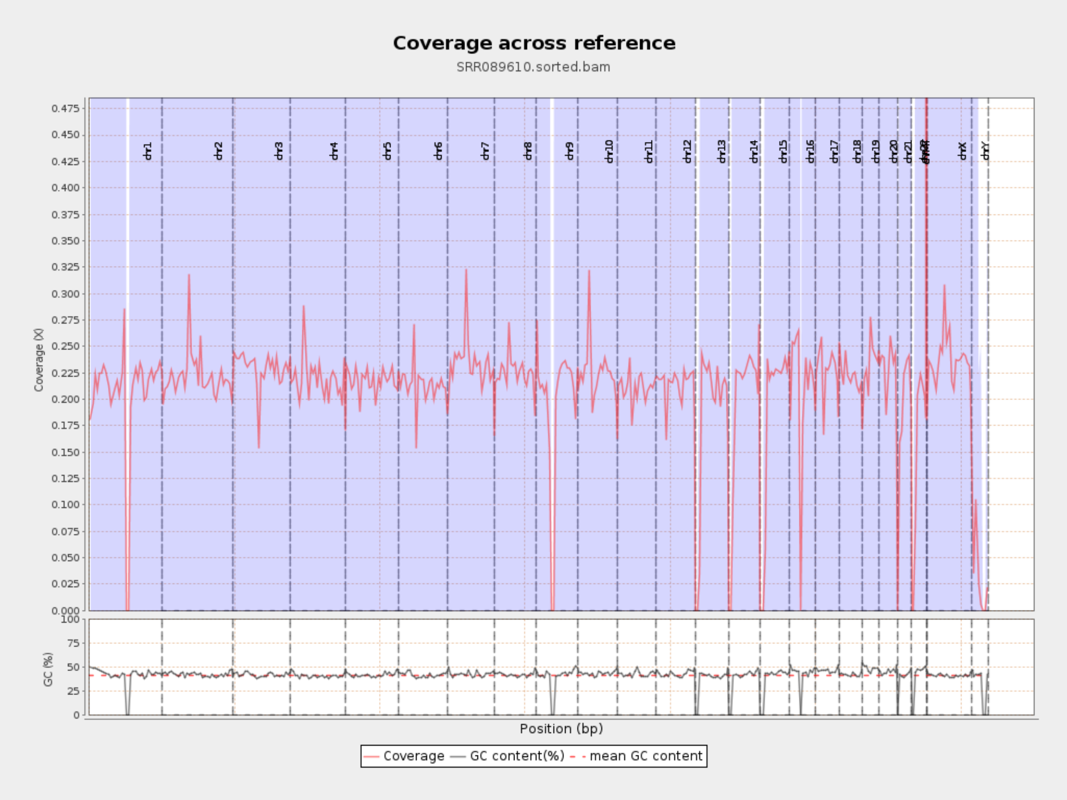
| | |
|---|---|
| General error rate | 0.45% |
| Mismatches | 2,922,213 |
| Insertions | 25,886 |
| Mapped reads with at least one insertion | 0.19% |
| Deletions | 80,344 |
| Mapped reads with at least one deletion | 0.58% |
| Homopolymer indels | 45.42% |

## 2.6. Chromosome stats

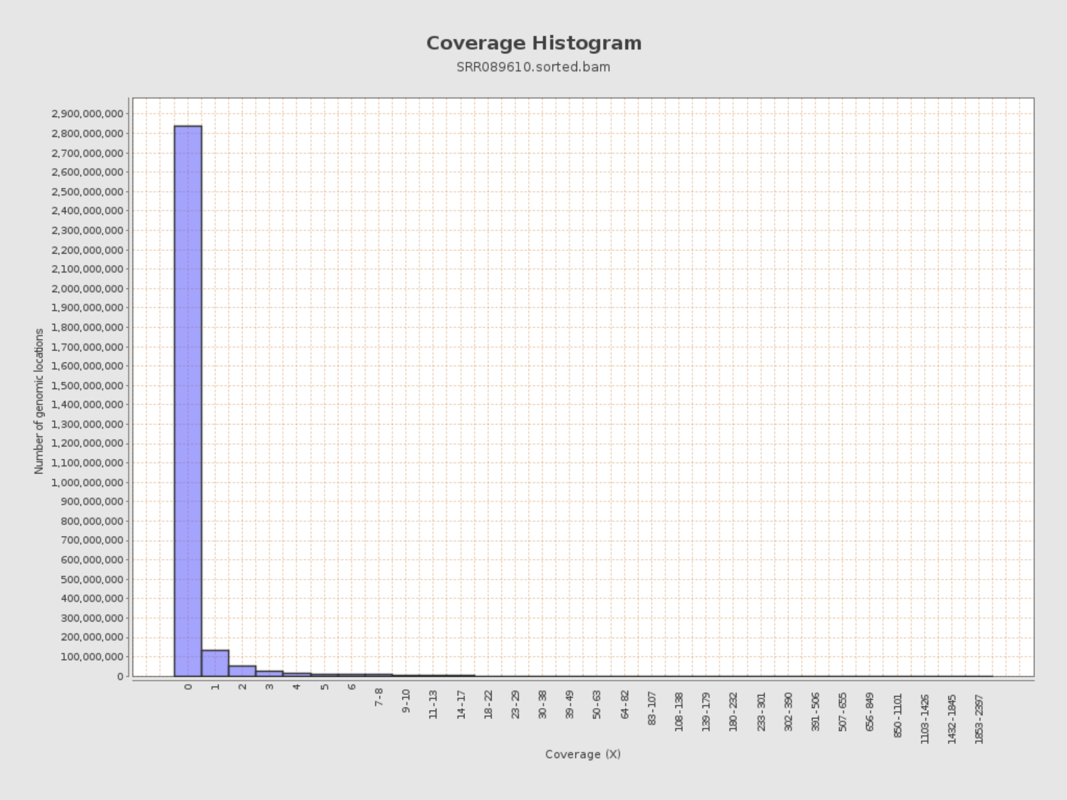
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 51015655 | 0.2047 | 2.0424 |
| chr2 | 243199373 | 54000329 | 0.222 | 1.7366 |
| chr3 | 198022430 | 45304083 | 0.2288 | 1.0948 |
| chr4 | 191154276 | 41852275 | 0.2189 | 1.142 |
| chr5 | 180915260 | 39361163 | 0.2176 | 1.0646 |
| chr6 | 171115067 | 36564951 | 0.2137 | 1.2231 |
| chr7 | 159138663 | 37567069 | 0.2361 | 1.9825 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 32962594 | 0.2252 | 1.6462 |
| chr9 | 141213431 | 26901005 | 0.1905 | 1.2383 |
| chr10 | 135534747 | 30623734 | 0.2259 | 1.4654 |
| chr11 | 135006516 | 28377130 | 0.2102 | 1.3094 |
| chr12 | 133851895 | 28618004 | 0.2138 | 1.0944 |
| chr13 | 115169878 | 20930679 | 0.1817 | 0.9851 |
| chr14 | 107349540 | 20396412 | 0.19 | 1.161 |
| chr15 | 102531392 | 18810198 | 0.1835 | 0.9923 |
| chr16 | 90354753 | 18950778 | 0.2097 | 1.1301 |
| chr17 | 81195210 | 18305814 | 0.2255 | 1.2457 |
| chr18 | 78077248 | 17387107 | 0.2227 | 1.8256 |
| chr19 | 59128983 | 13799940 | 0.2334 | 1.9823 |
| chr20 | 63025520 | 14384871 | 0.2282 | 1.1737 |
| chr21 | 48129895 | 8930911 | 0.1856 | 1.126 |
| chr22 | 51304566 | 7508373 | 0.1463 | 0.8876 |
| chrMT | 16571 | 76491 | 4.616 | 5.4649 |
| chrX | 155270560 | 36742633 | 0.2366 | 1.2959 |
| chrY | 59373566 | 1966342 | 0.0331 | 0.6716 |

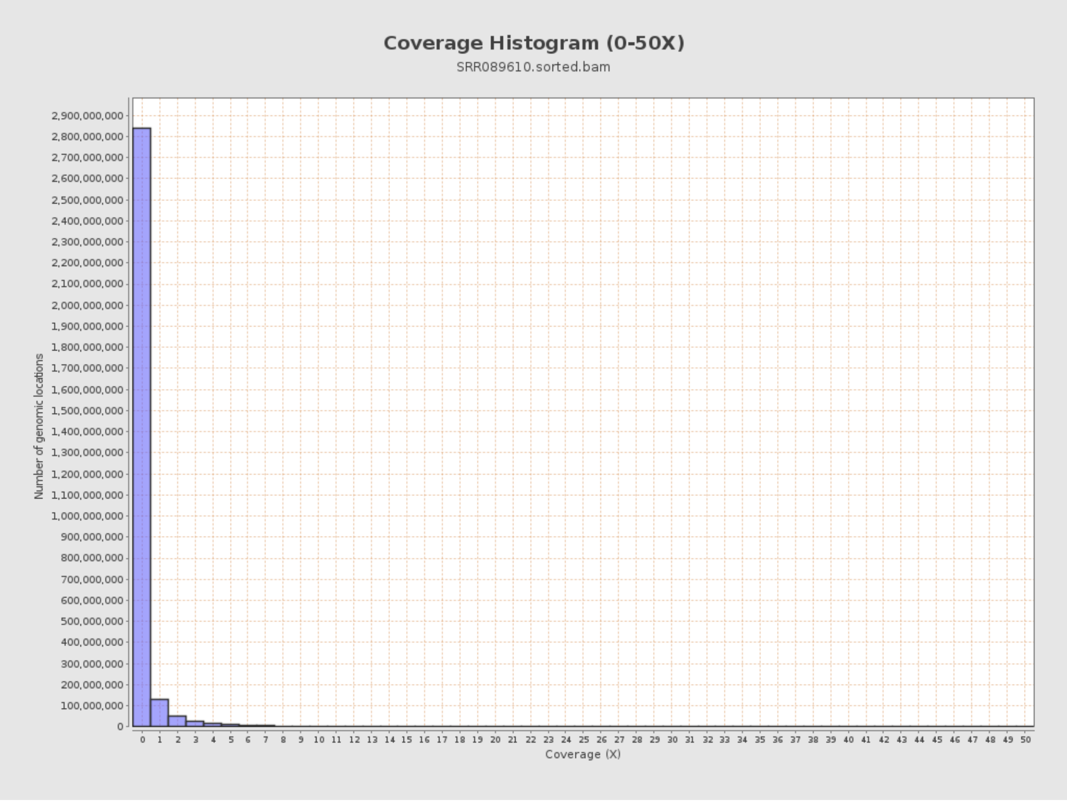
# 3. Results : Coverage across reference



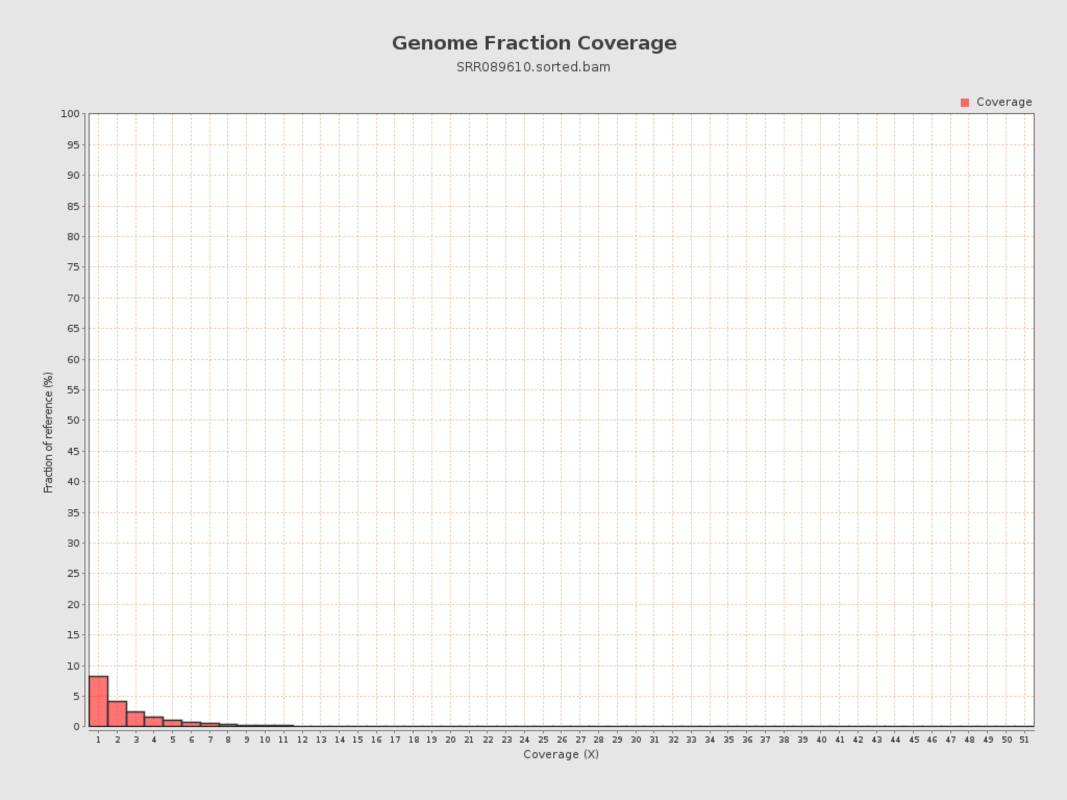
# 4. Results : Coverage Histogram



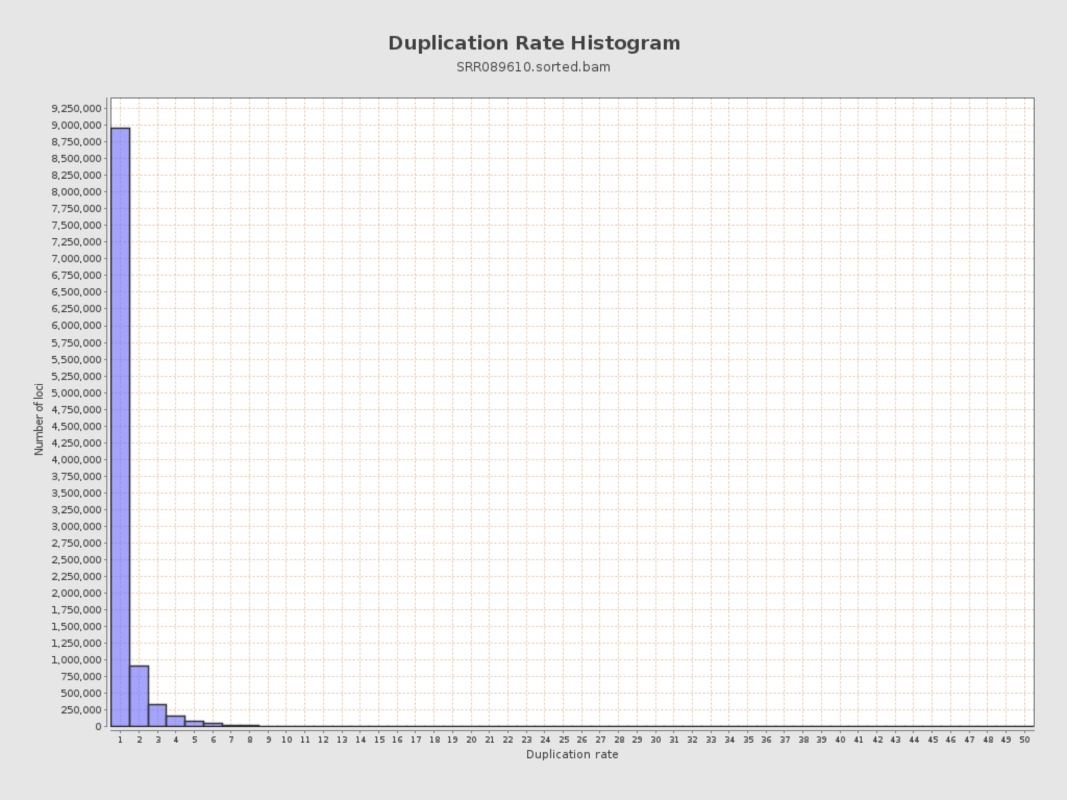
# 5. Results : Coverage Histogram (0-50X)



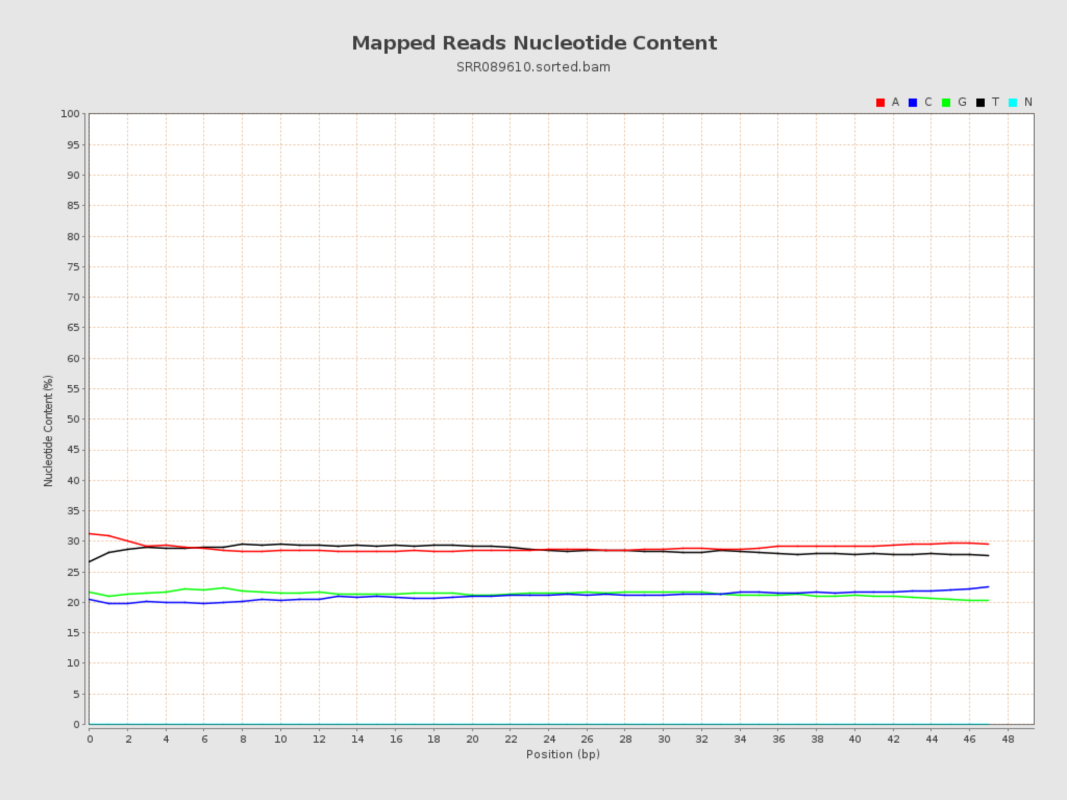
# 6. Results : Genome Fraction Coverage



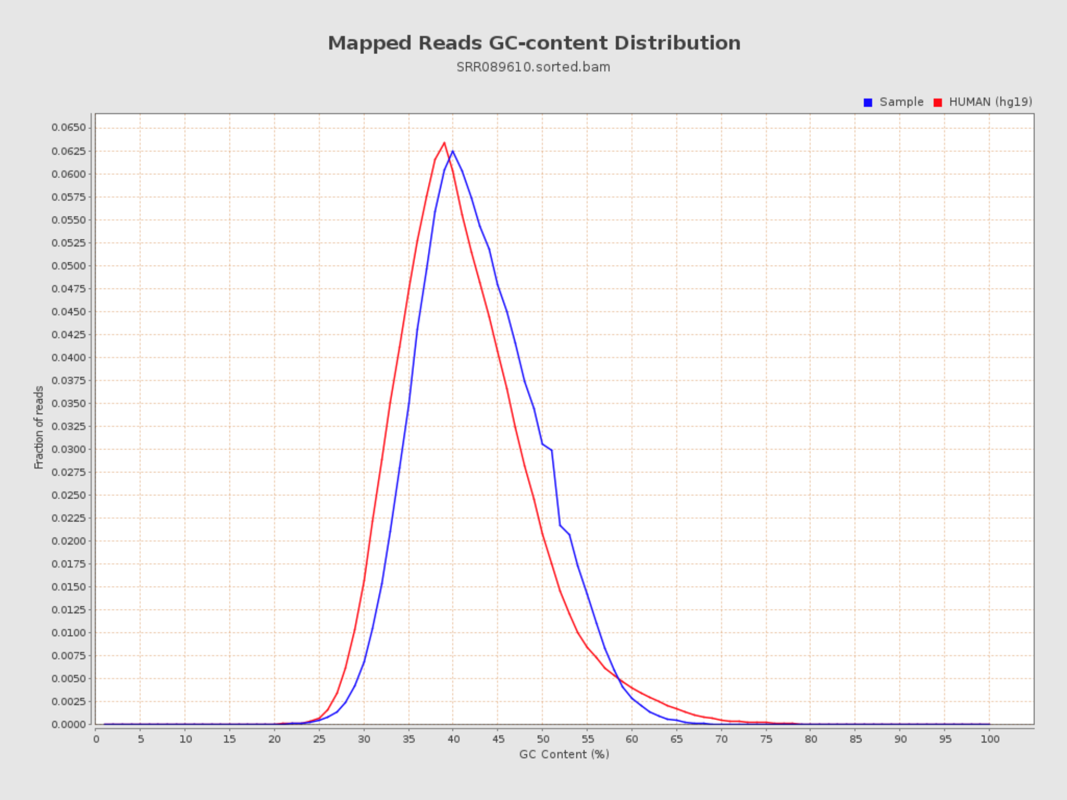
# 7. Results : Duplication Rate Histogram



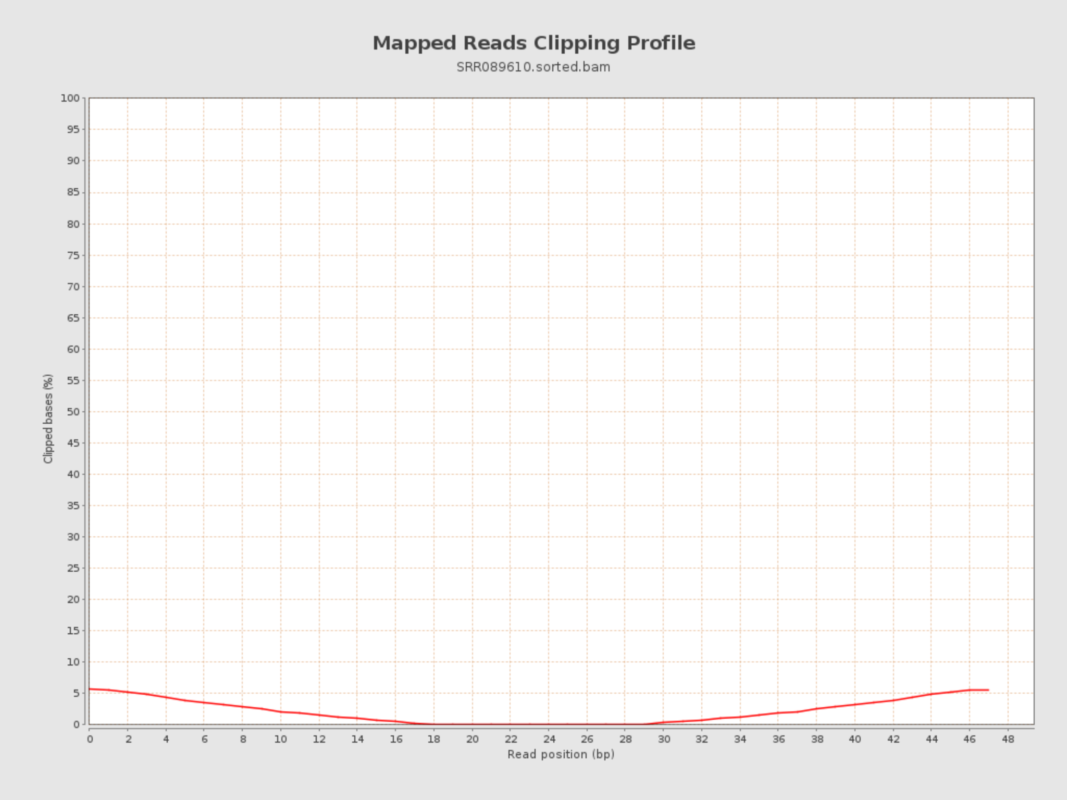
# 8. Results : Mapped Reads Nucleotide Content



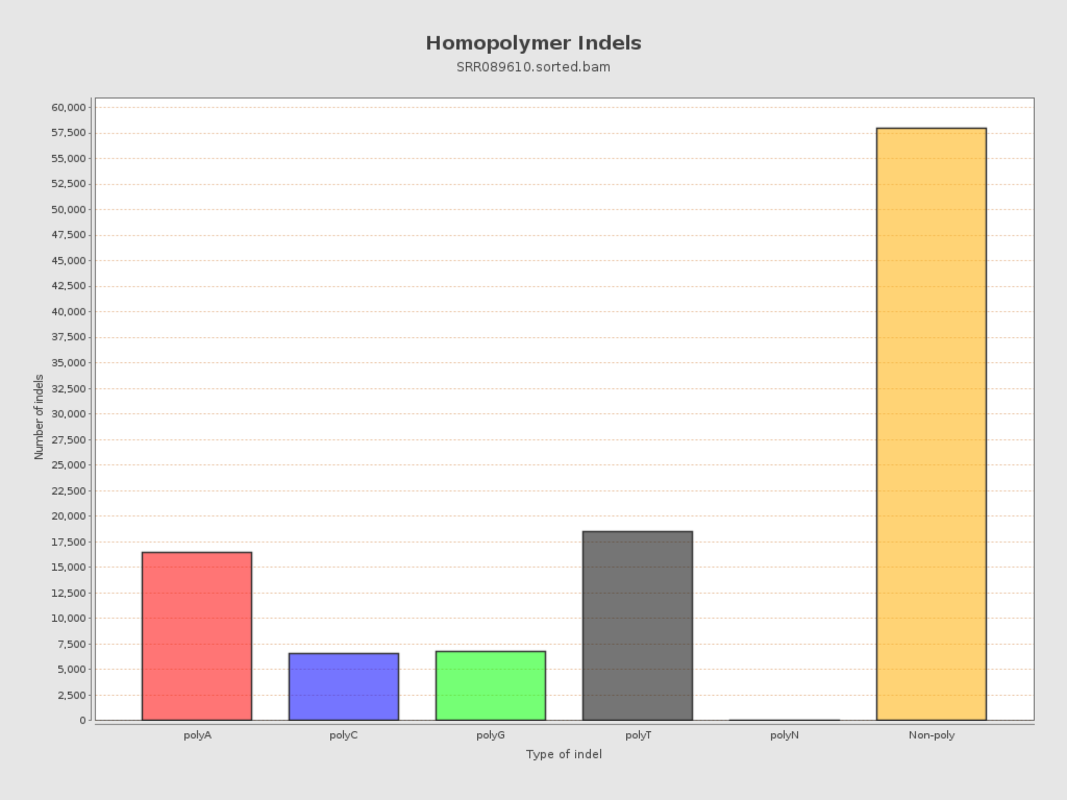
# 9. Results : Mapped Reads GC-content Distribution



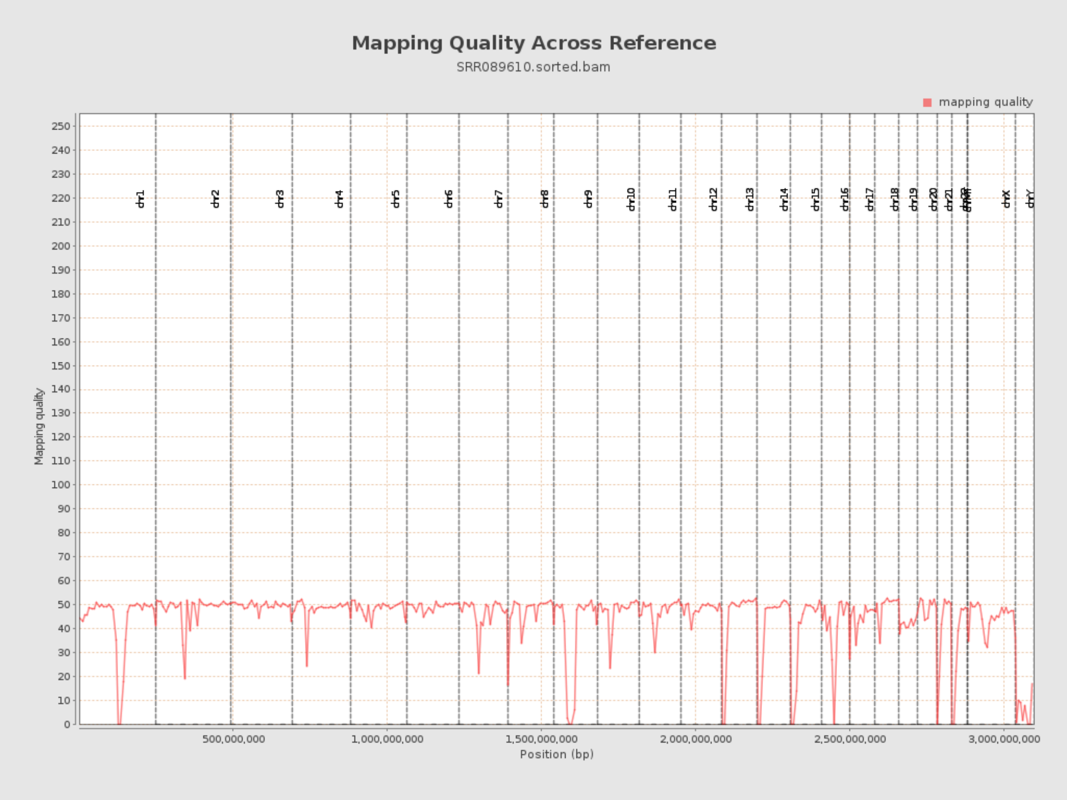
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram