# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 12:20:21*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080957.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_SRR3080957 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080957.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 12:20:18 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3080957.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,622,842 |
| Mapped reads | 4,185,417 / 90.54% |
| Unmapped reads | 437,425 / 9.46% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 52,962 / 1.15% |
| Read min/max/mean length | 30 / 76 / 76.4 |
| Duplicated reads (estimated) | 214,293 / 4.64% |
| Duplication rate | 3.96% |
| Clipped reads | 1,424,469 / 30.81% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 84,124,690 / 29.06% |
| Number/percentage of C's | 51,763,122 / 17.88% |
| Number/percentage of T's | 92,114,630 / 31.82% |
| Number/percentage of G's | 60,112,738 / 20.76% |
| Number/percentage of N's | 1,415,839 / 0.49% |
| GC Percentage | 38.64% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0936 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6816 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.57 |

## 2.5. Mismatches and indels

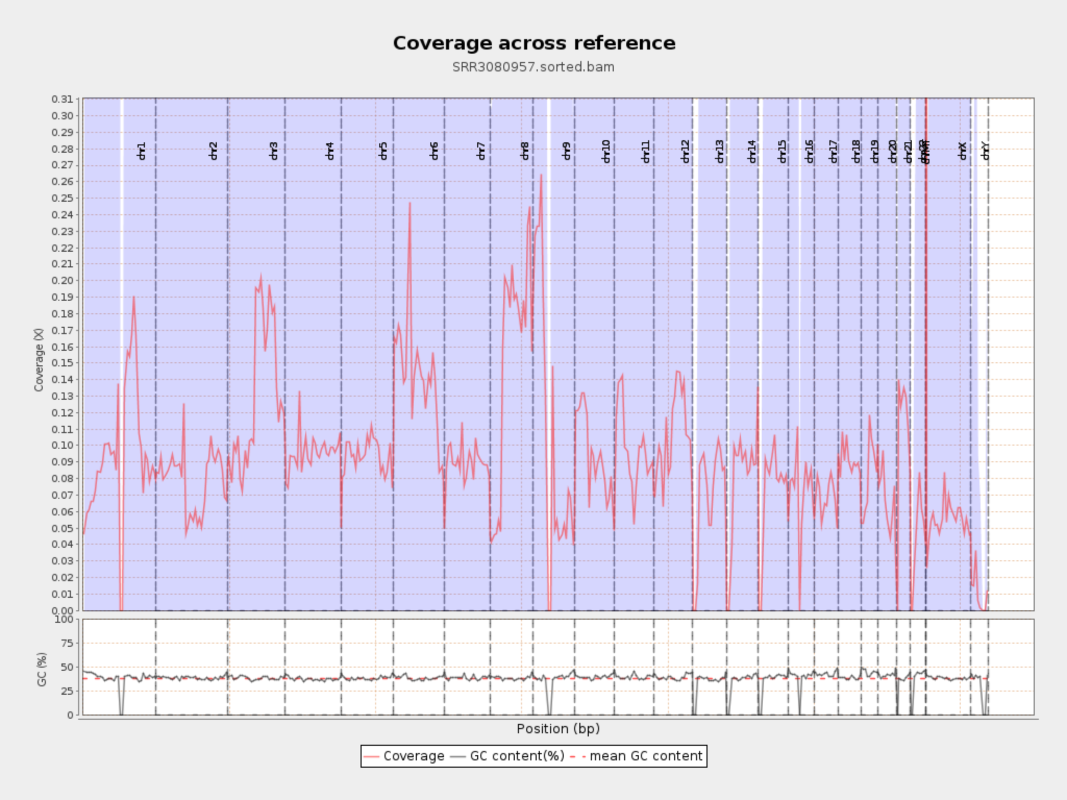
| | |
|---|---|
| General error rate | 1.16% |
| Mismatches | 3,331,021 |
| Insertions | 22,450 |
| Mapped reads with at least one insertion | 0.53% |
| Deletions | 65,345 |
| Mapped reads with at least one deletion | 1.54% |
| Homopolymer indels | 49.69% |

## 2.6. Chromosome stats

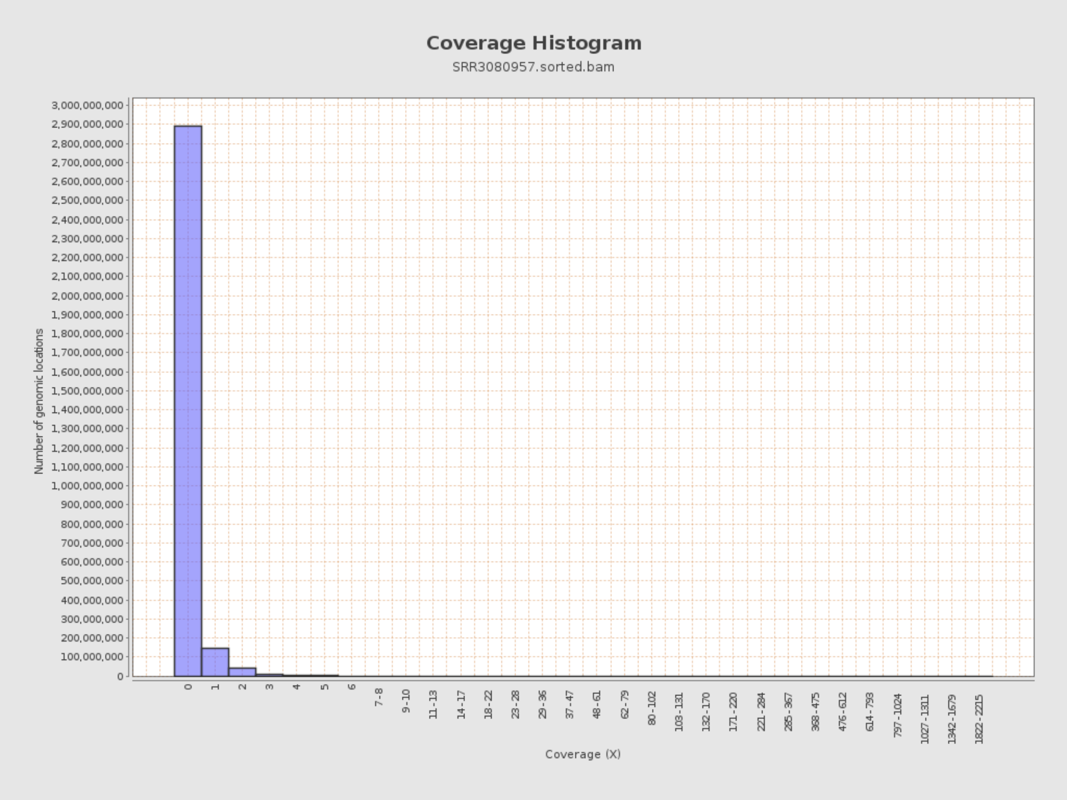
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 23586082 | 0.0946 | 1.1067 |
| chr2 | 243199373 | 19333532 | 0.0795 | 0.5743 |
| chr3 | 198022430 | 25790041 | 0.1302 | 0.4827 |
| chr4 | 191154276 | 18381601 | 0.0962 | 0.4384 |
| chr5 | 180915260 | 16936845 | 0.0936 | 0.4086 |
| chr6 | 171115067 | 24848290 | 0.1452 | 0.7591 |
| chr7 | 159138663 | 14278833 | 0.0897 | 0.5958 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 22426832 | 0.1532 | 1.4508 |
| chr9 | 141213431 | 14872829 | 0.1053 | 0.7395 |
| chr10 | 135534747 | 12917356 | 0.0953 | 0.5698 |
| chr11 | 135006516 | 13199645 | 0.0978 | 0.4896 |
| chr12 | 133851895 | 14300054 | 0.1068 | 0.4571 |
| chr13 | 115169878 | 7937726 | 0.0689 | 0.3446 |
| chr14 | 107349540 | 8350728 | 0.0778 | 0.4551 |
| chr15 | 102531392 | 7245672 | 0.0707 | 0.3497 |
| chr16 | 90354753 | 6379597 | 0.0706 | 0.4529 |
| chr17 | 81195210 | 5672135 | 0.0699 | 0.3616 |
| chr18 | 78077248 | 7151305 | 0.0916 | 1.296 |
| chr19 | 59128983 | 4880470 | 0.0825 | 0.7811 |
| chr20 | 63025520 | 4224760 | 0.067 | 0.3683 |
| chr21 | 48129895 | 5362953 | 0.1114 | 0.544 |
| chr22 | 51304566 | 2301124 | 0.0449 | 0.2745 |
| chrMT | 16571 | 46377 | 2.7987 | 2.4034 |
| chrX | 155270560 | 8580838 | 0.0553 | 0.3422 |
| chrY | 59373566 | 633538 | 0.0107 | 0.2128 |

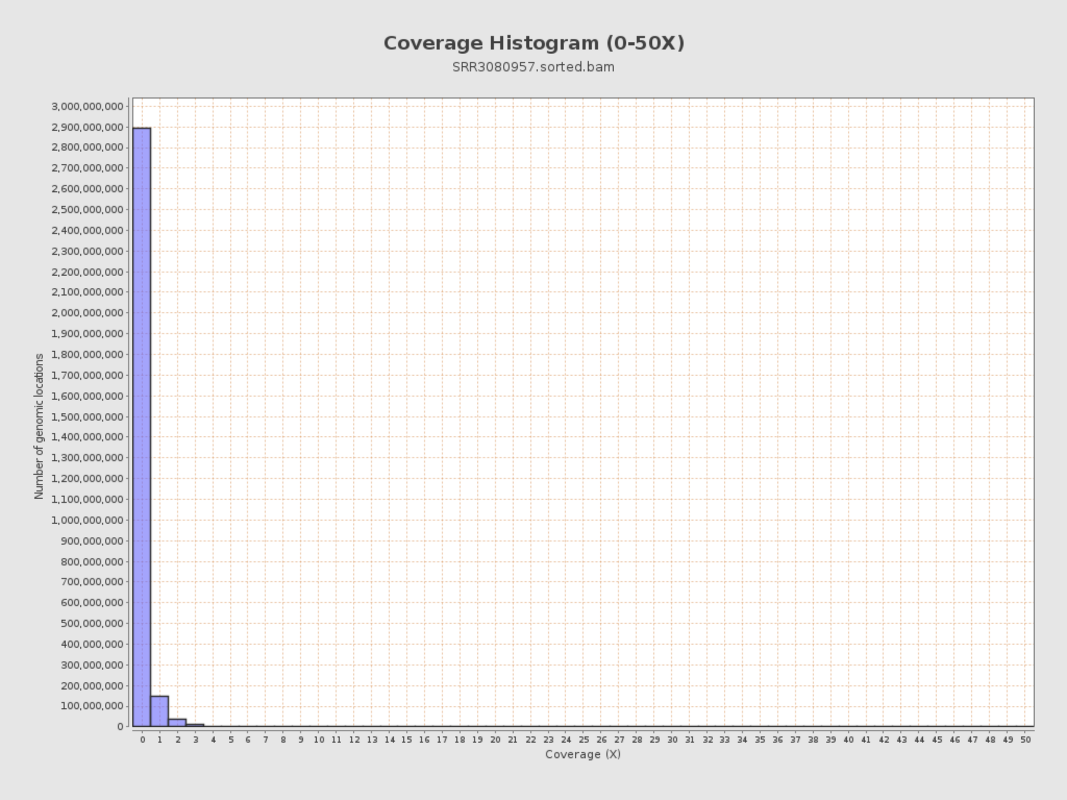
# 3. Results : Coverage across reference



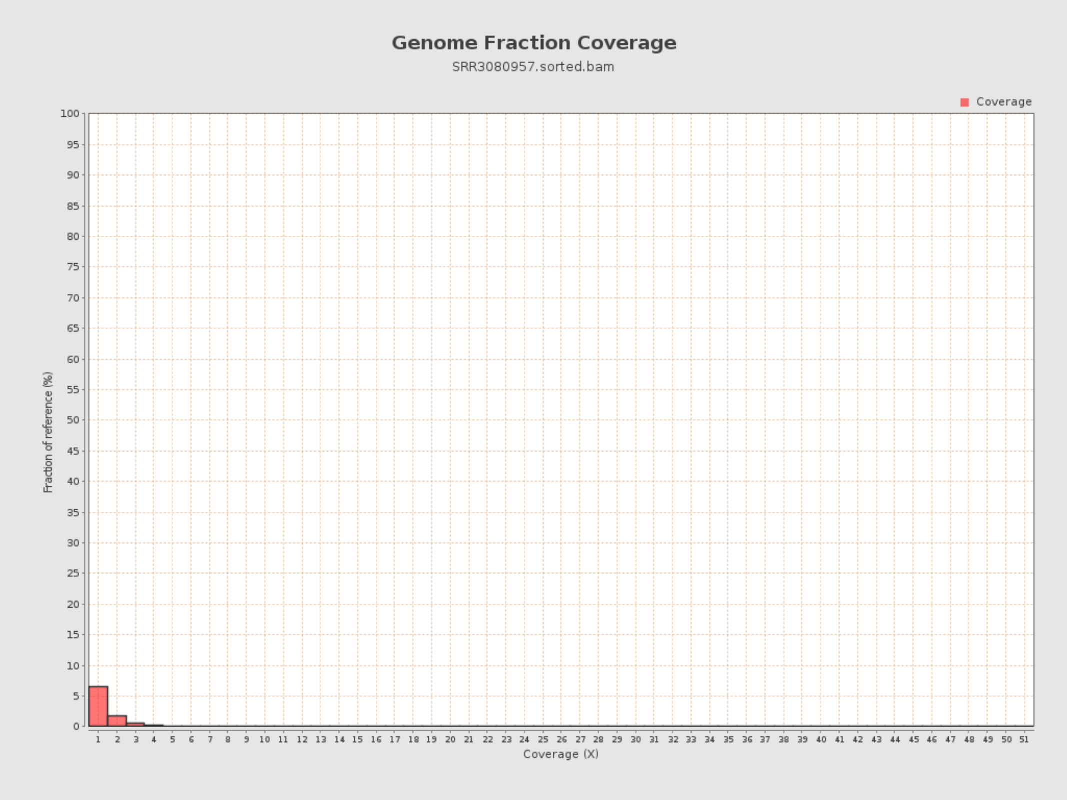
# 4. Results : Coverage Histogram



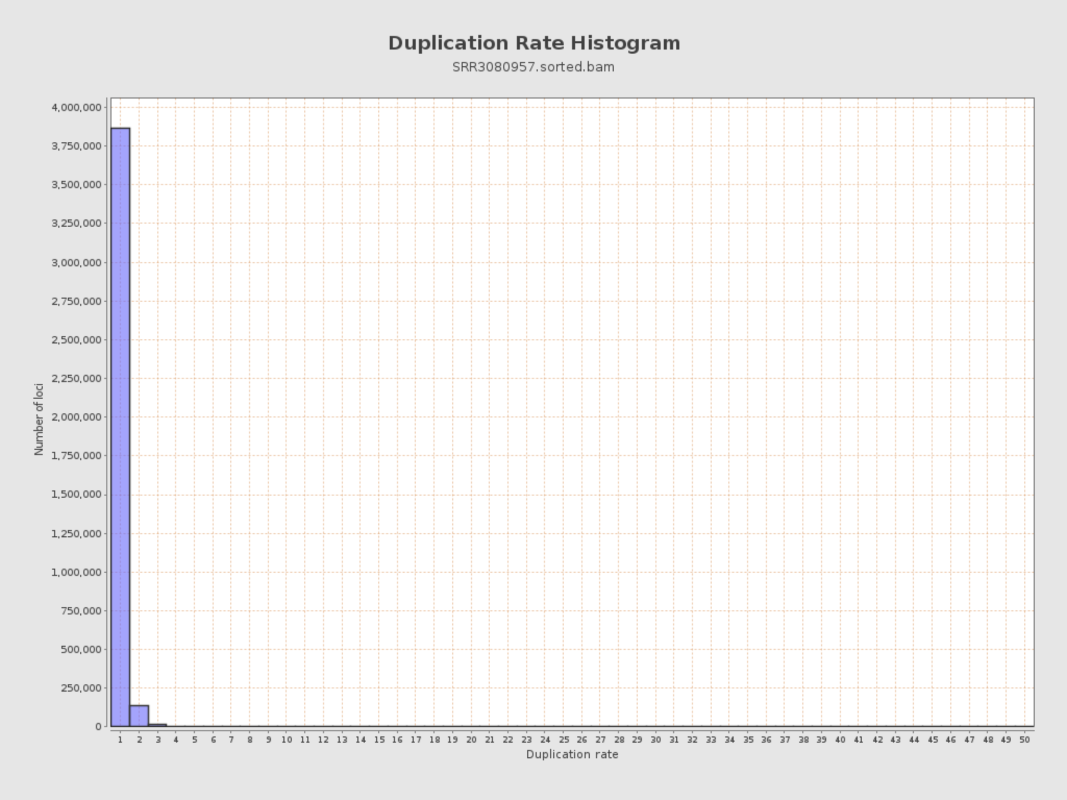
# 5. Results : Coverage Histogram (0-50X)



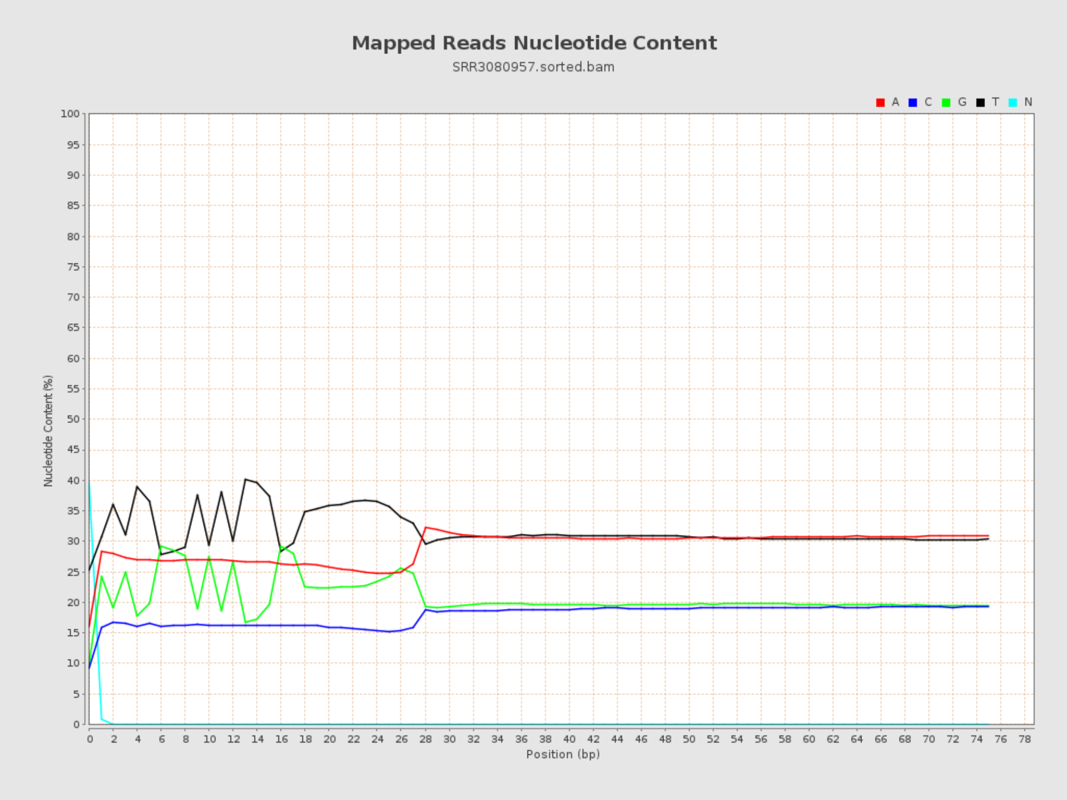
# 6. Results : Genome Fraction Coverage



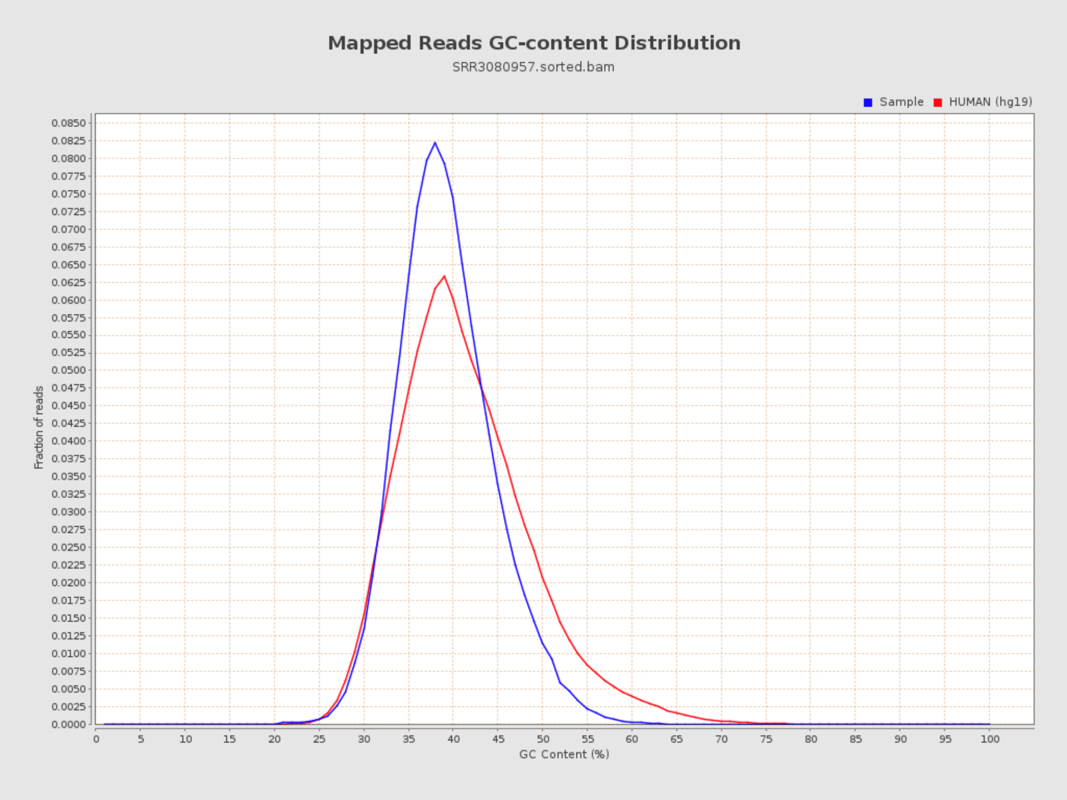
# 7. Results : Duplication Rate Histogram



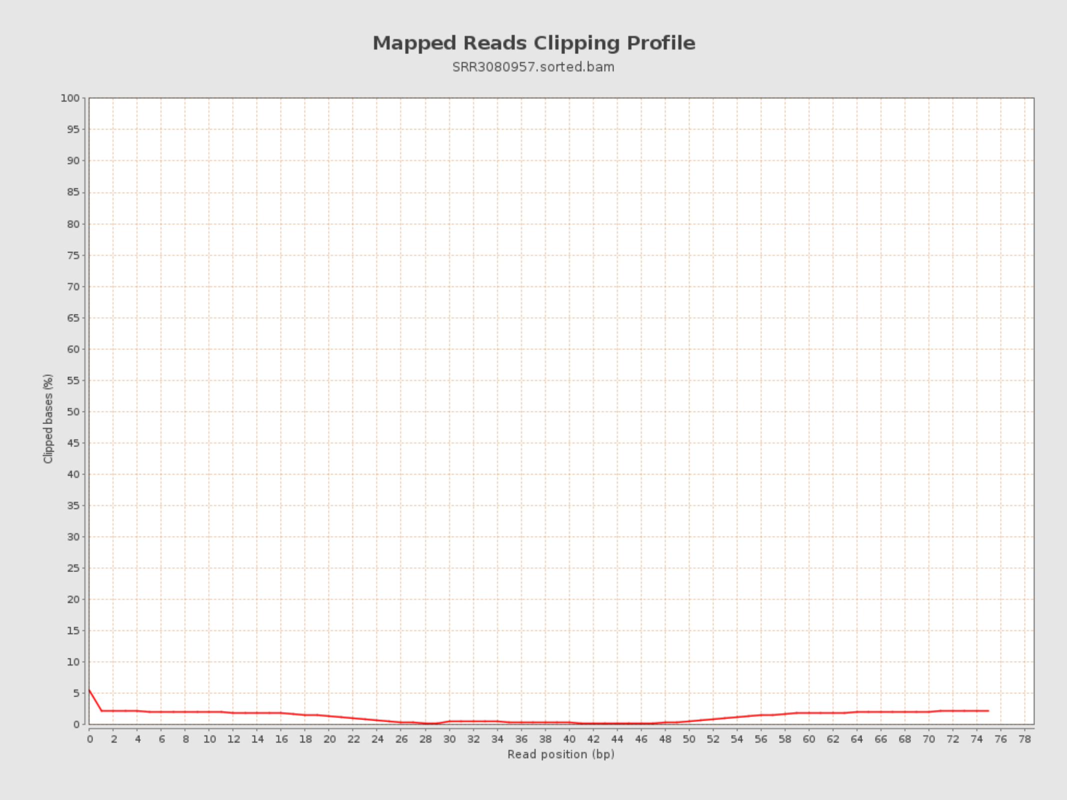
# 8. Results : Mapped Reads Nucleotide Content



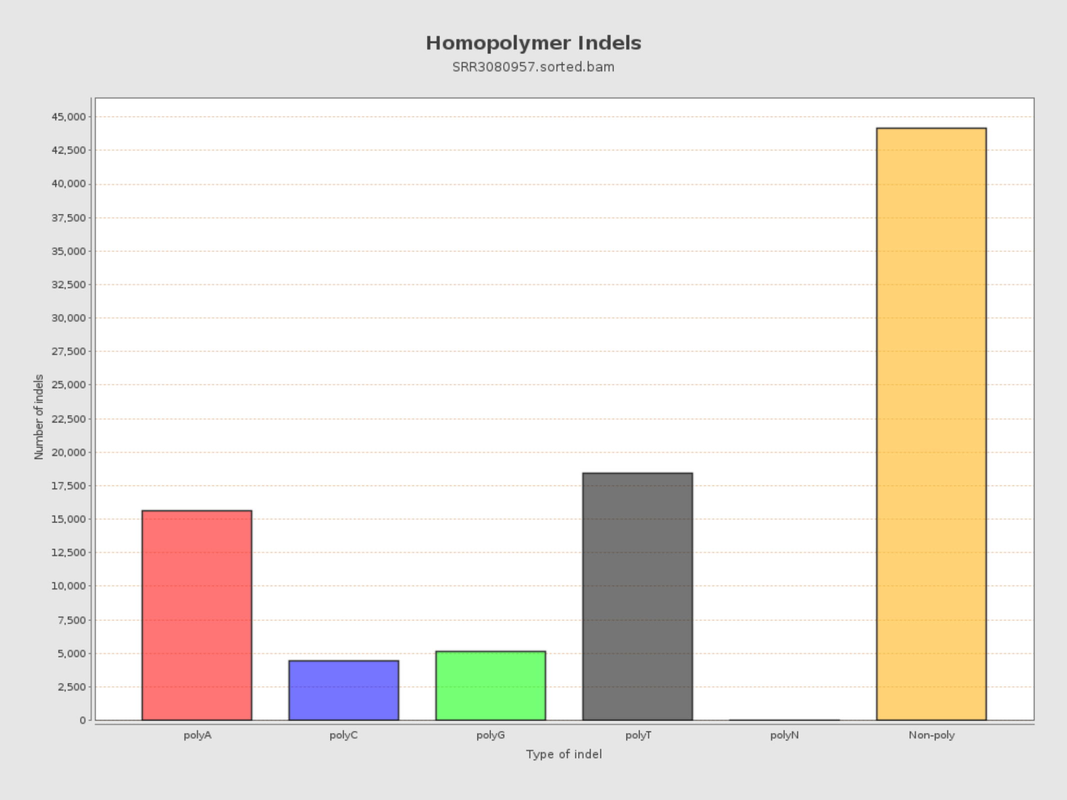
# 9. Results : Mapped Reads GC-content Distribution



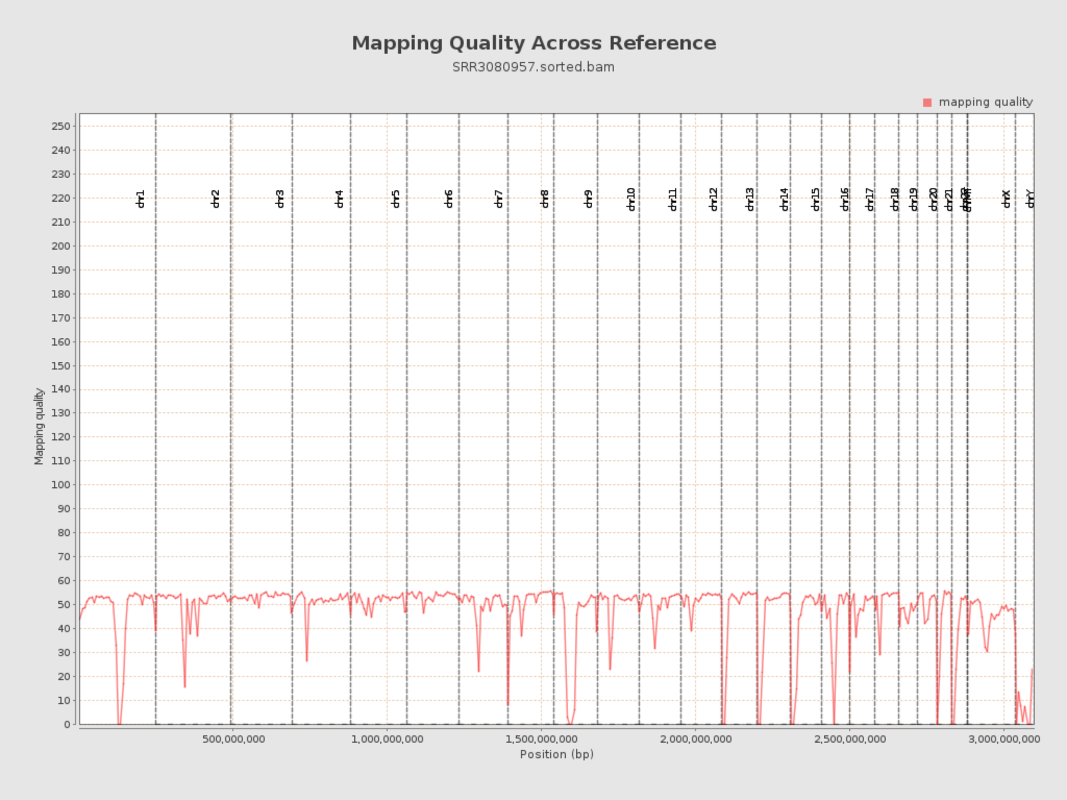
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram