# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/19 17:45:17*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR089607.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_SRR089607 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089607.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Apr 19 17:45:17 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR089607.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 20,713,429 |
| Mapped reads | 17,606,419 / 85% |
| Unmapped reads | 3,107,010 / 15% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 627 / 0% |
| Read min/max/mean length | 30 / 48 / 48 |
| Duplicated reads (estimated) | 3,383,967 / 16.34% |
| Duplication rate | 13.18% |
| Clipped reads | 2,102,397 / 10.15% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 239,704,188 / 29.03% |
| Number/percentage of C's | 178,241,760 / 21.59% |
| Number/percentage of T's | 231,724,094 / 28.07% |
| Number/percentage of G's | 175,947,112 / 21.31% |
| Number/percentage of N's | 17,825 / 0% |
| GC Percentage | 42.9% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.2668 |
| | |

| | |
|---|---|
| Standard Deviation | 1.6267 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.48 |

## 2.5. Mismatches and indels

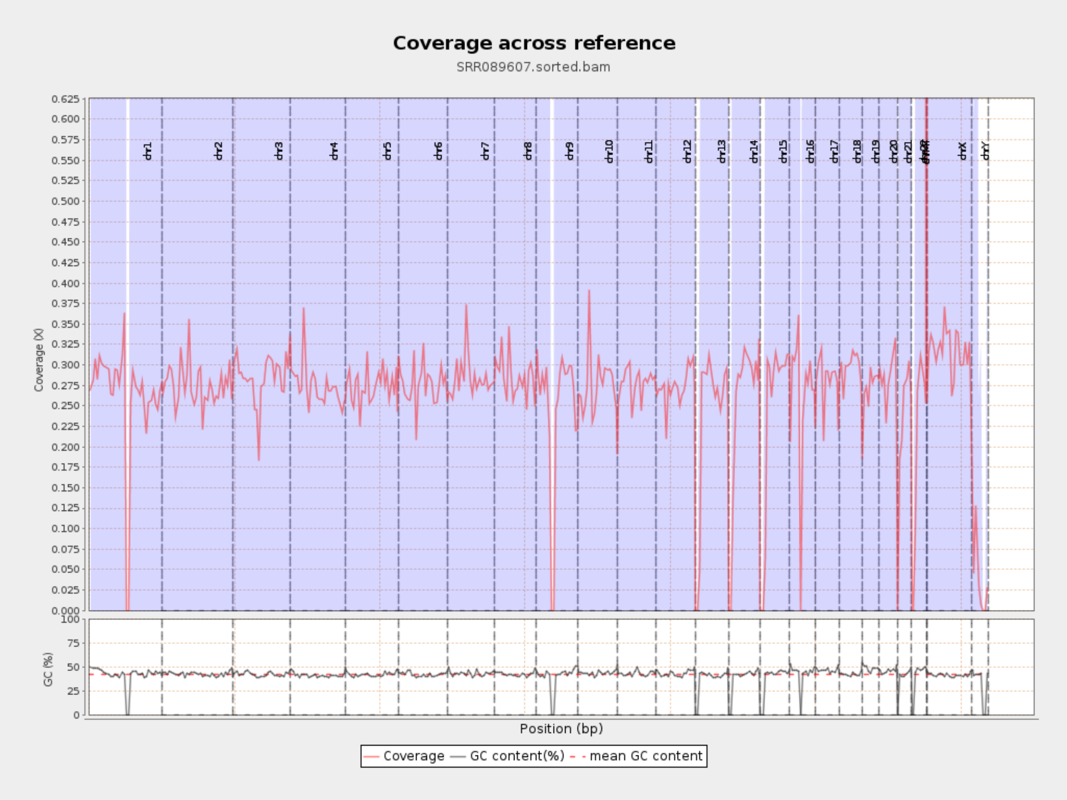
| | |
|---|---|
| General error rate | 0.45% |
| Mismatches | 3,663,423 |
| Insertions | 32,377 |
| Mapped reads with at least one insertion | 0.18% |
| Deletions | 108,435 |
| Mapped reads with at least one deletion | 0.61% |
| Homopolymer indels | 43.37% |

## 2.6. Chromosome stats

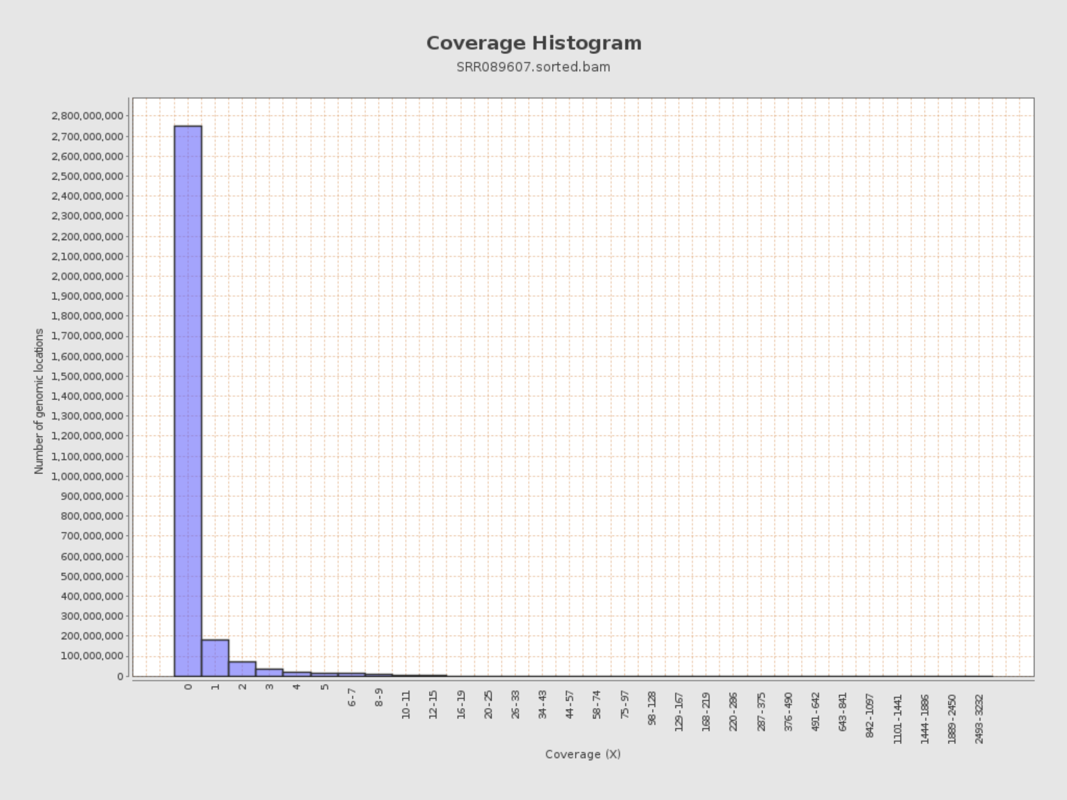
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 65139778 | 0.2613 | 2.5401 |
| chr2 | 243199373 | 67131414 | 0.276 | 1.9471 |
| chr3 | 198022430 | 56293634 | 0.2843 | 1.1521 |
| chr4 | 191154276 | 52243202 | 0.2733 | 1.236 |
| chr5 | 180915260 | 49591078 | 0.2741 | 1.141 |
| chr6 | 171115067 | 47421374 | 0.2771 | 1.4388 |
| chr7 | 159138663 | 45293335 | 0.2846 | 2.1779 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 41855479 | 0.286 | 1.7815 |
| chr9 | 141213431 | 34552091 | 0.2447 | 1.4317 |
| chr10 | 135534747 | 37534643 | 0.2769 | 1.7447 |
| chr11 | 135006516 | 37428678 | 0.2772 | 1.5753 |
| chr12 | 133851895 | 36536108 | 0.273 | 1.1832 |
| chr13 | 115169878 | 26985676 | 0.2343 | 1.0541 |
| chr14 | 107349540 | 26436068 | 0.2463 | 1.279 |
| chr15 | 102531392 | 24411899 | 0.2381 | 1.0833 |
| chr16 | 90354753 | 23834450 | 0.2638 | 1.2493 |
| chr17 | 81195210 | 22754546 | 0.2802 | 1.4195 |
| chr18 | 78077248 | 23321366 | 0.2987 | 2.3081 |
| chr19 | 59128983 | 16134455 | 0.2729 | 2.2298 |
| chr20 | 63025520 | 17922981 | 0.2844 | 1.2756 |
| chr21 | 48129895 | 11004750 | 0.2286 | 1.2505 |
| chr22 | 51304566 | 10169791 | 0.1982 | 1.0889 |
| chrMT | 16571 | 155103 | 9.3599 | 11.078 |
| chrX | 155270560 | 49131214 | 0.3164 | 1.5134 |
| chrY | 59373566 | 2512713 | 0.0423 | 0.7387 |

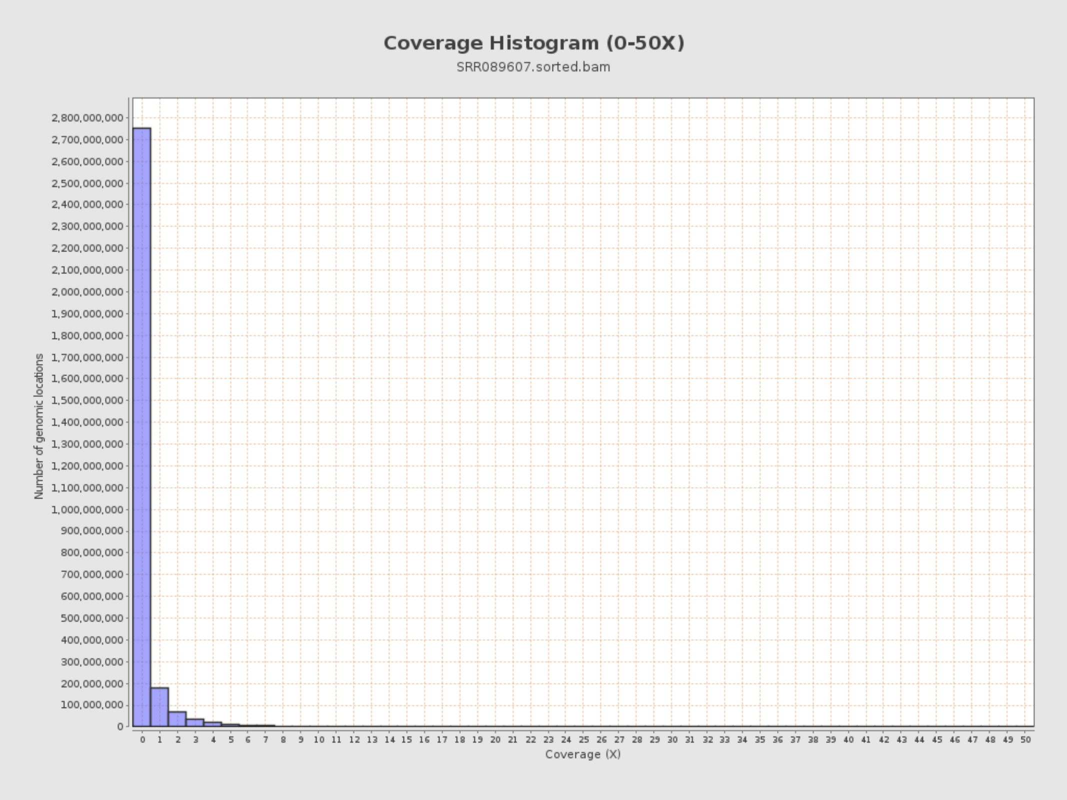
# 3. Results : Coverage across reference



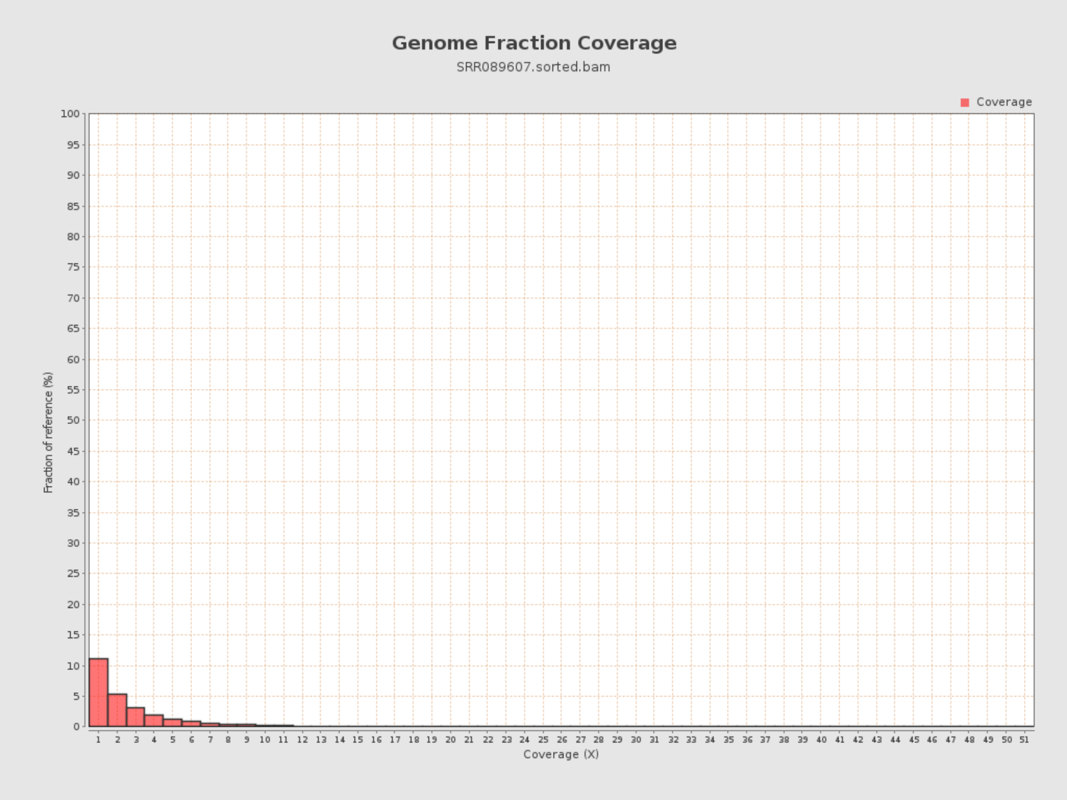
# 4. Results : Coverage Histogram



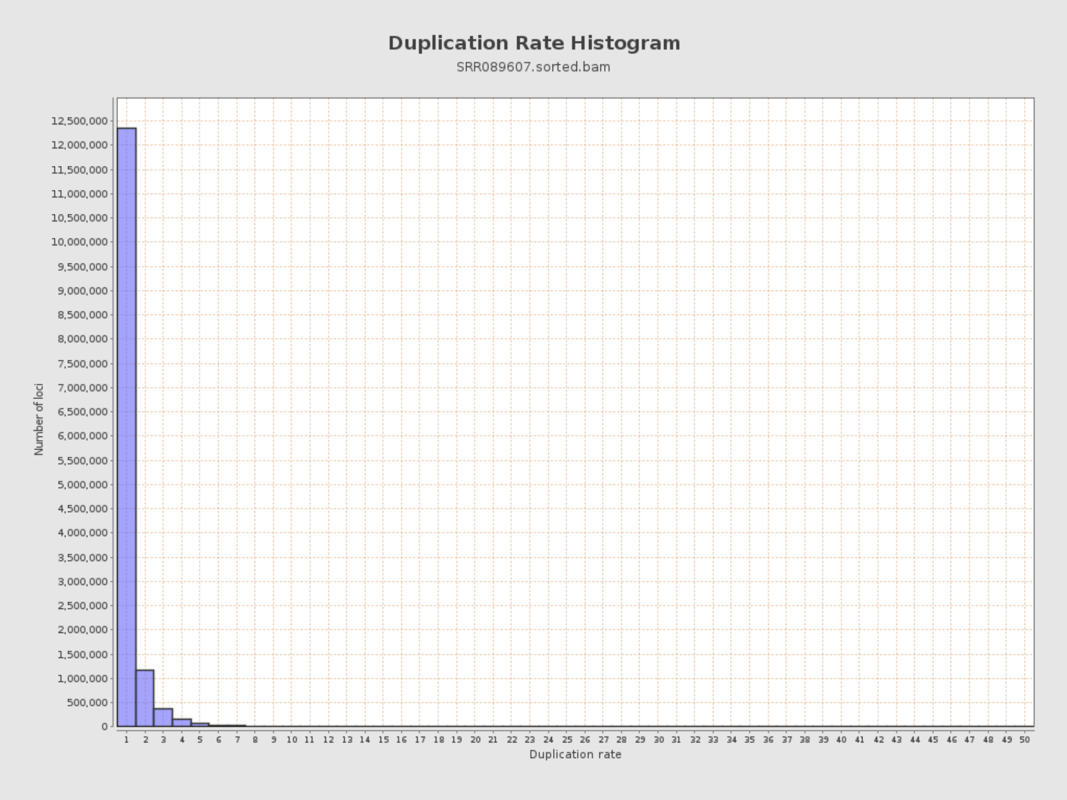
# 5. Results : Coverage Histogram (0-50X)



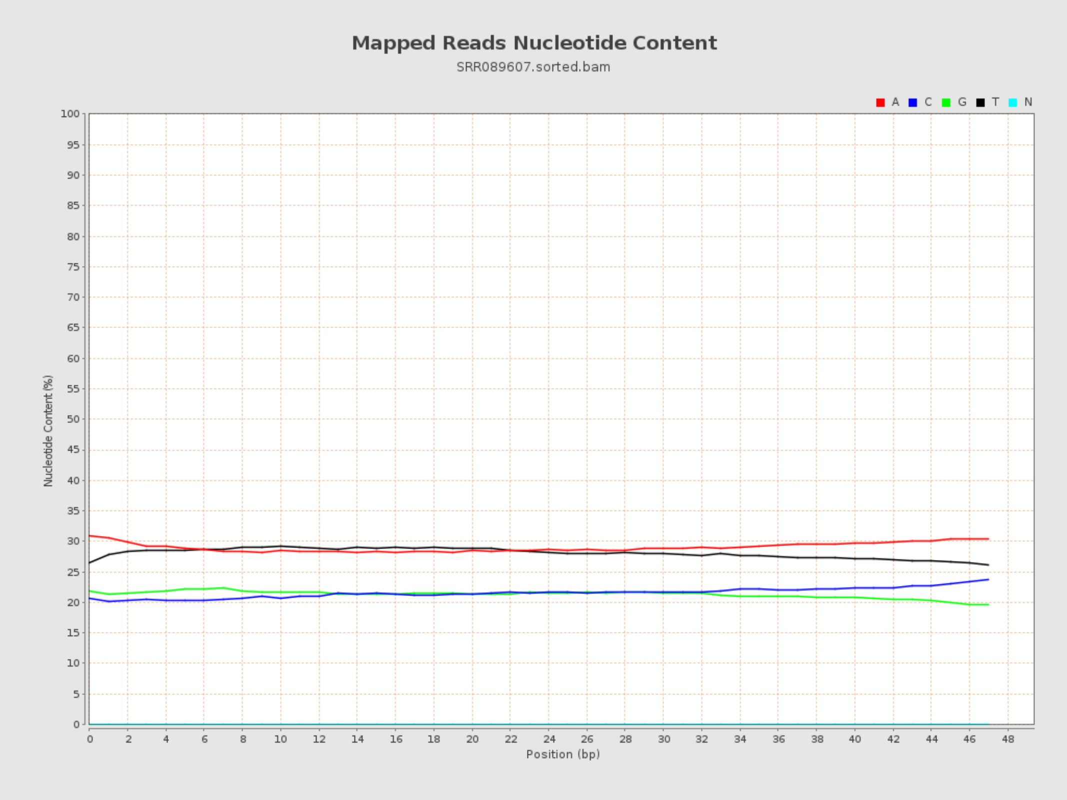
# 6. Results : Genome Fraction Coverage



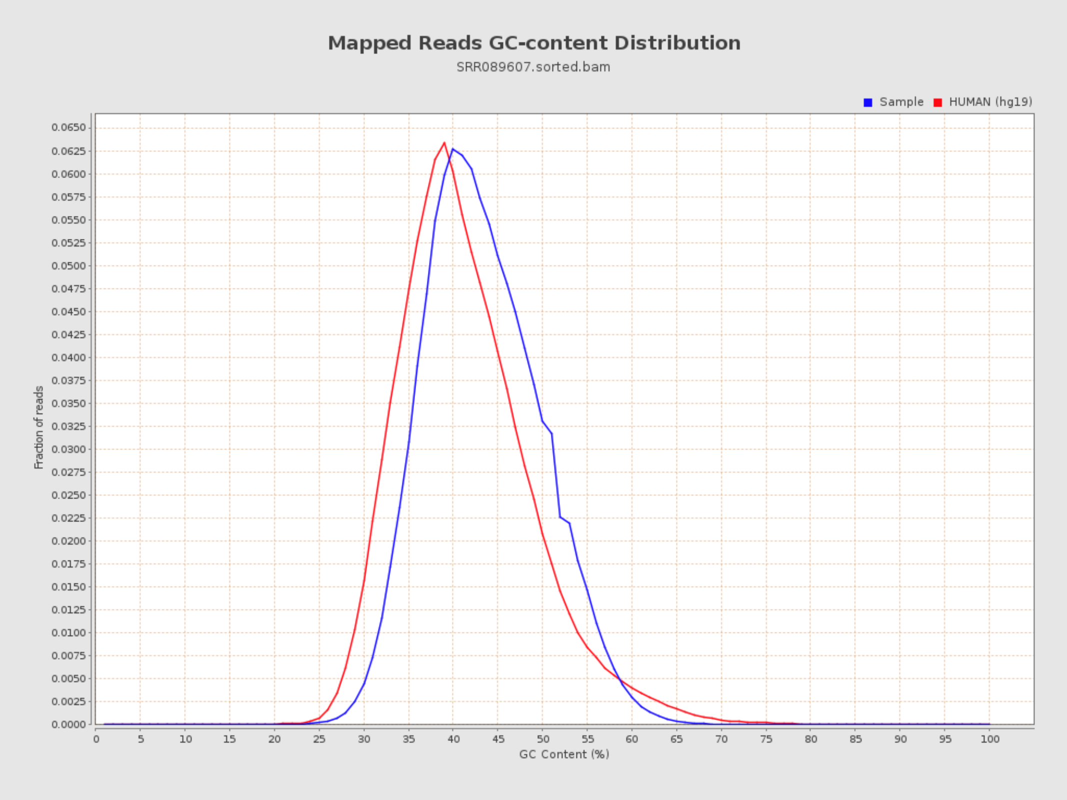
# 7. Results : Duplication Rate Histogram



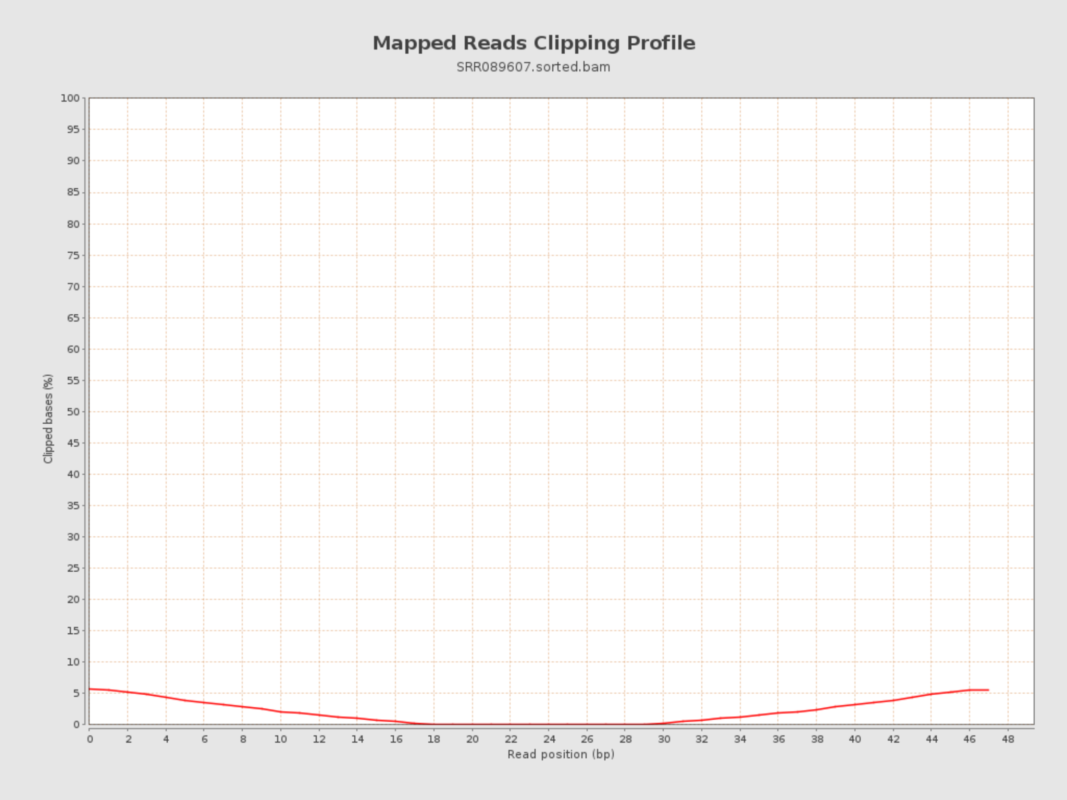
# 8. Results : Mapped Reads Nucleotide Content



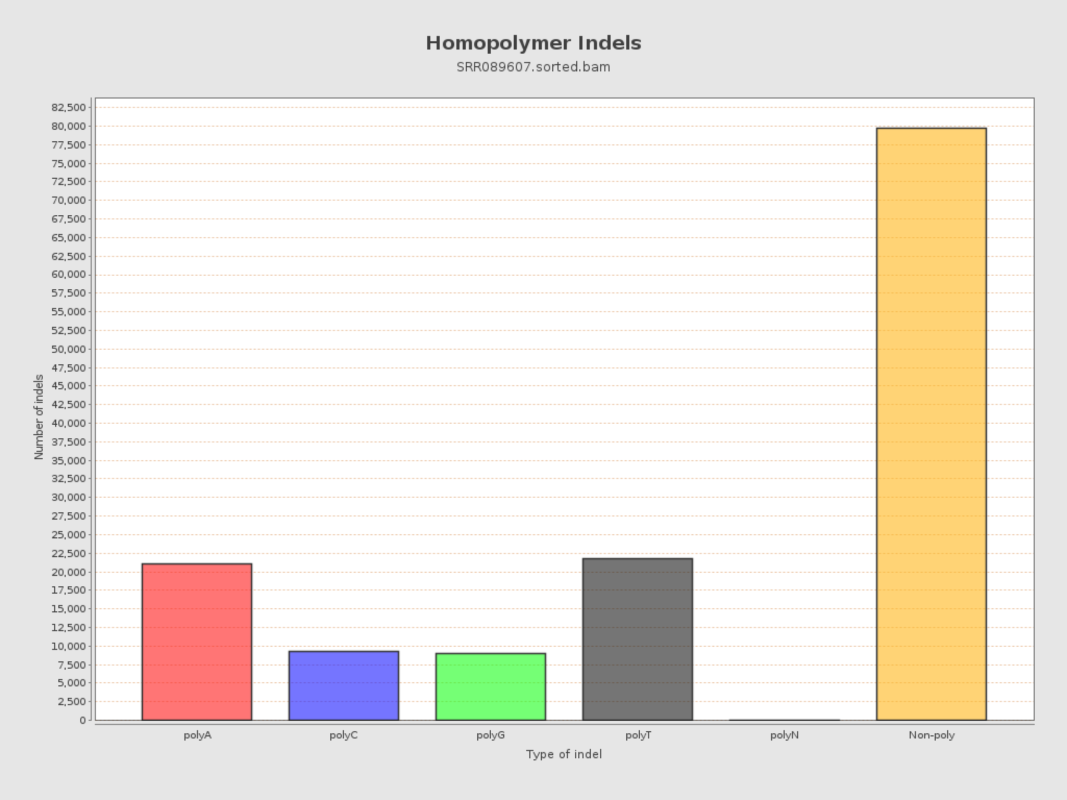
# 9. Results : Mapped Reads GC-content Distribution



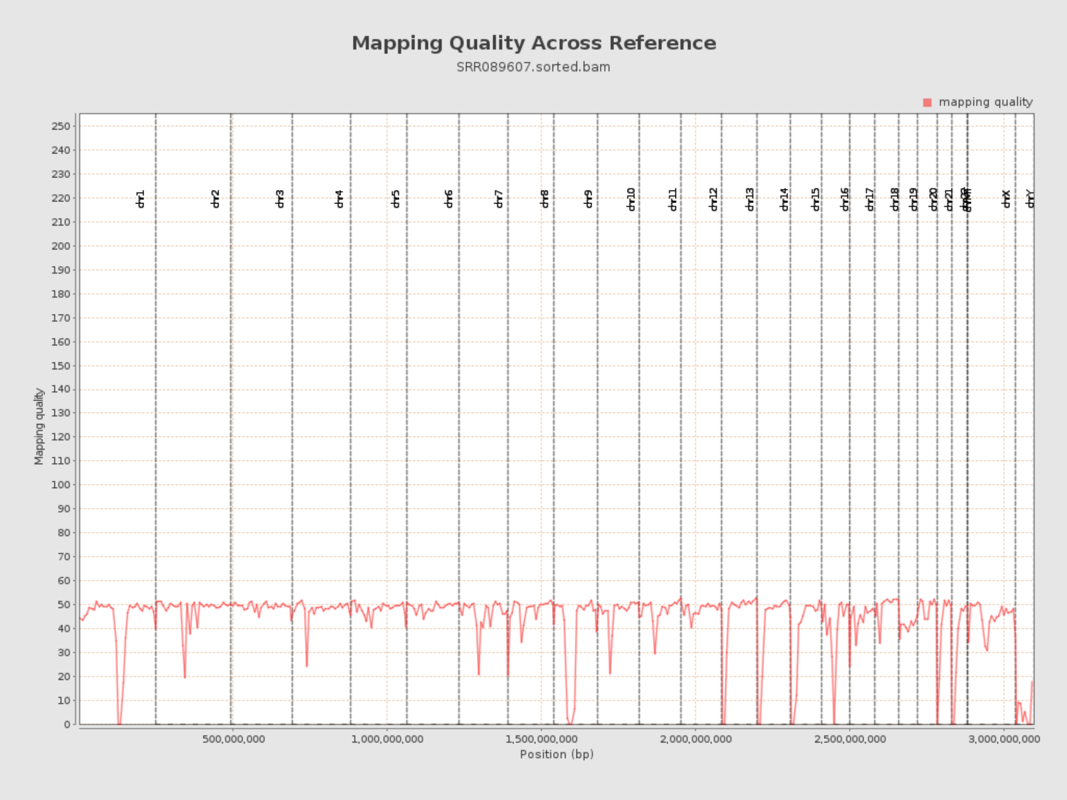
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram