# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/20 05:49:55*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR089757.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_SRR089757 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089757.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Apr 20 05:49:55 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR089757.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 18,765,791 |
| Mapped reads | 15,270,320 / 81.37% |
| Unmapped reads | 3,495,471 / 18.63% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 781 / 0% |
| Read min/max/mean length | 30 / 48 / 48 |
| Duplicated reads (estimated) | 2,718,942 / 14.49% |
| Duplication rate | 12.29% |
| Clipped reads | 1,533,626 / 8.17% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 210,445,240 / 29.3% |
| Number/percentage of C's | 147,325,135 / 20.51% |
| Number/percentage of T's | 206,180,966 / 28.71% |
| Number/percentage of G's | 154,274,369 / 21.48% |
| Number/percentage of N's | 14,042 / 0% |
| GC Percentage | 41.99% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.2321 |
| | |

| | |
|---|---|
| Standard Deviation | 1.2718 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.23 |

## 2.5. Mismatches and indels

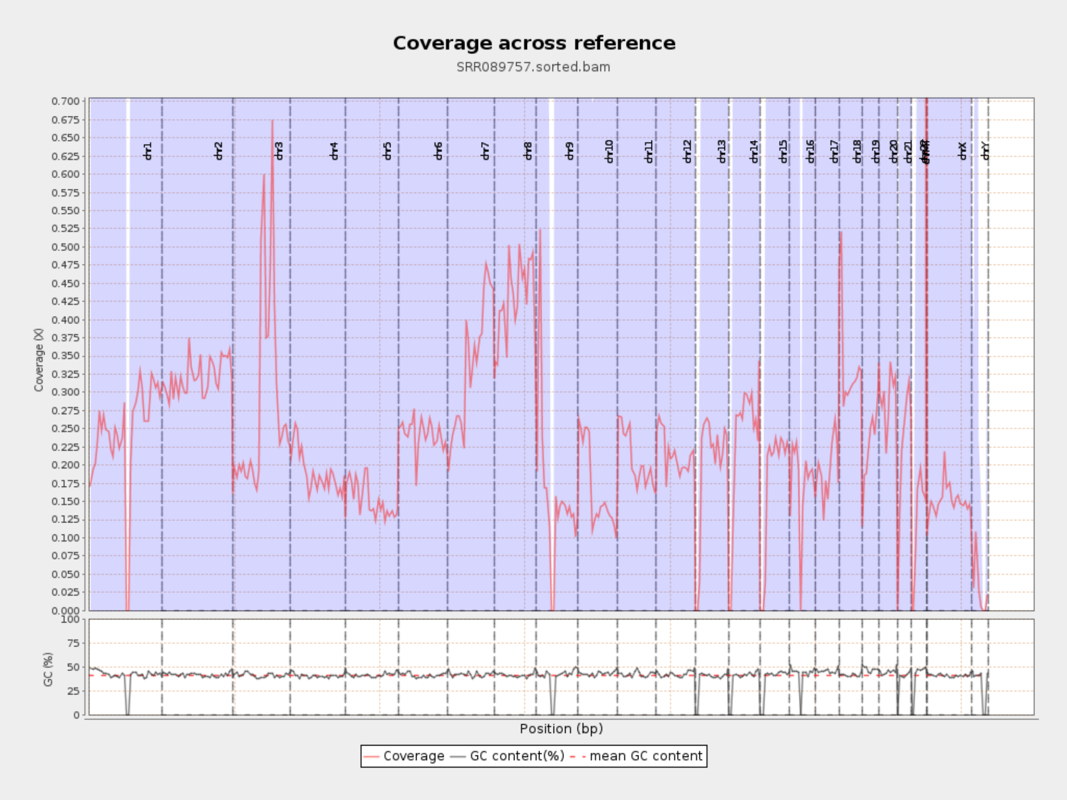
| | |
|---|---|
| General error rate | 0.47% |
| Mismatches | 3,305,832 |
| Insertions | 27,013 |
| Mapped reads with at least one insertion | 0.18% |
| Deletions | 87,242 |
| Mapped reads with at least one deletion | 0.57% |
| Homopolymer indels | 45.78% |

## 2.6. Chromosome stats

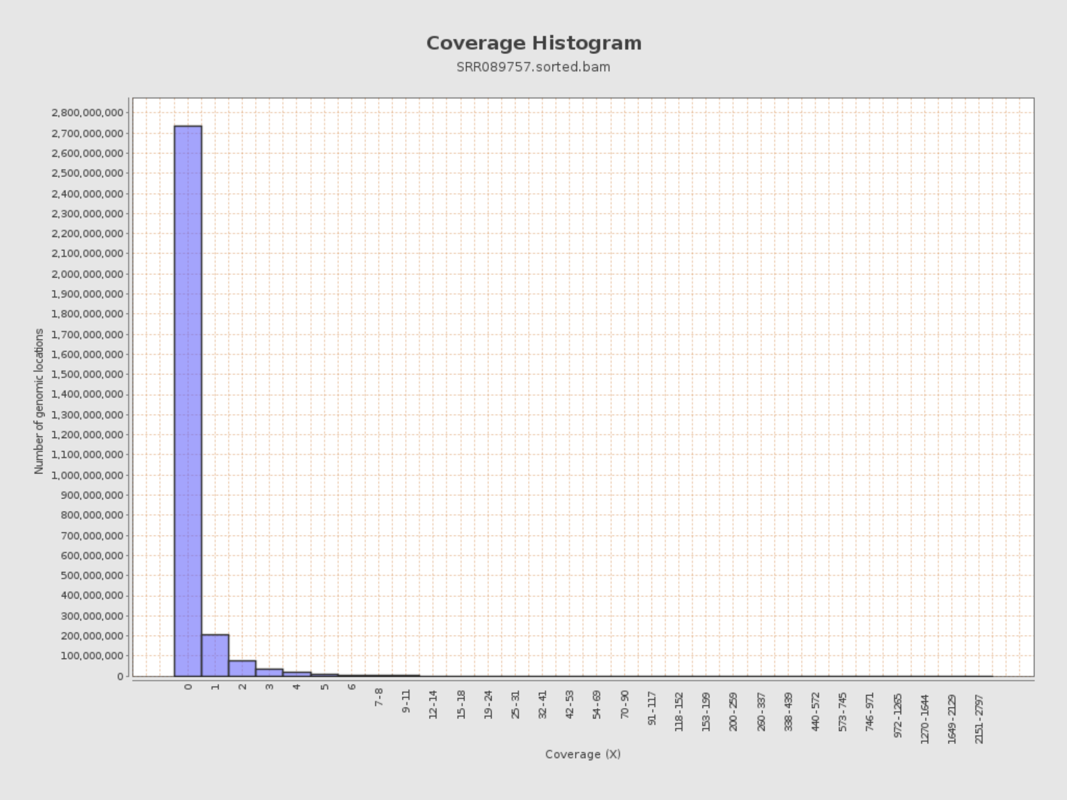
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 60852081 | 0.2441 | 1.923 |
| chr2 | 243199373 | 78316329 | 0.322 | 1.4669 |
| chr3 | 198022430 | 56800939 | 0.2868 | 0.9953 |
| chr4 | 191154276 | 36278357 | 0.1898 | 0.8057 |
| chr5 | 180915260 | 27538986 | 0.1522 | 0.6918 |
| chr6 | 171115067 | 41529945 | 0.2427 | 0.9464 |
| chr7 | 159138663 | 54091797 | 0.3399 | 2.3781 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 62955839 | 0.4301 | 1.987 |
| chr9 | 141213431 | 23009721 | 0.1629 | 0.9778 |
| chr10 | 135534747 | 22963786 | 0.1694 | 1.0796 |
| chr11 | 135006516 | 27904247 | 0.2067 | 1.0265 |
| chr12 | 133851895 | 28694454 | 0.2144 | 0.8534 |
| chr13 | 115169878 | 22469139 | 0.1951 | 0.791 |
| chr14 | 107349540 | 24445253 | 0.2277 | 0.885 |
| chr15 | 102531392 | 18248656 | 0.178 | 0.7563 |
| chr16 | 90354753 | 15853756 | 0.1755 | 0.8206 |
| chr17 | 81195210 | 15608332 | 0.1922 | 0.865 |
| chr18 | 78077248 | 26412920 | 0.3383 | 1.7674 |
| chr19 | 59128983 | 13810353 | 0.2336 | 1.3244 |
| chr20 | 63025520 | 18129064 | 0.2876 | 1.0405 |
| chr21 | 48129895 | 10743800 | 0.2232 | 0.9609 |
| chr22 | 51304566 | 6161419 | 0.1201 | 0.6279 |
| chrMT | 16571 | 332763 | 20.081 | 14.7283 |
| chrX | 155270560 | 23387389 | 0.1506 | 0.7658 |
| chrY | 59373566 | 1833956 | 0.0309 | 0.9582 |

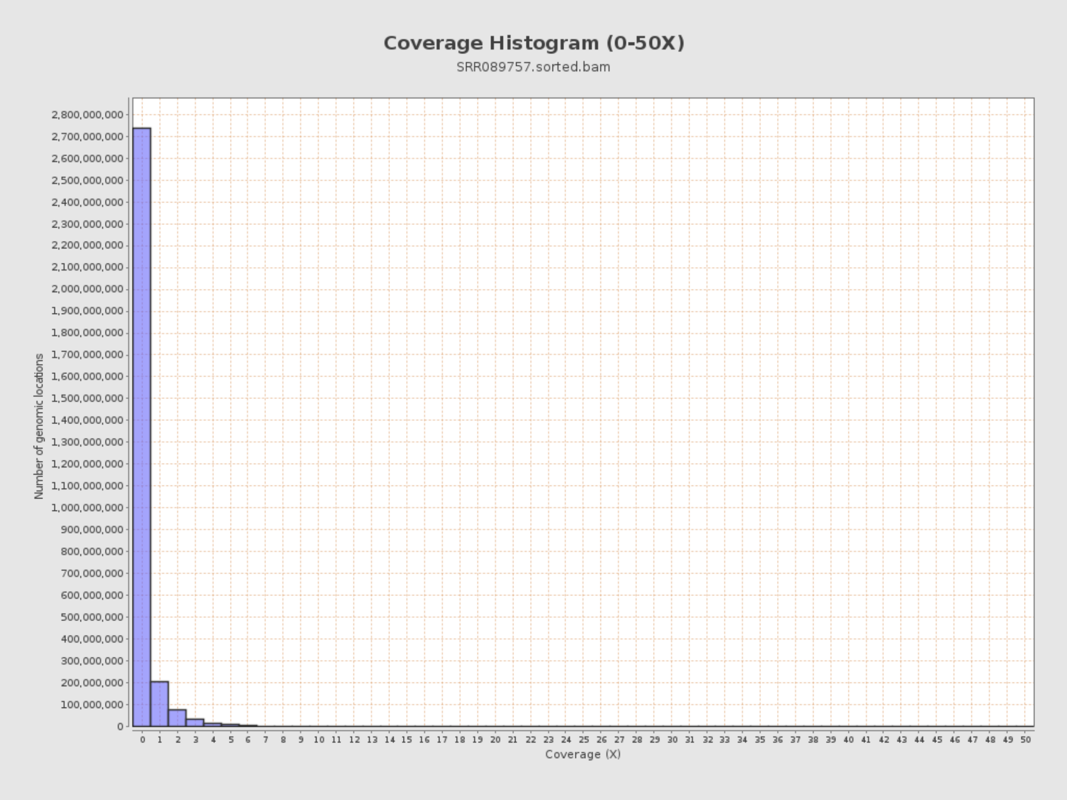
# 3. Results : Coverage across reference



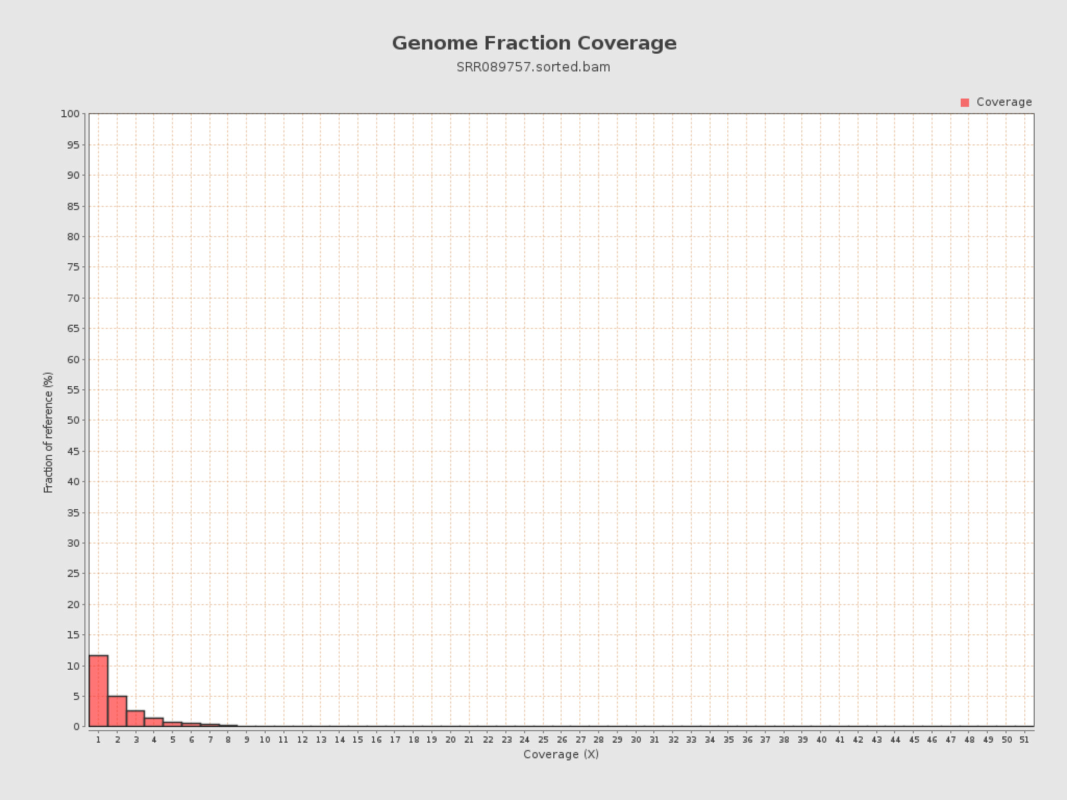
# 4. Results : Coverage Histogram



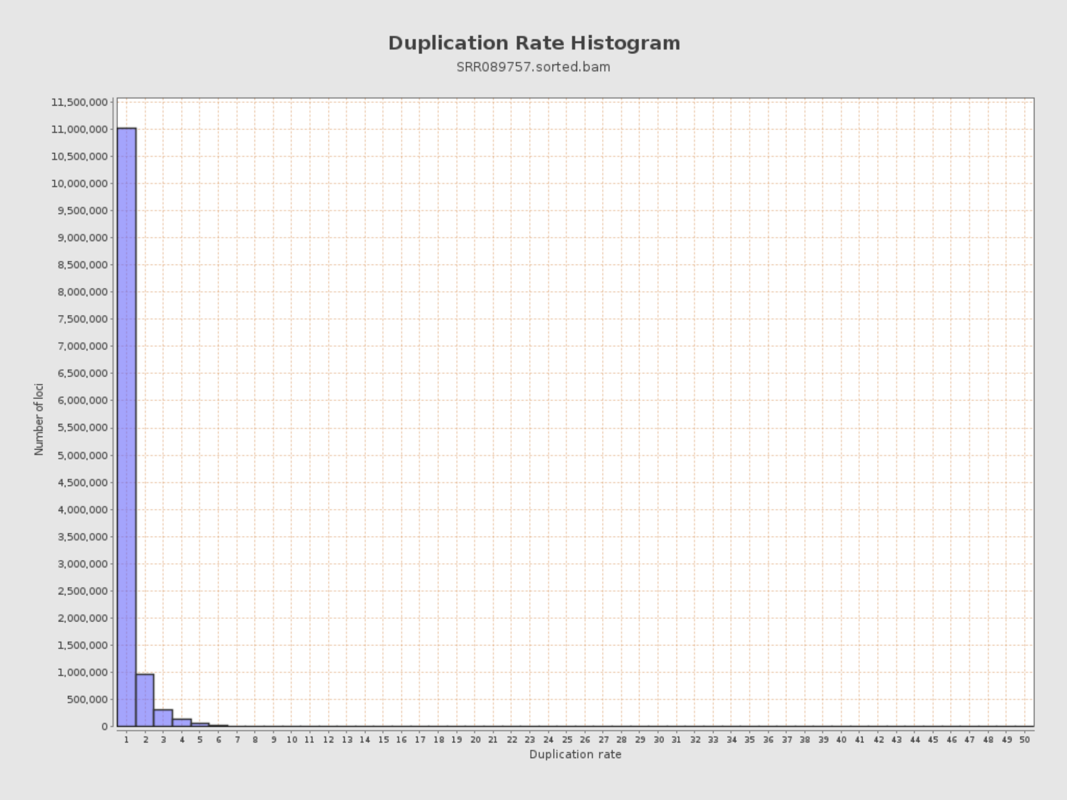
# 5. Results : Coverage Histogram (0-50X)



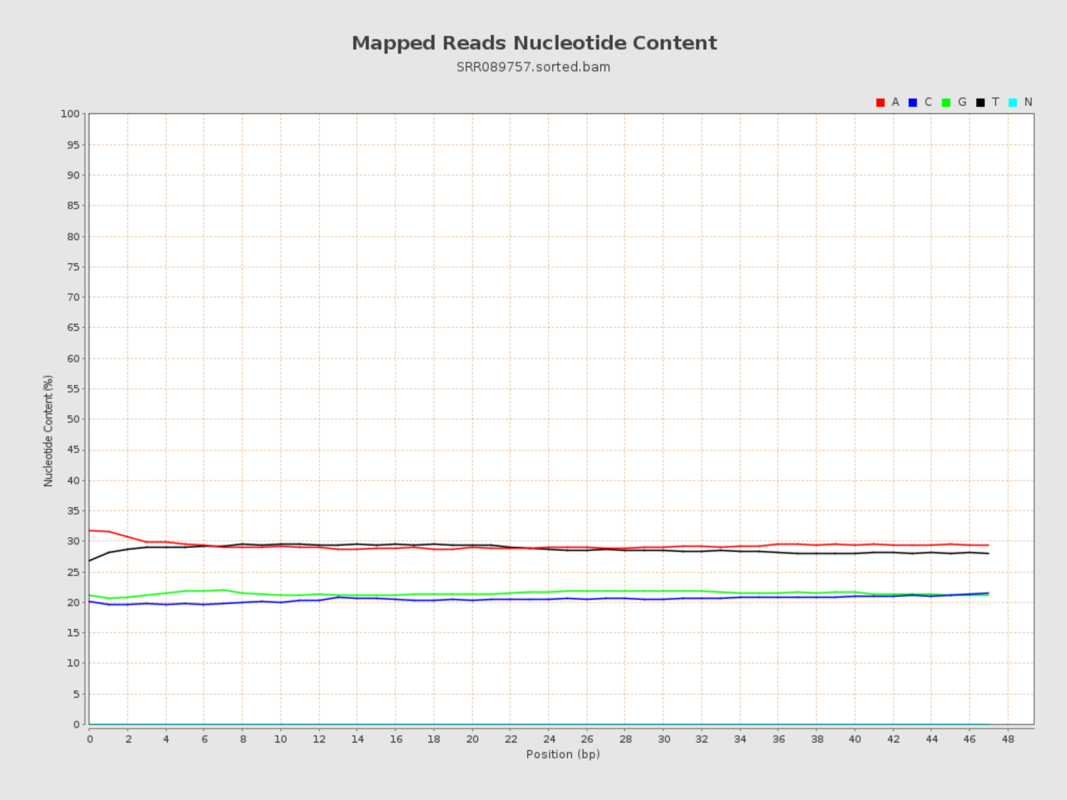
# 6. Results : Genome Fraction Coverage



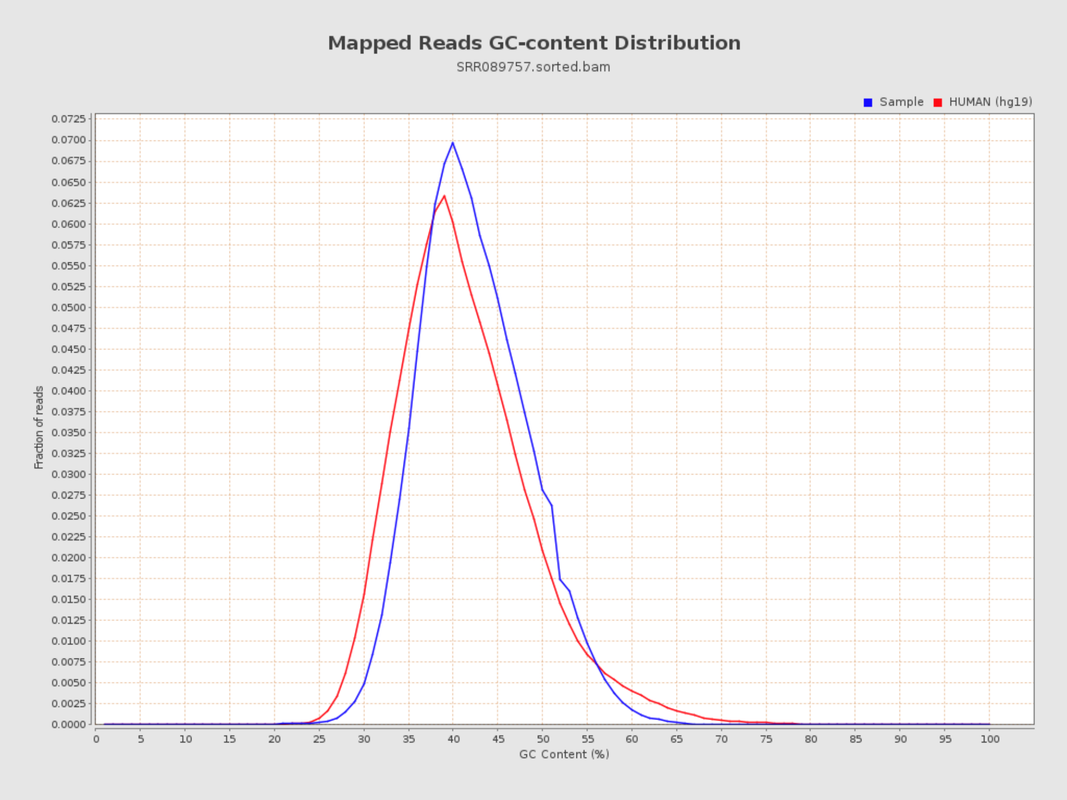
# 7. Results : Duplication Rate Histogram



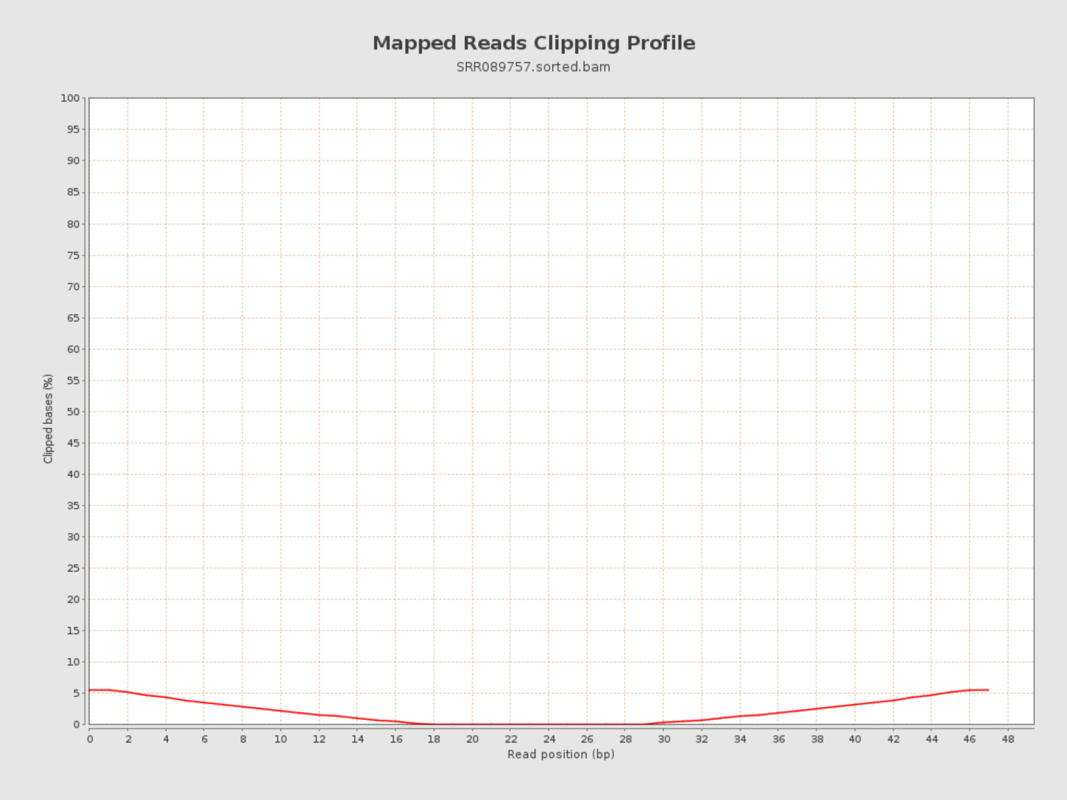
# 8. Results : Mapped Reads Nucleotide Content



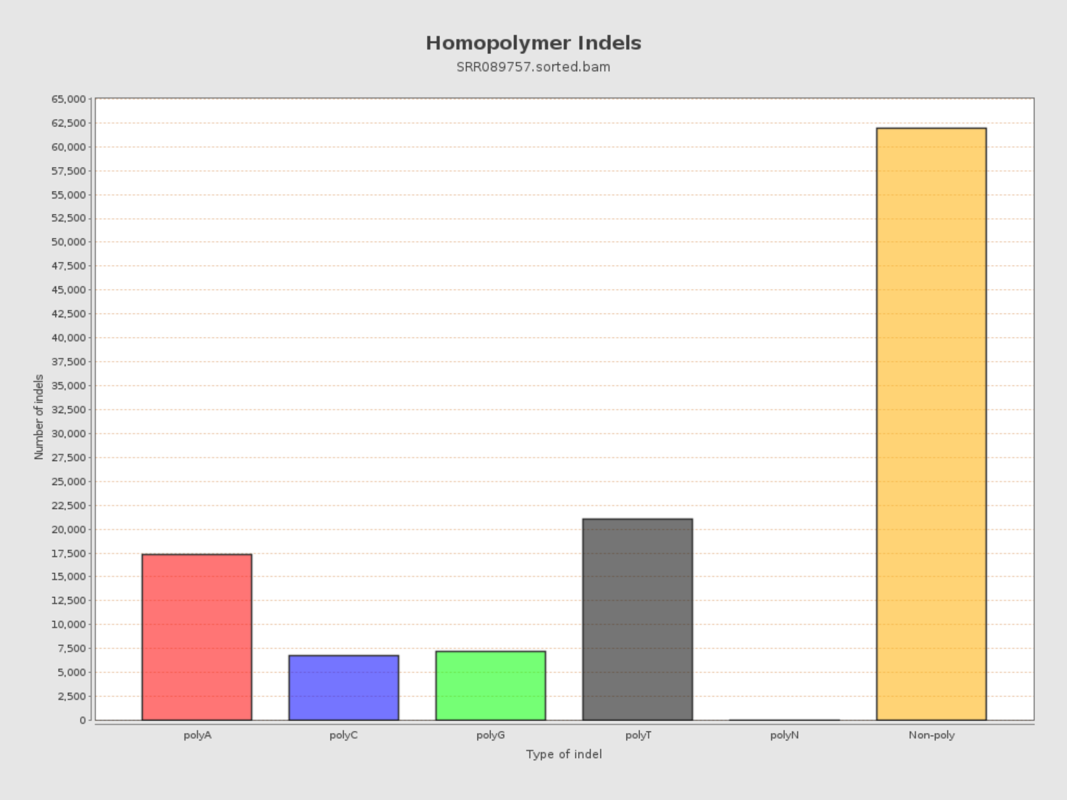
# 9. Results : Mapped Reads GC-content Distribution



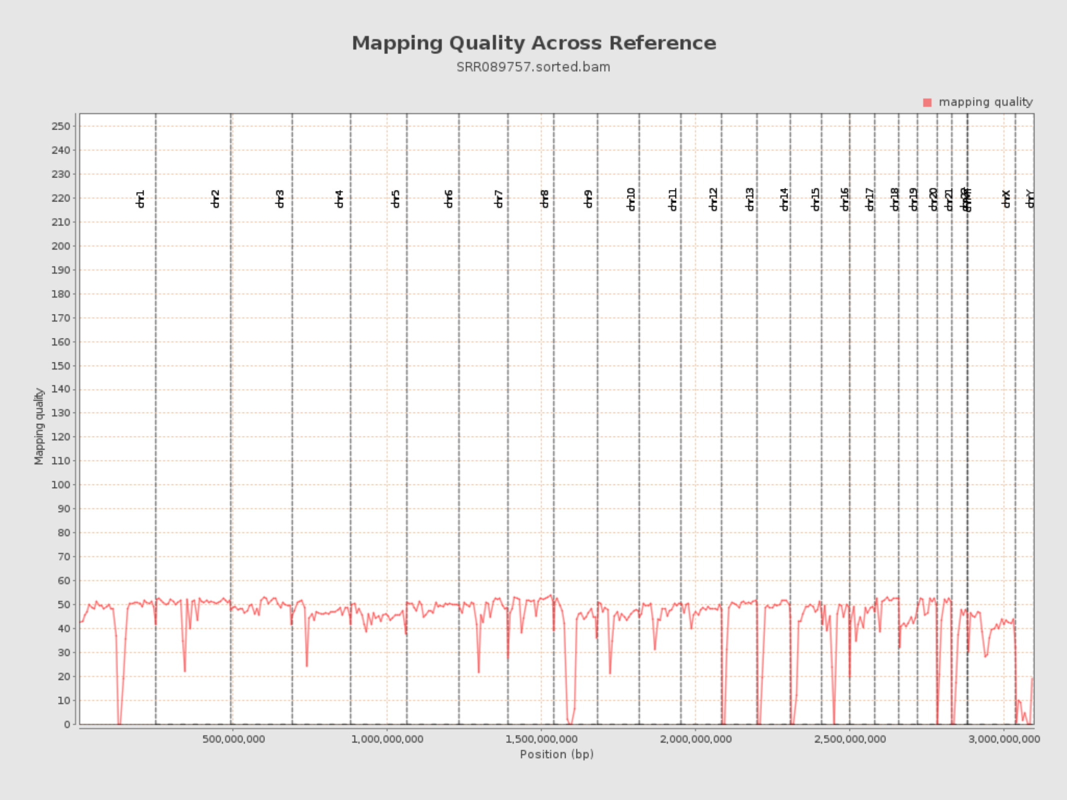
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram