# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 06:42:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237807.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_SRR6237807 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237807.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 17 06:42:19 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6237807.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,943,002 |
| Mapped reads | 2,111,906 / 71.76% |
| Unmapped reads | 831,096 / 28.24% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 11,627 / 0.4% |
| Read min/max/mean length | 30 / 76 / 76.14 |
| Duplicated reads (estimated) | 153,013 / 5.2% |
| Duplication rate | 6.14% |
| Clipped reads | 1,167,670 / 39.68% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 37,343,209 / 27.76% |
| Number/percentage of C's | 26,869,123 / 19.97% |
| Number/percentage of T's | 40,321,874 / 29.97% |
| Number/percentage of G's | 29,876,785 / 22.21% |
| Number/percentage of N's | 118,414 / 0.09% |
| GC Percentage | 42.18% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0435 |
| | |

| | |
|---|---|
| Standard Deviation | 0.393 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.6 |

## 2.5. Mismatches and indels

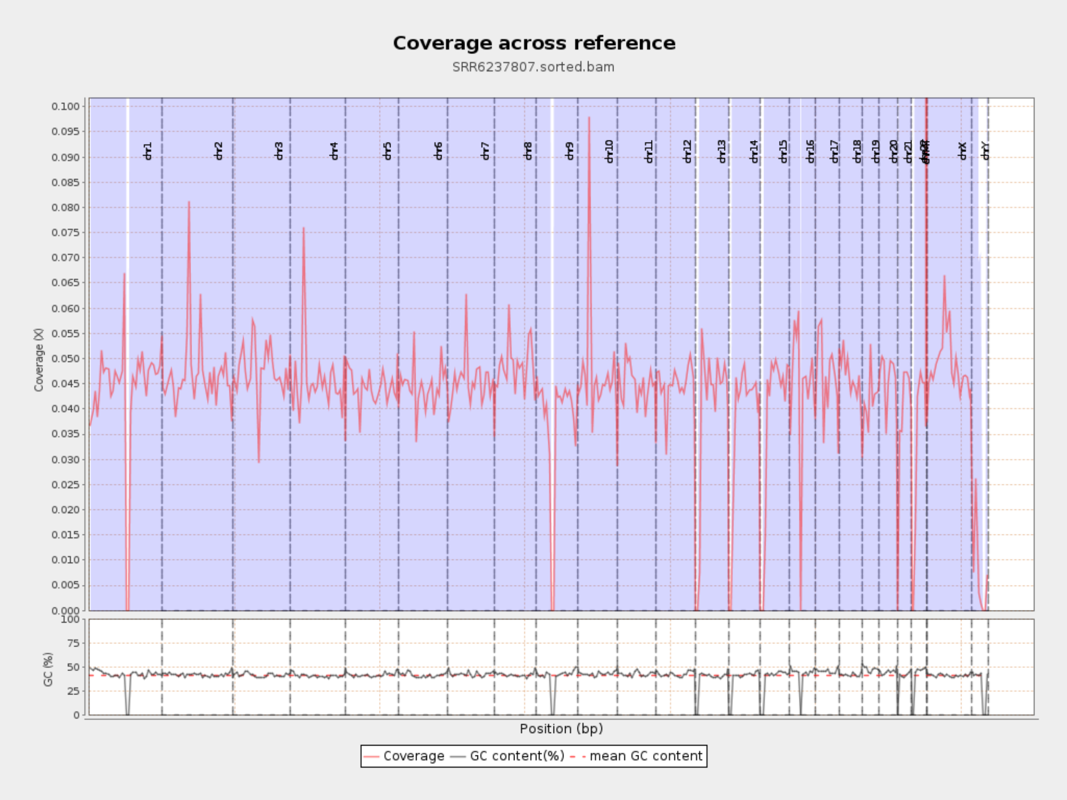
| | |
|---|---|
| General error rate | 0.83% |
| Mismatches | 1,095,790 |
| Insertions | 10,249 |
| Mapped reads with at least one insertion | 0.48% |
| Deletions | 29,662 |
| Mapped reads with at least one deletion | 1.39% |
| Homopolymer indels | 47.23% |

## 2.6. Chromosome stats

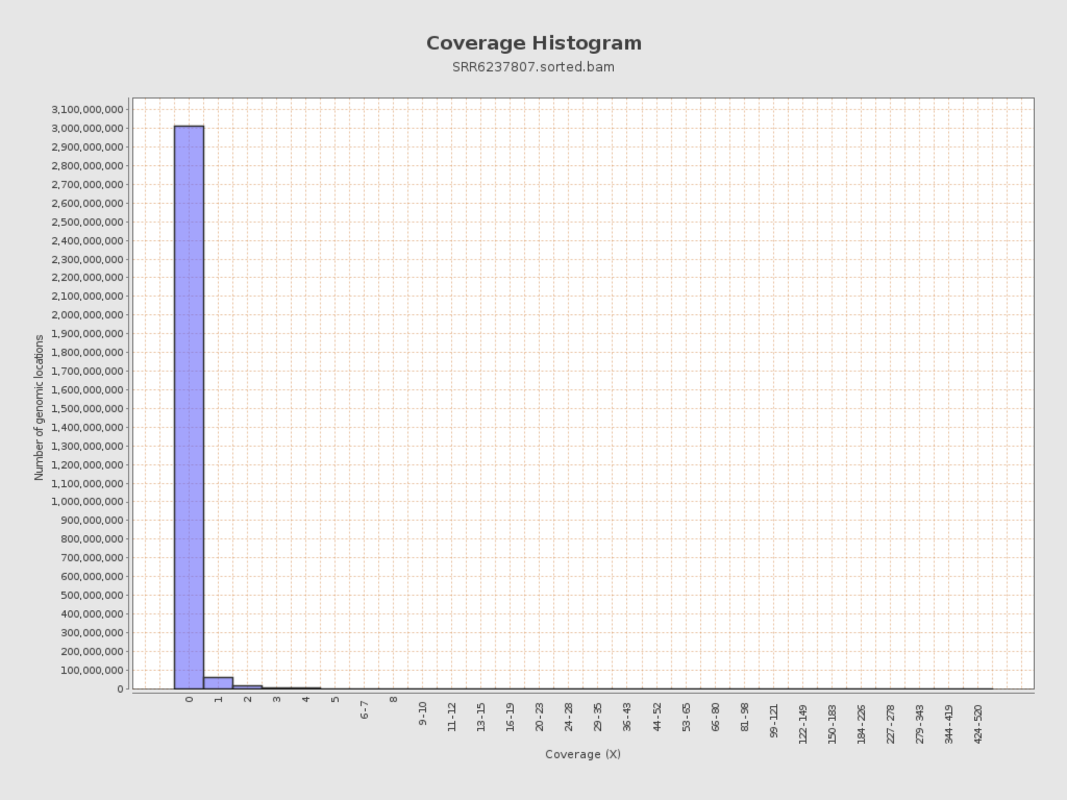
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 10876442 | 0.0436 | 0.5558 |
| chr2 | 243199373 | 11469858 | 0.0472 | 0.4261 |
| chr3 | 198022430 | 9429240 | 0.0476 | 0.3288 |
| chr4 | 191154276 | 8699227 | 0.0455 | 0.3509 |
| chr5 | 180915260 | 8005268 | 0.0442 | 0.3123 |
| chr6 | 171115067 | 7587099 | 0.0443 | 0.3401 |
| chr7 | 159138663 | 7235932 | 0.0455 | 0.4476 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7119641 | 0.0486 | 0.4043 |
| chr9 | 141213431 | 5153257 | 0.0365 | 0.3564 |
| chr10 | 135534747 | 6430435 | 0.0474 | 0.5221 |
| chr11 | 135006516 | 6052664 | 0.0448 | 0.4089 |
| chr12 | 133851895 | 5985006 | 0.0447 | 0.3154 |
| chr13 | 115169878 | 4493229 | 0.039 | 0.2943 |
| chr14 | 107349540 | 3960678 | 0.0369 | 0.2973 |
| chr15 | 102531392 | 3844398 | 0.0375 | 0.2838 |
| chr16 | 90354753 | 3980326 | 0.0441 | 0.349 |
| chr17 | 81195210 | 3741730 | 0.0461 | 0.3548 |
| chr18 | 78077248 | 3636051 | 0.0466 | 0.6142 |
| chr19 | 59128983 | 2466217 | 0.0417 | 0.4411 |
| chr20 | 63025520 | 2904498 | 0.0461 | 0.3349 |
| chr21 | 48129895 | 1835550 | 0.0381 | 0.3214 |
| chr22 | 51304566 | 1595863 | 0.0311 | 0.2623 |
| chrMT | 16571 | 66851 | 4.0342 | 3.578 |
| chrX | 155270560 | 7575559 | 0.0488 | 0.3515 |
| chrY | 59373566 | 435121 | 0.0073 | 0.214 |

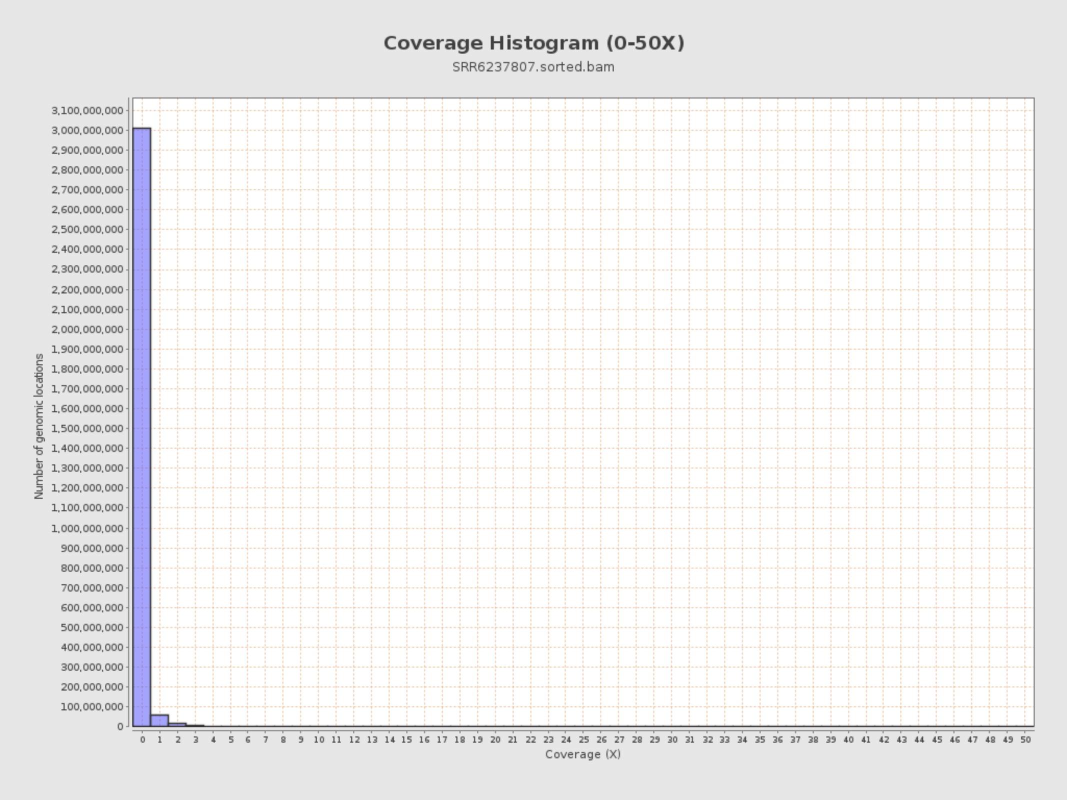
# 3. Results : Coverage across reference



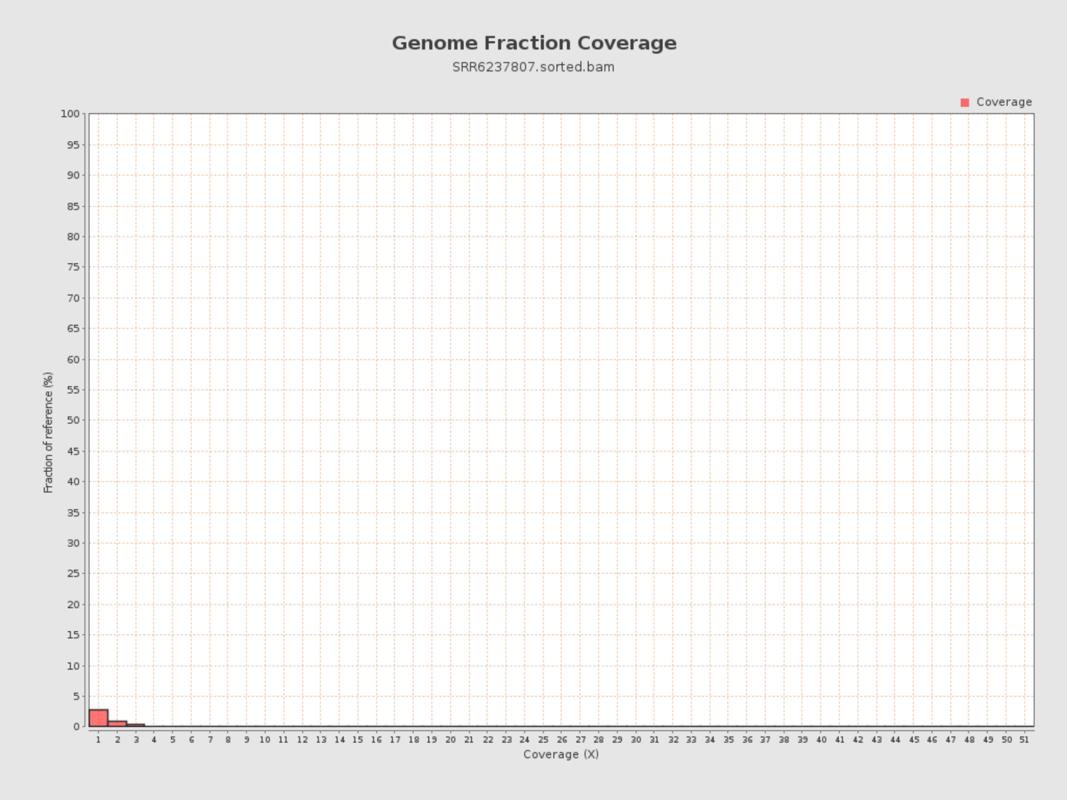
# 4. Results : Coverage Histogram



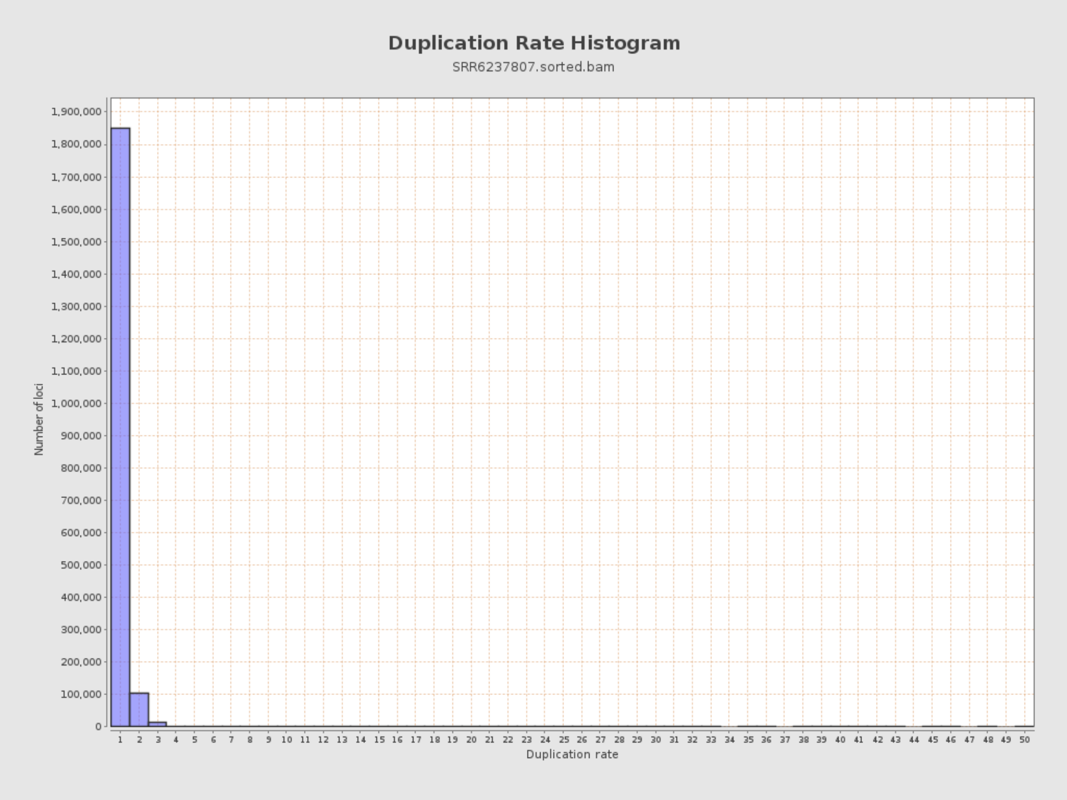
# 5. Results : Coverage Histogram (0-50X)



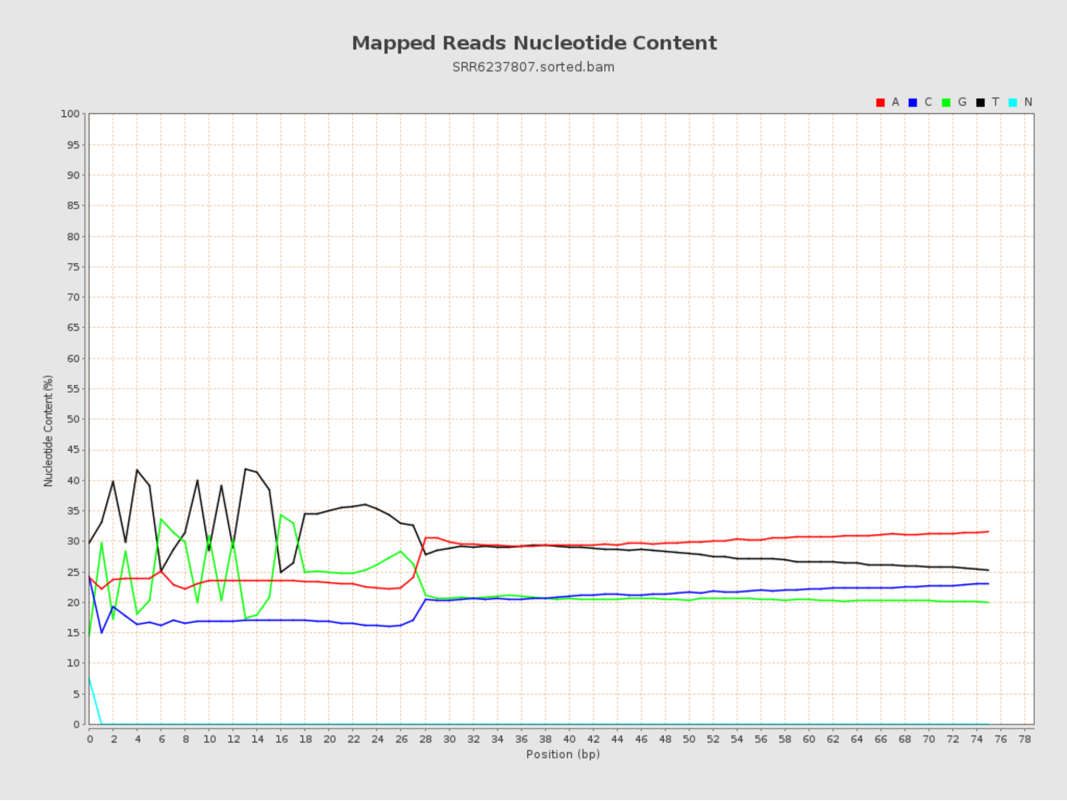
# 6. Results : Genome Fraction Coverage



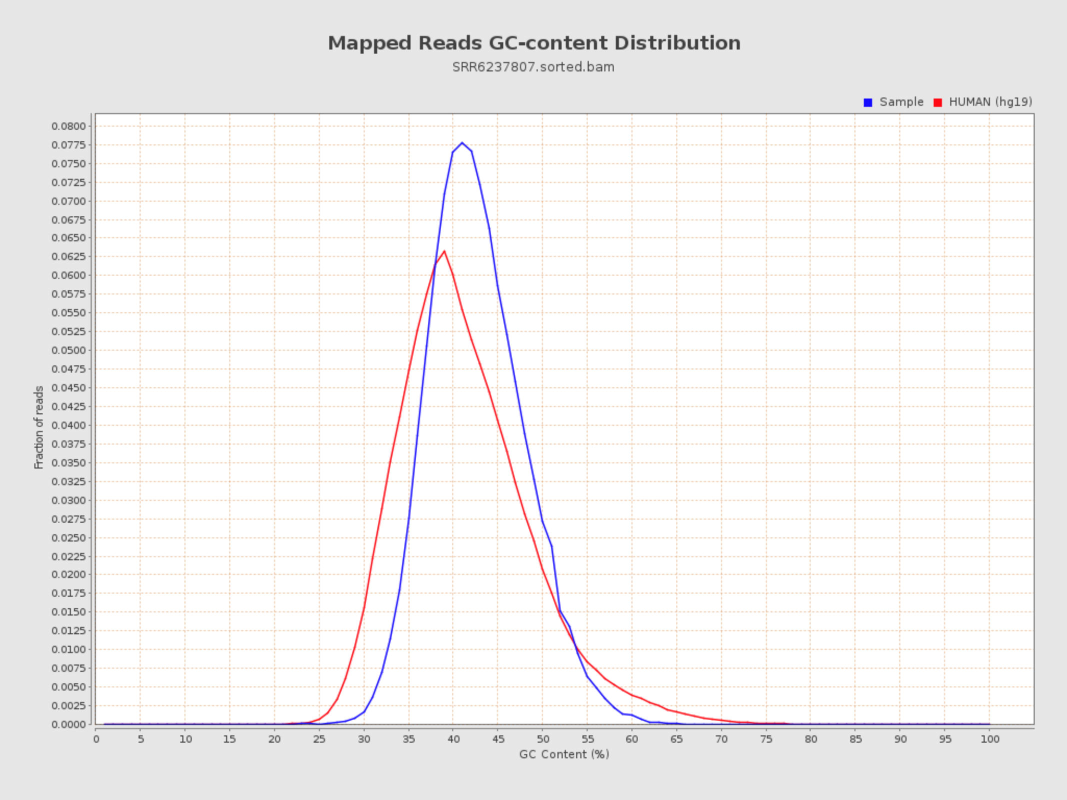
# 7. Results : Duplication Rate Histogram



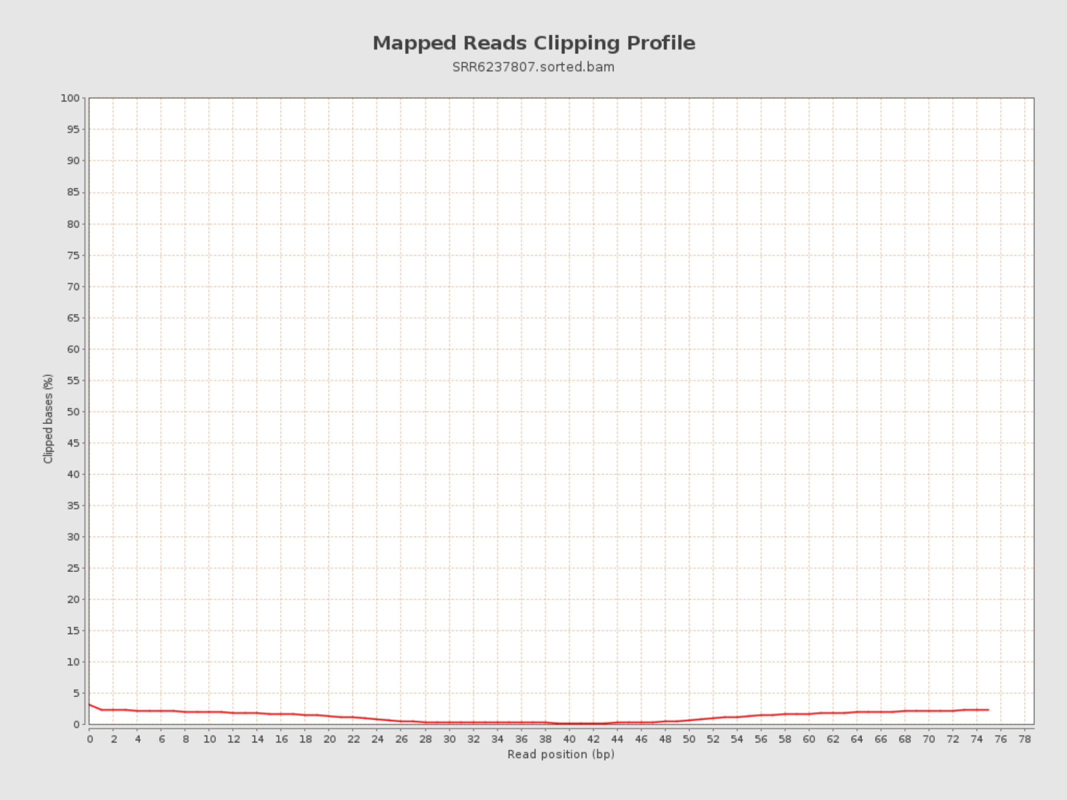
# 8. Results : Mapped Reads Nucleotide Content



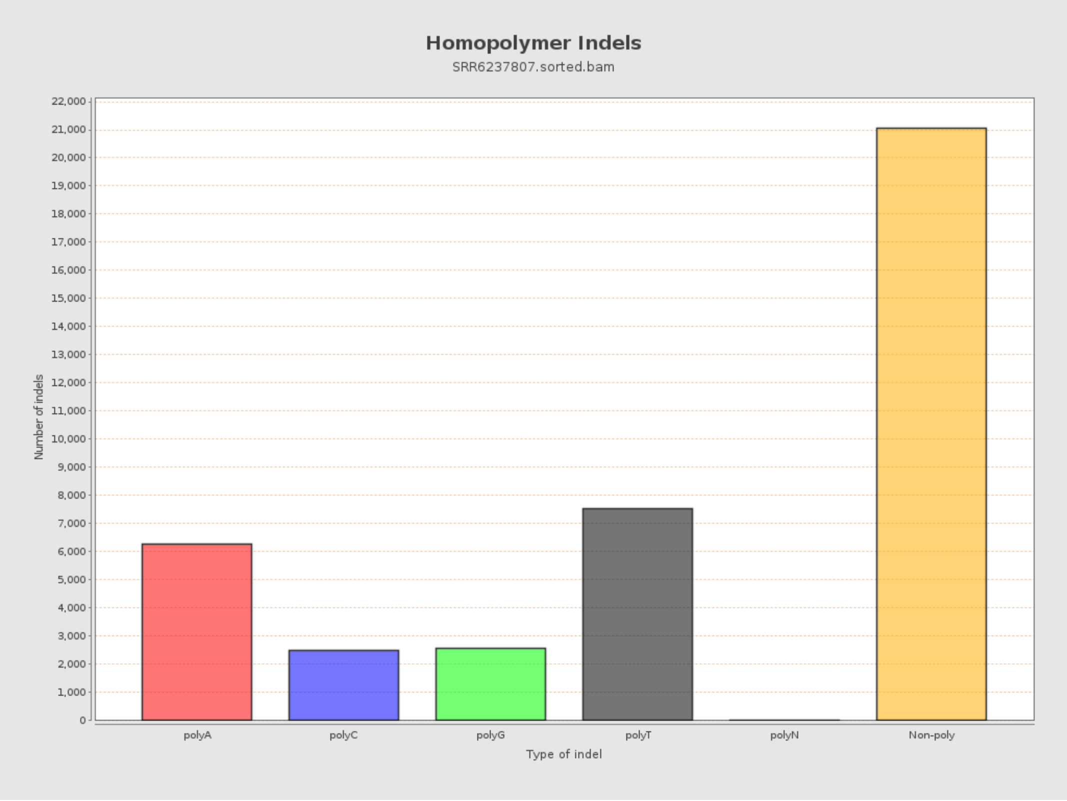
# 9. Results : Mapped Reads GC-content Distribution



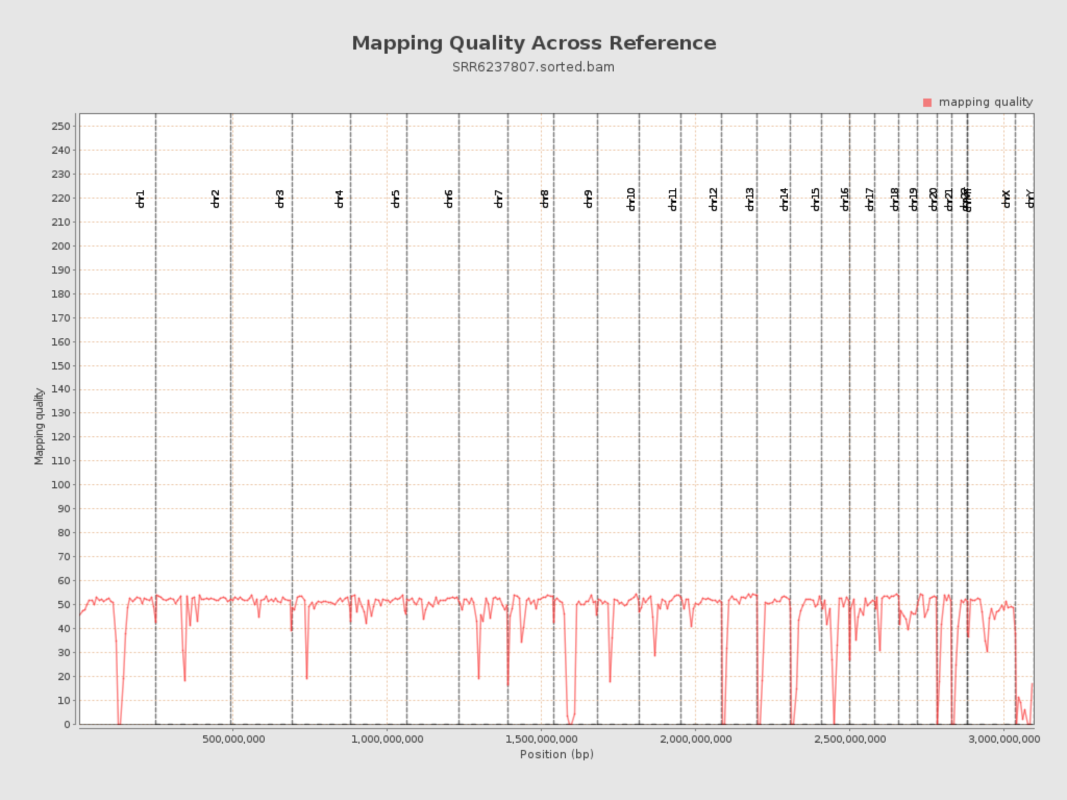
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram