# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 04:52:03*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3087919.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_SRR3087919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3087919.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 04:51:18 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3087919.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,911,283 |
| Mapped reads | 1,126,904 / 58.96% |
| Unmapped reads | 784,379 / 41.04% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 5,672 / 0.3% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 27,655 / 1.45% |
| Duplication rate | 2.03% |
| Clipped reads | 668,912 / 35% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 20,209,550 / 29.04% |
| Number/percentage of C's | 13,372,682 / 19.21% |
| Number/percentage of T's | 20,671,843 / 29.7% |
| Number/percentage of G's | 15,341,422 / 22.04% |
| Number/percentage of N's | 769 / 0% |
| GC Percentage | 41.26% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0225 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1938 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.12 |

## 2.5. Mismatches and indels

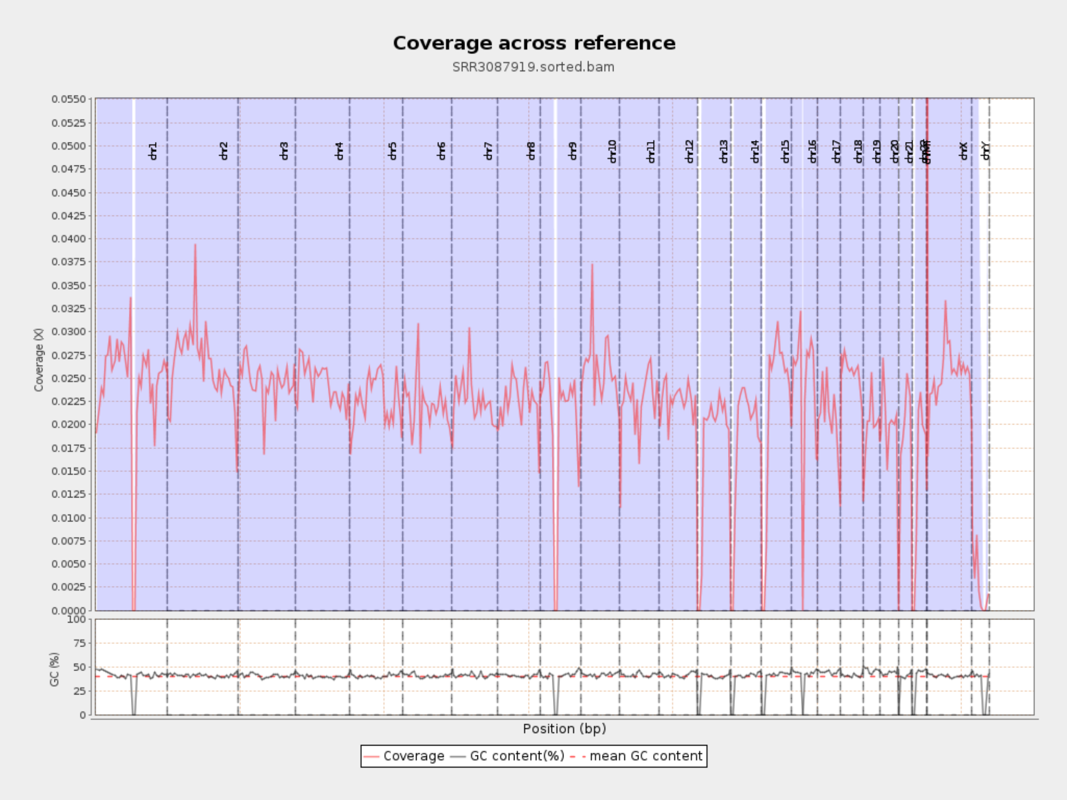
| | |
|---|---|
| General error rate | 0.85% |
| Mismatches | 586,699 |
| Insertions | 4,840 |
| Mapped reads with at least one insertion | 0.43% |
| Deletions | 13,663 |
| Mapped reads with at least one deletion | 1.2% |
| Homopolymer indels | 45.68% |

## 2.6. Chromosome stats

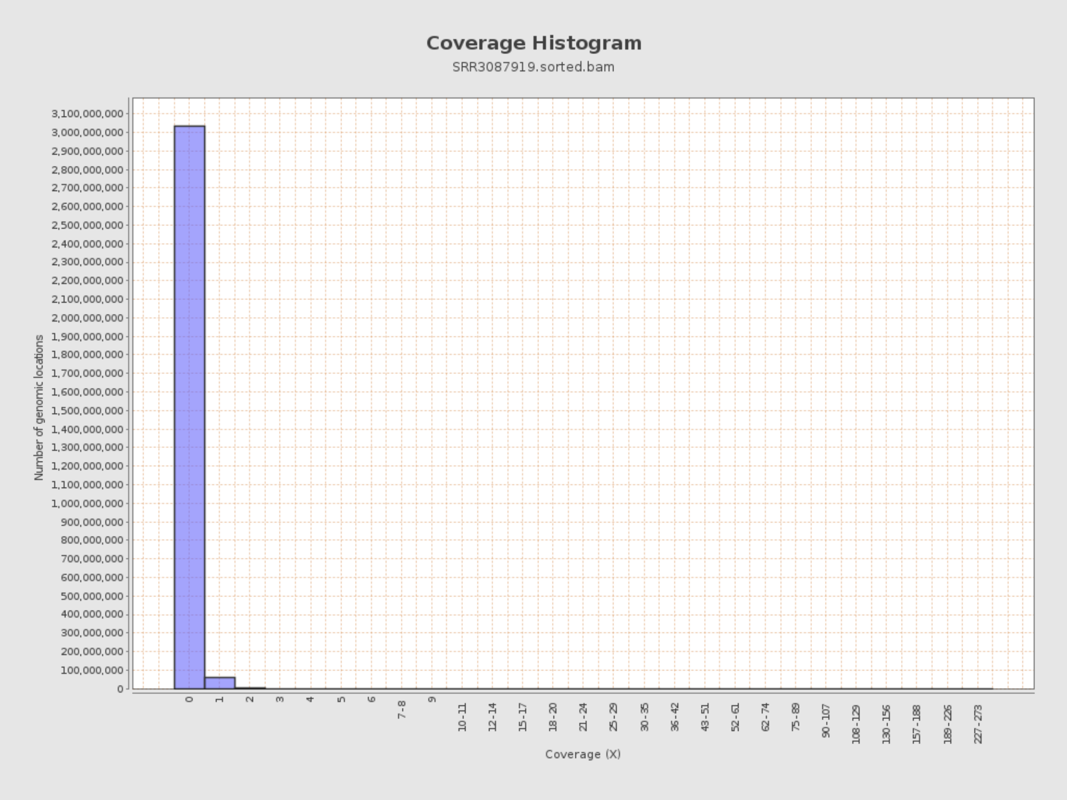
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6000796 | 0.0241 | 0.2806 |
| chr2 | 243199373 | 6447597 | 0.0265 | 0.2267 |
| chr3 | 198022430 | 4872732 | 0.0246 | 0.1669 |
| chr4 | 191154276 | 4666986 | 0.0244 | 0.1681 |
| chr5 | 180915260 | 4119553 | 0.0228 | 0.1602 |
| chr6 | 171115067 | 3790998 | 0.0222 | 0.175 |
| chr7 | 159138663 | 3603209 | 0.0226 | 0.2048 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3300296 | 0.0225 | 0.2049 |
| chr9 | 141213431 | 2880690 | 0.0204 | 0.1799 |
| chr10 | 135534747 | 3550790 | 0.0262 | 0.211 |
| chr11 | 135006516 | 3069196 | 0.0227 | 0.1807 |
| chr12 | 133851895 | 3014907 | 0.0225 | 0.16 |
| chr13 | 115169878 | 2013872 | 0.0175 | 0.1405 |
| chr14 | 107349540 | 1956794 | 0.0182 | 0.148 |
| chr15 | 102531392 | 2225969 | 0.0217 | 0.1586 |
| chr16 | 90354753 | 2150176 | 0.0238 | 0.1743 |
| chr17 | 81195210 | 1695486 | 0.0209 | 0.1688 |
| chr18 | 78077248 | 2011820 | 0.0258 | 0.3244 |
| chr19 | 59128983 | 1183687 | 0.02 | 0.2156 |
| chr20 | 63025520 | 1269206 | 0.0201 | 0.1526 |
| chr21 | 48129895 | 889582 | 0.0185 | 0.1479 |
| chr22 | 51304566 | 737779 | 0.0144 | 0.1261 |
| chrMT | 16571 | 37301 | 2.251 | 1.9522 |
| chrX | 155270560 | 3967324 | 0.0256 | 0.1818 |
| chrY | 59373566 | 160840 | 0.0027 | 0.0647 |

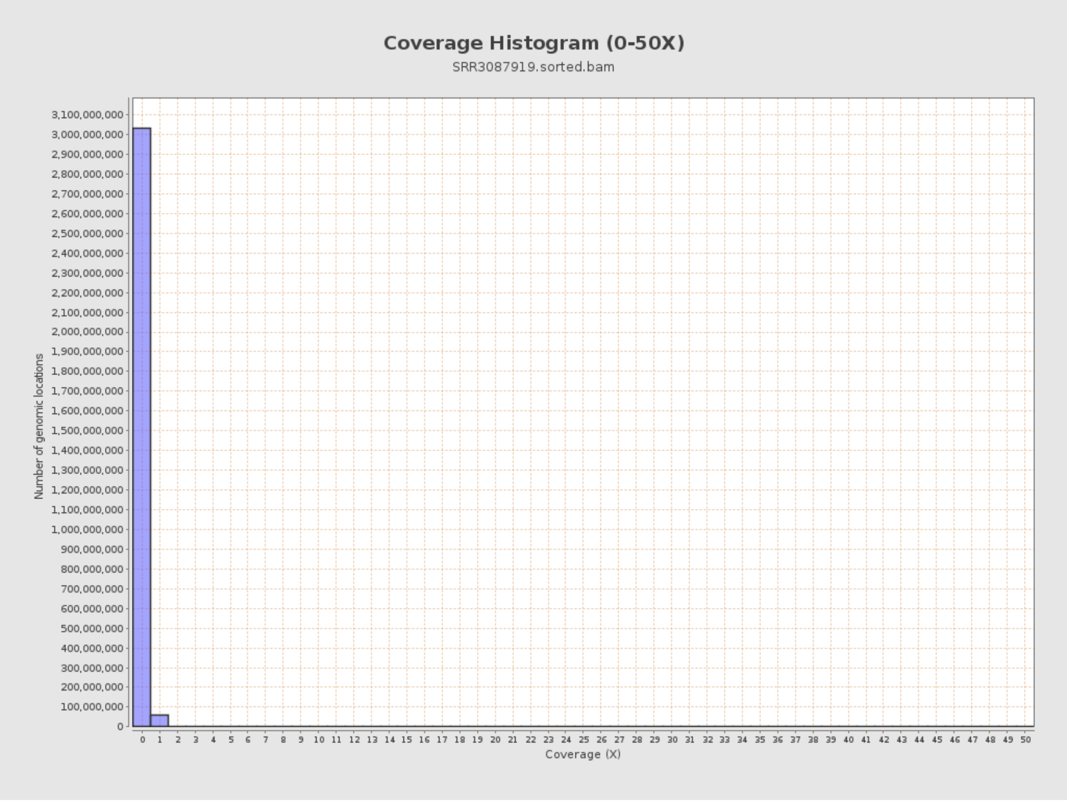
# 3. Results : Coverage across reference



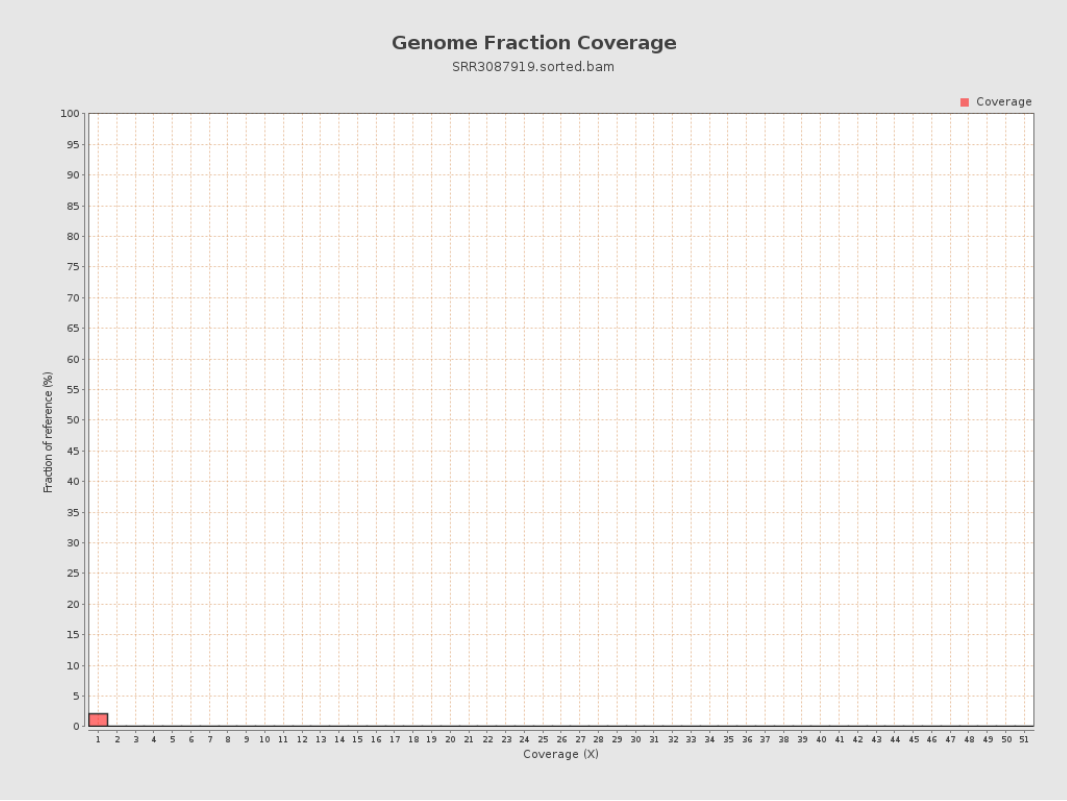
# 4. Results : Coverage Histogram



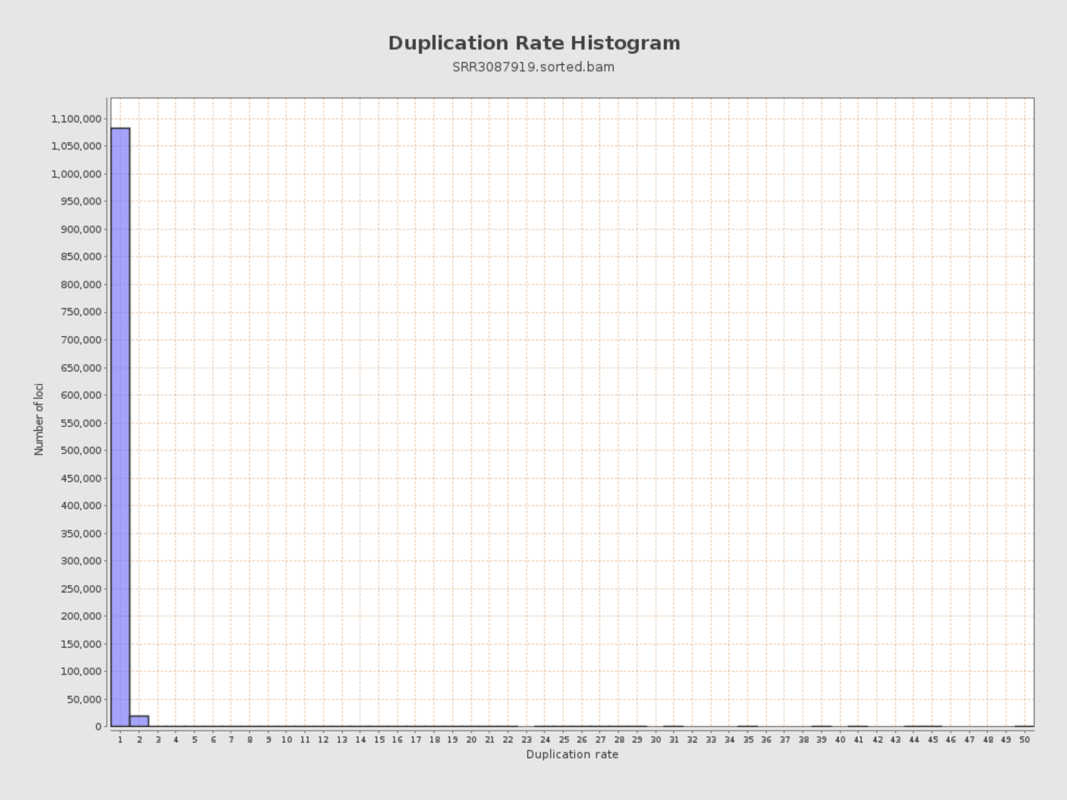
# 5. Results : Coverage Histogram (0-50X)



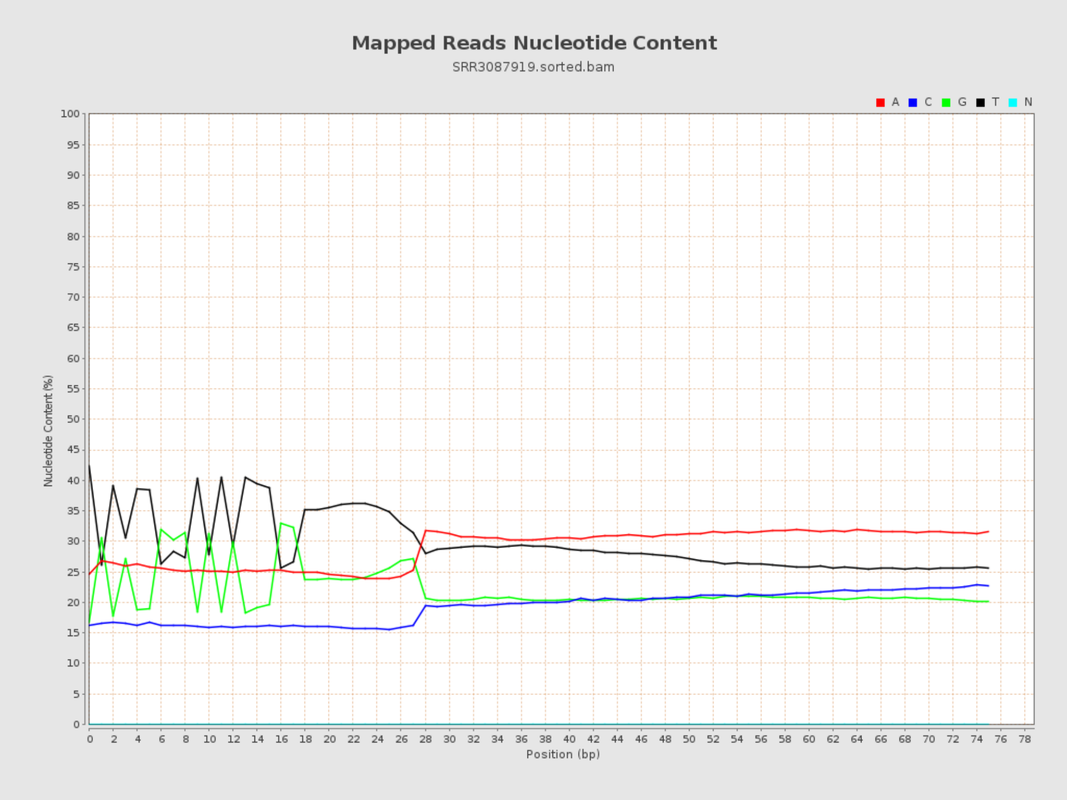
# 6. Results : Genome Fraction Coverage



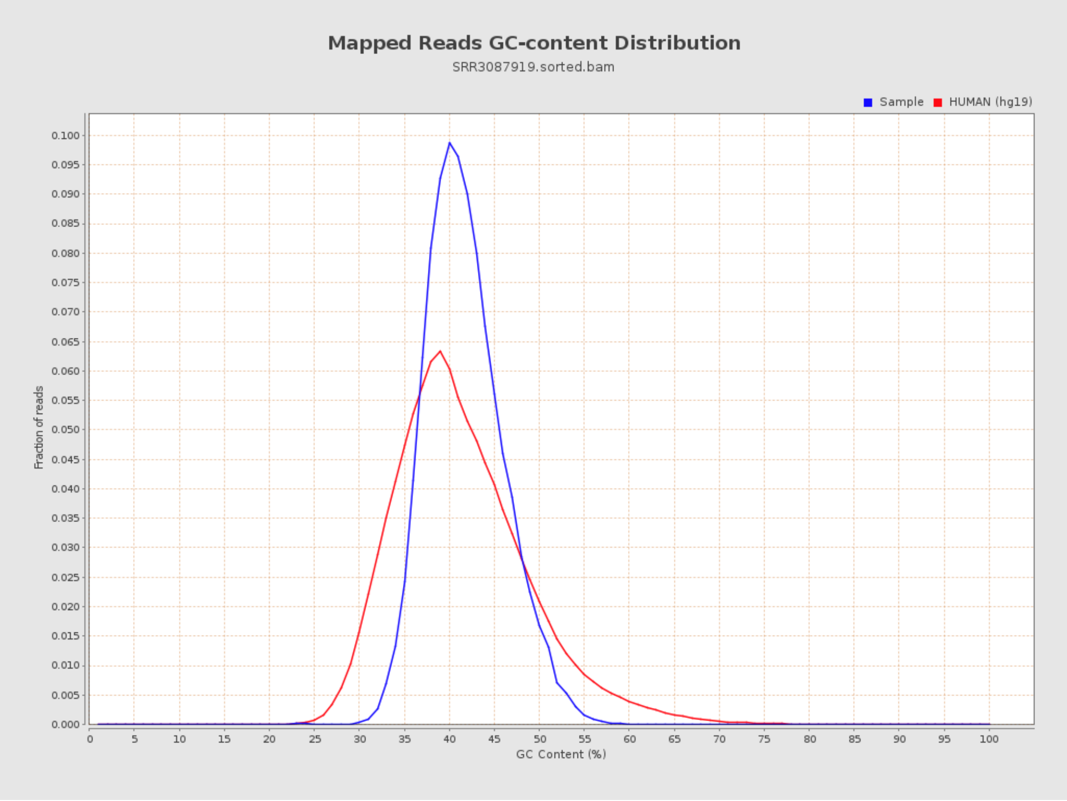
# 7. Results : Duplication Rate Histogram



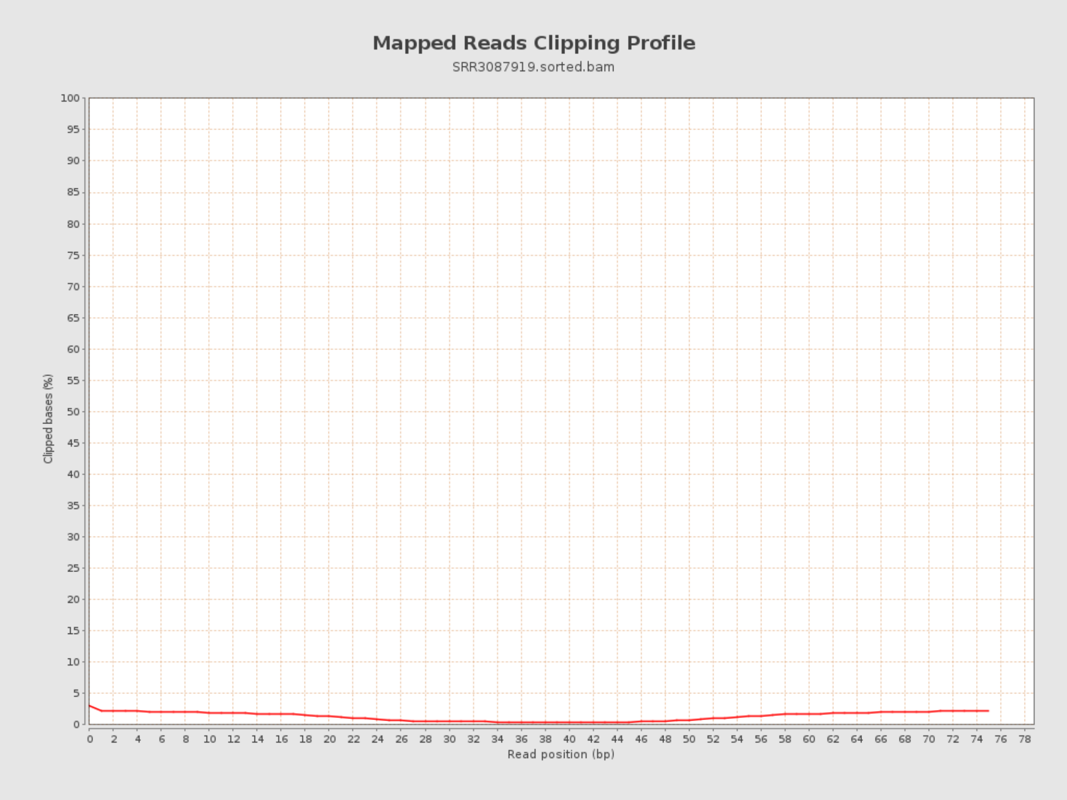
# 8. Results : Mapped Reads Nucleotide Content



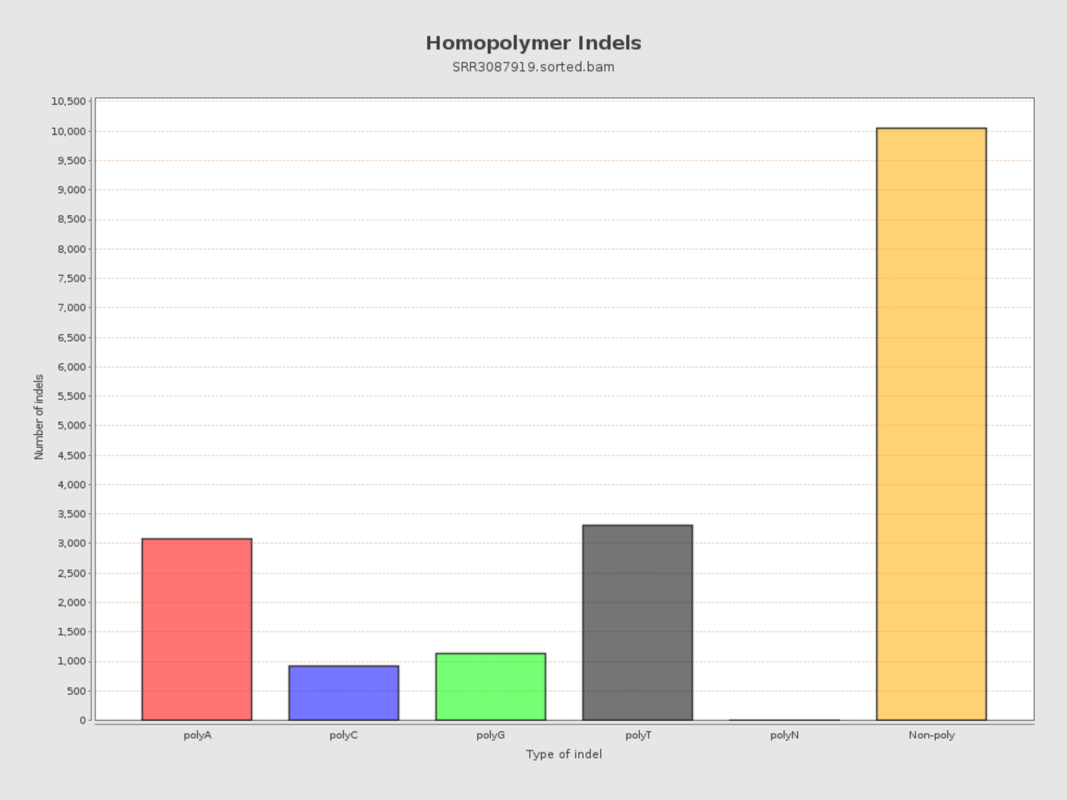
# 9. Results : Mapped Reads GC-content Distribution



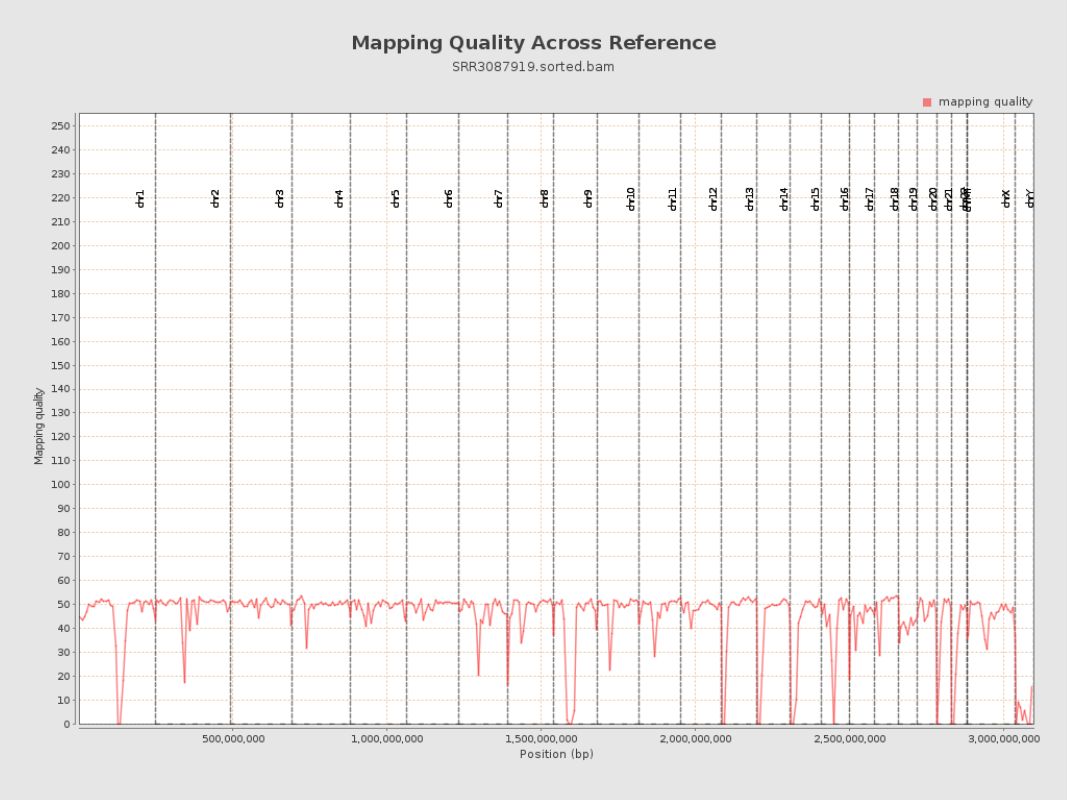
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram