# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 04:55:52*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237599.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_SRR6237599 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237599.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 17 04:55:51 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6237599.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,737,080 |
| Mapped reads | 2,107,785 / 77.01% |
| Unmapped reads | 629,295 / 22.99% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 10,518 / 0.38% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 161,657 / 5.91% |
| Duplication rate | 5.35% |
| Clipped reads | 1,339,163 / 48.93% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 34,911,065 / 26.72% |
| Number/percentage of C's | 22,595,344 / 17.29% |
| Number/percentage of T's | 41,807,595 / 32% |
| Number/percentage of G's | 31,104,316 / 23.81% |
| Number/percentage of N's | 235,581 / 0.18% |
| GC Percentage | 41.1% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0422 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3909 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.01 |

## 2.5. Mismatches and indels

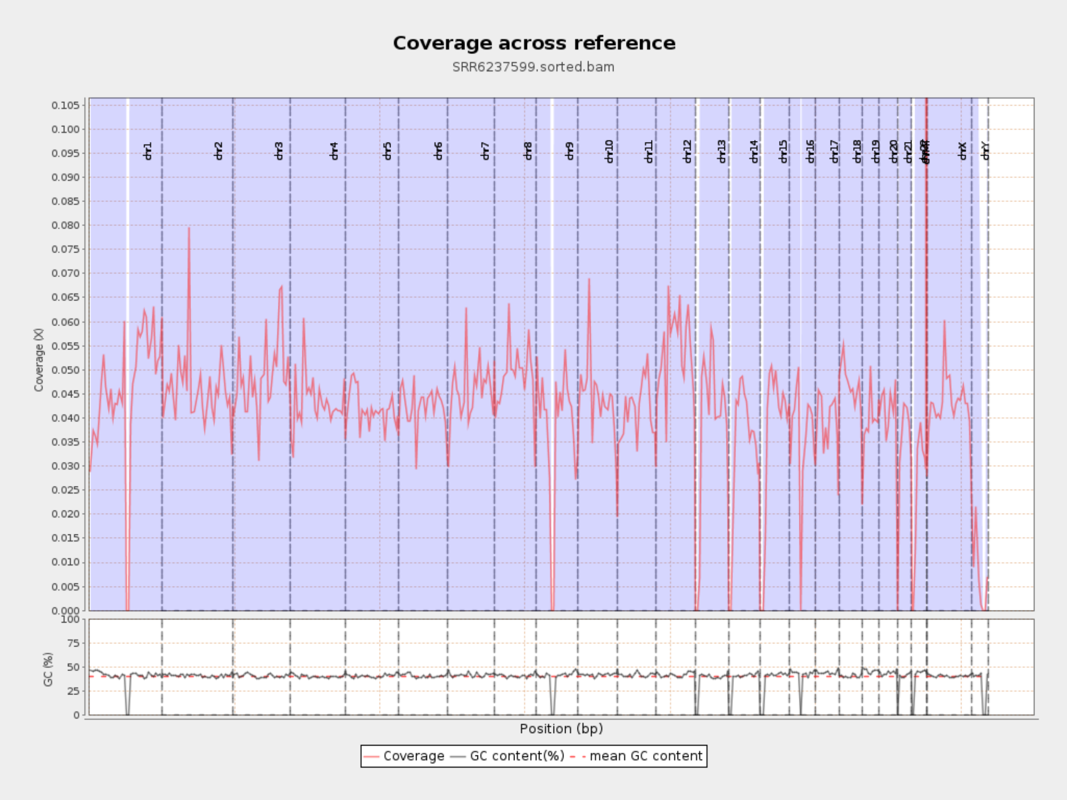
| | |
|---|---|
| General error rate | 1.06% |
| Mismatches | 1,357,809 |
| Insertions | 12,017 |
| Mapped reads with at least one insertion | 0.57% |
| Deletions | 52,492 |
| Mapped reads with at least one deletion | 2.46% |
| Homopolymer indels | 49.07% |

## 2.6. Chromosome stats

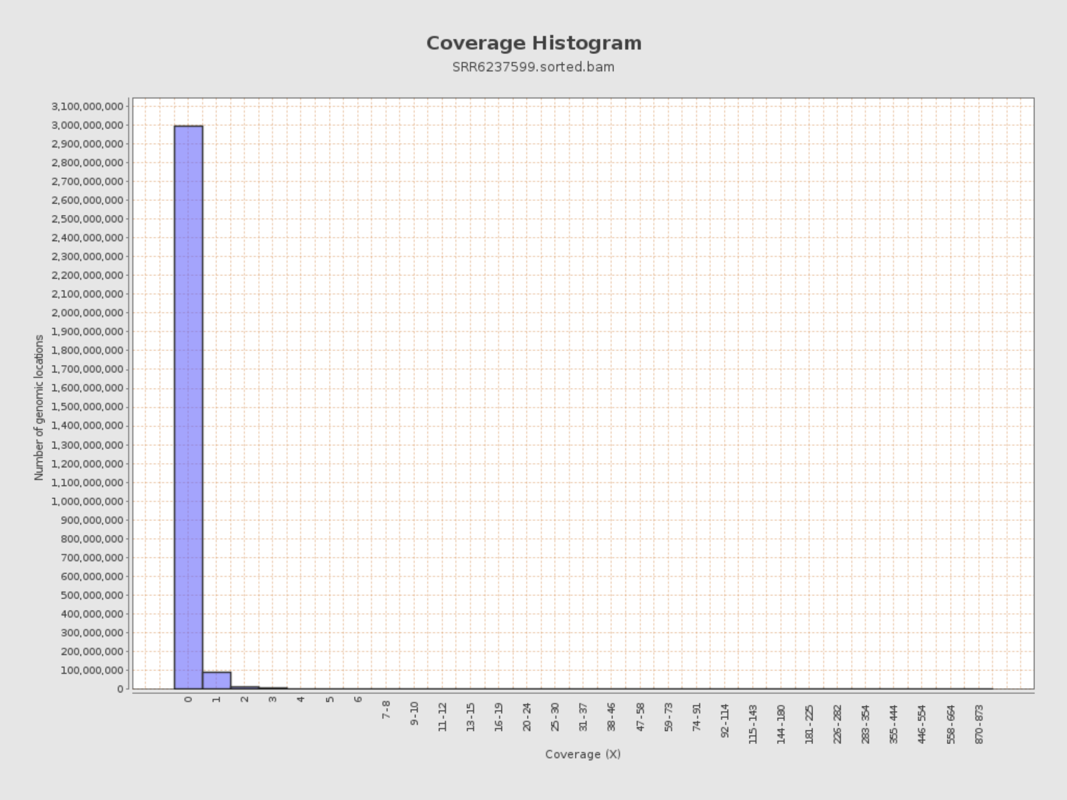
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 11300856 | 0.0453 | 0.5245 |
| chr2 | 243199373 | 11270131 | 0.0463 | 0.5567 |
| chr3 | 198022430 | 9627622 | 0.0486 | 0.3057 |
| chr4 | 191154276 | 8250040 | 0.0432 | 0.2932 |
| chr5 | 180915260 | 7585696 | 0.0419 | 0.2701 |
| chr6 | 171115067 | 7252348 | 0.0424 | 0.3262 |
| chr7 | 159138663 | 7295423 | 0.0458 | 0.5222 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7124730 | 0.0487 | 0.4623 |
| chr9 | 141213431 | 5268015 | 0.0373 | 0.3919 |
| chr10 | 135534747 | 6060105 | 0.0447 | 0.368 |
| chr11 | 135006516 | 5568445 | 0.0412 | 0.3842 |
| chr12 | 133851895 | 7268897 | 0.0543 | 0.3285 |
| chr13 | 115169878 | 4396840 | 0.0382 | 0.2776 |
| chr14 | 107349540 | 3613602 | 0.0337 | 0.2718 |
| chr15 | 102531392 | 3718437 | 0.0363 | 0.2655 |
| chr16 | 90354753 | 3275995 | 0.0363 | 0.2857 |
| chr17 | 81195210 | 3149394 | 0.0388 | 0.29 |
| chr18 | 78077248 | 3704417 | 0.0474 | 0.7008 |
| chr19 | 59128983 | 2324610 | 0.0393 | 0.3815 |
| chr20 | 63025520 | 2622221 | 0.0416 | 0.2873 |
| chr21 | 48129895 | 1638682 | 0.034 | 0.2724 |
| chr22 | 51304566 | 1224850 | 0.0239 | 0.206 |
| chrMT | 16571 | 93618 | 5.6495 | 4.4435 |
| chrX | 155270560 | 6677916 | 0.043 | 0.3113 |
| chrY | 59373566 | 425521 | 0.0072 | 0.1619 |

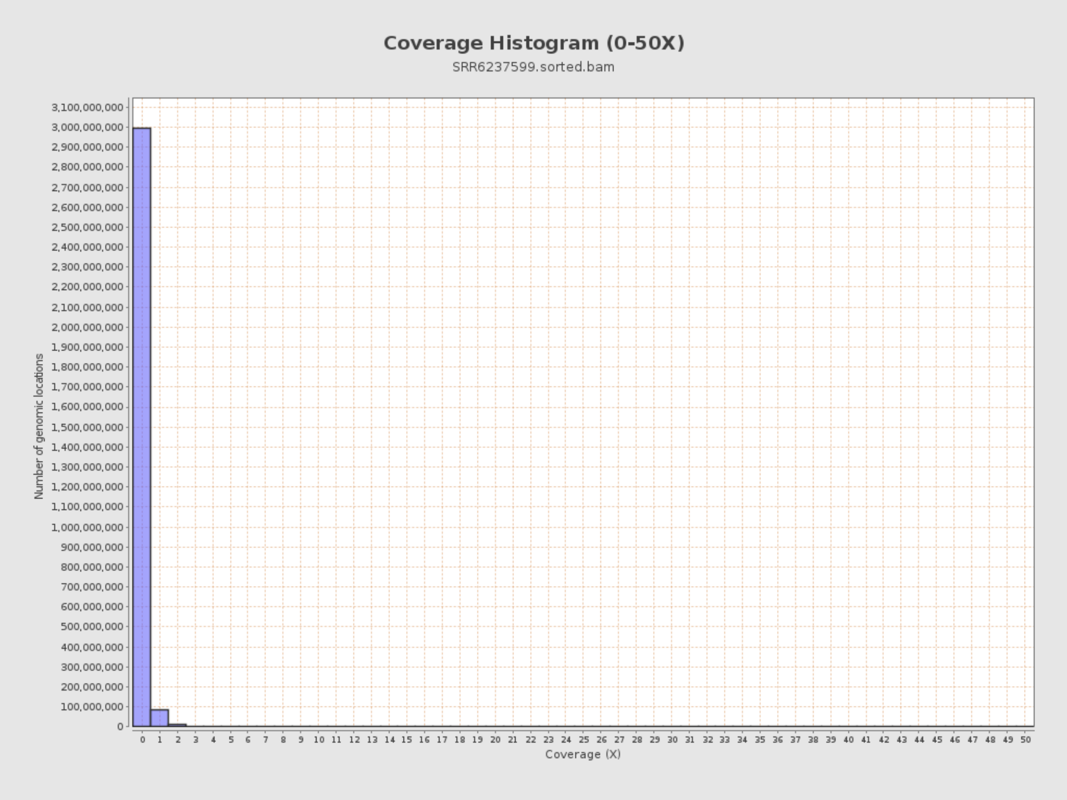
# 3. Results : Coverage across reference



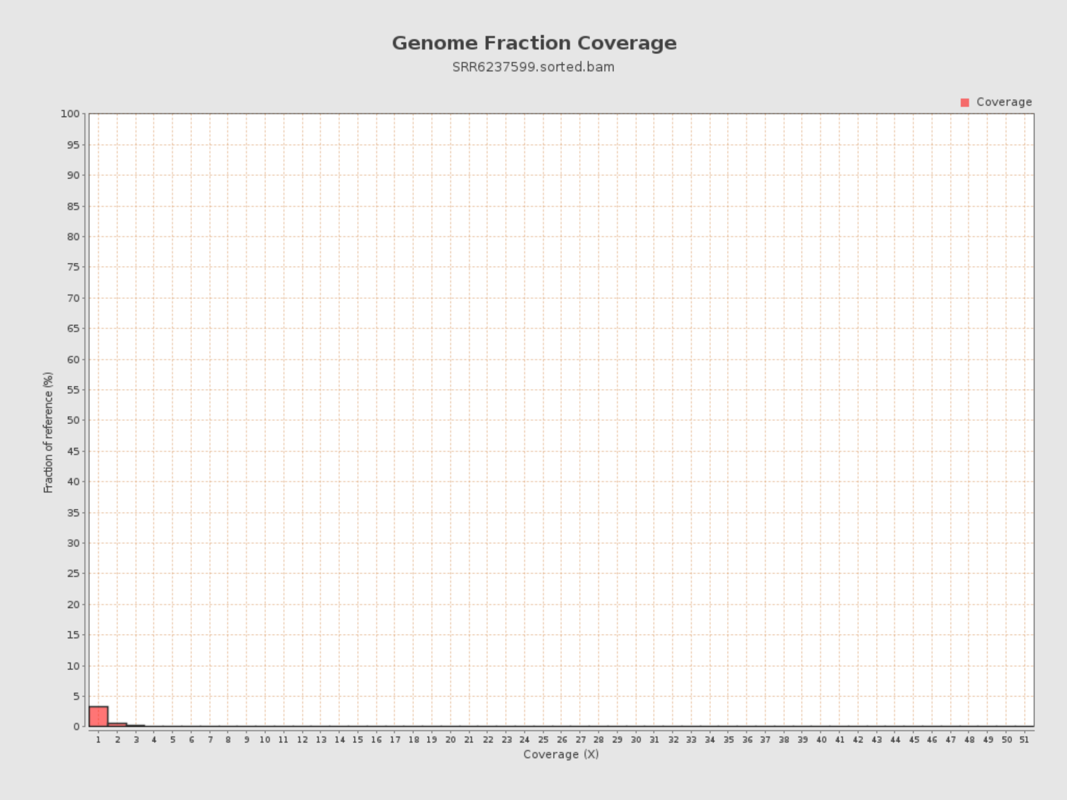
# 4. Results : Coverage Histogram



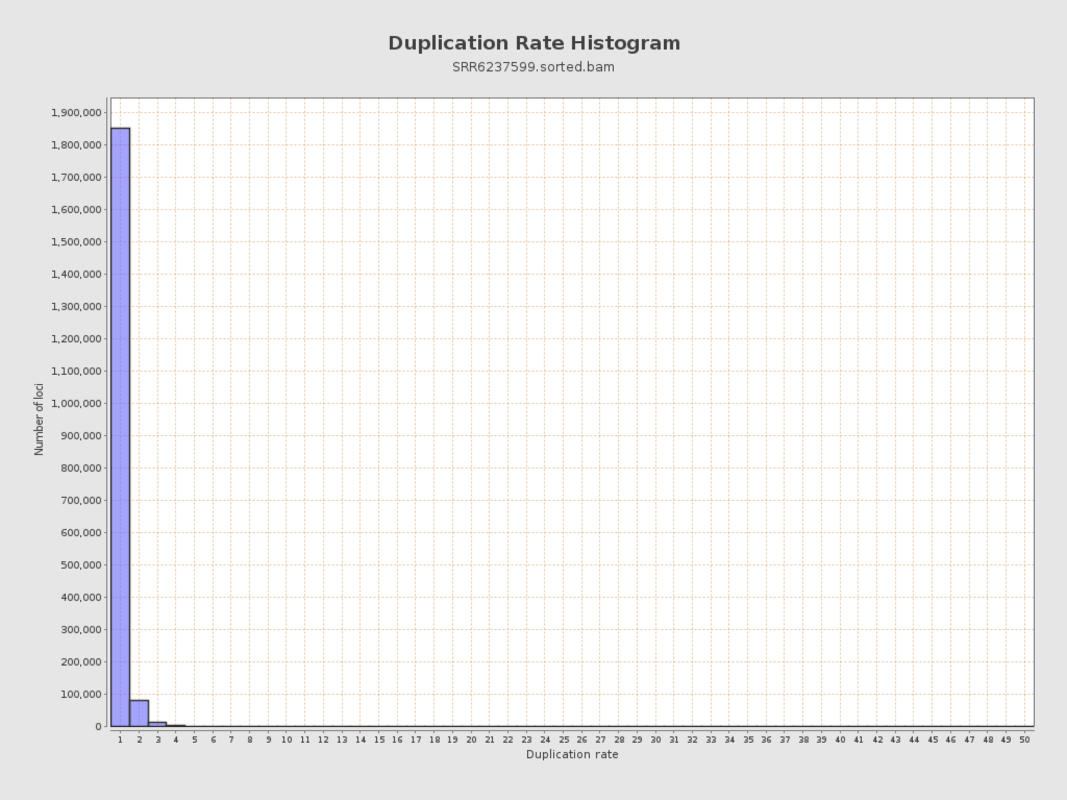
# 5. Results : Coverage Histogram (0-50X)



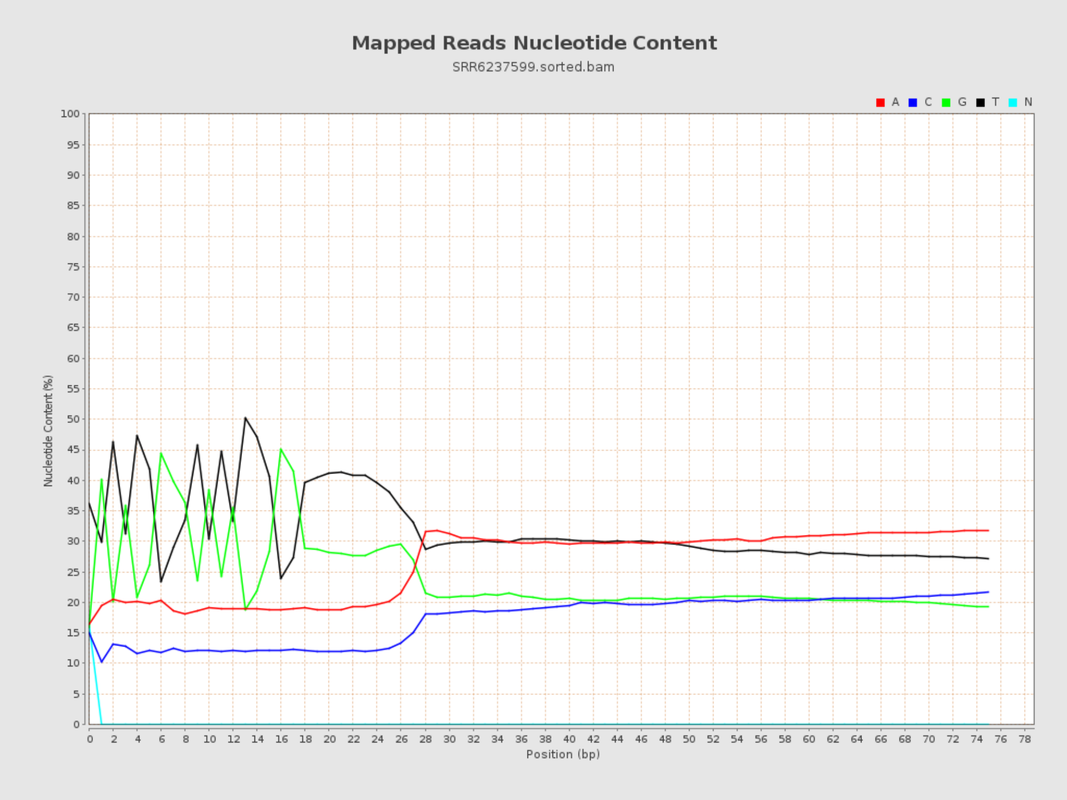
# 6. Results : Genome Fraction Coverage



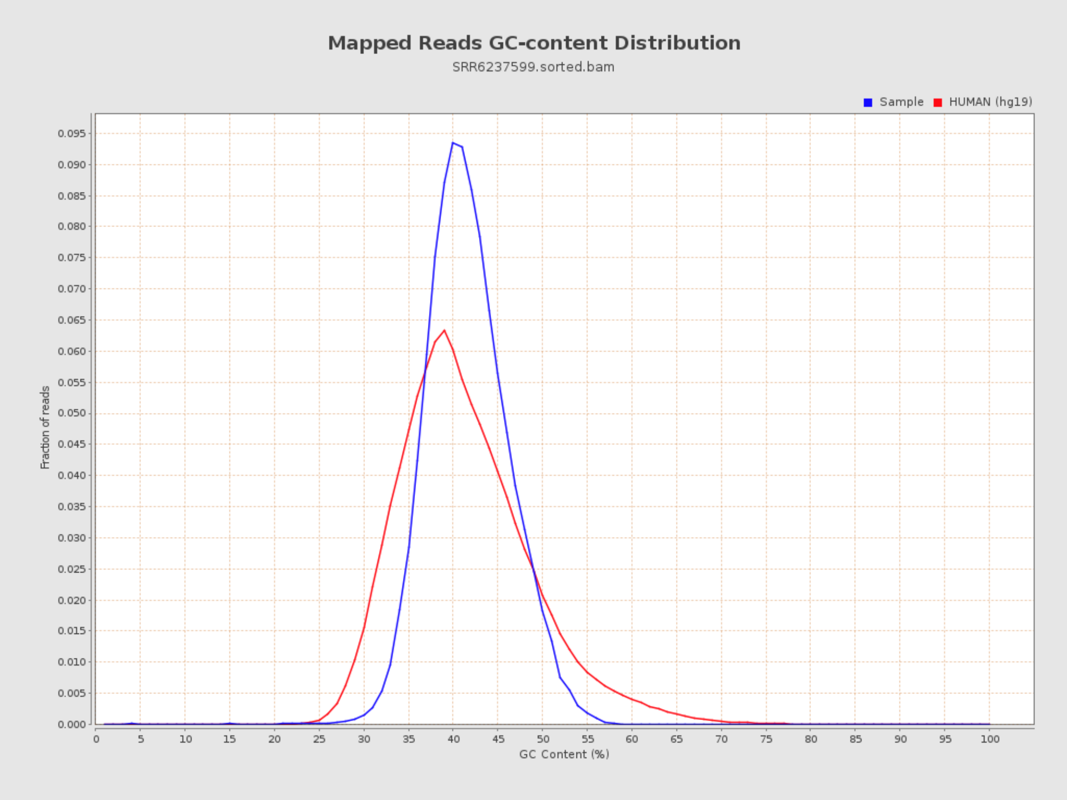
# 7. Results : Duplication Rate Histogram



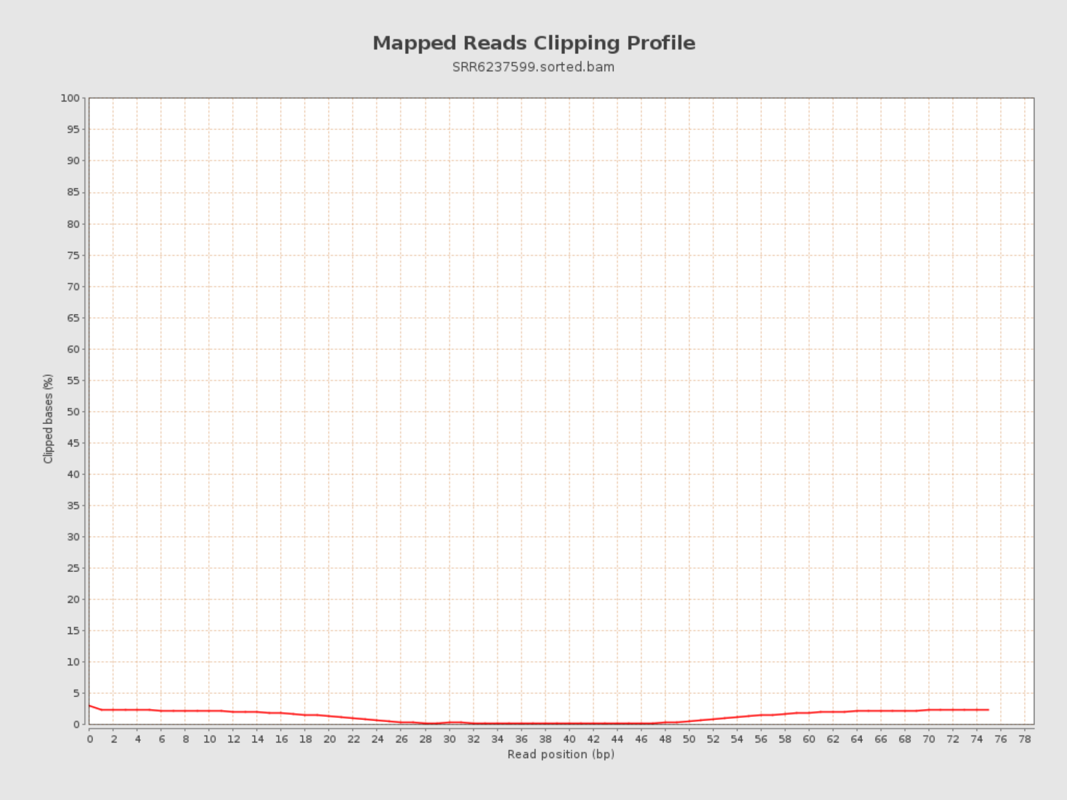
# 8. Results : Mapped Reads Nucleotide Content



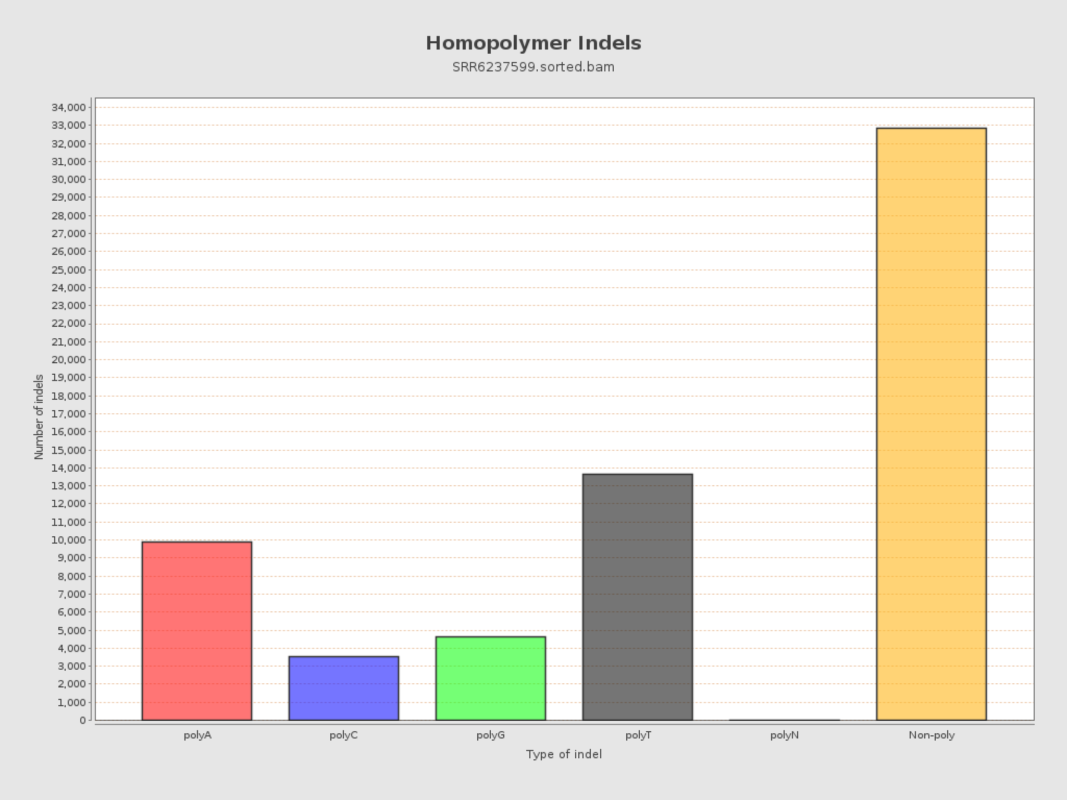
# 9. Results : Mapped Reads GC-content Distribution



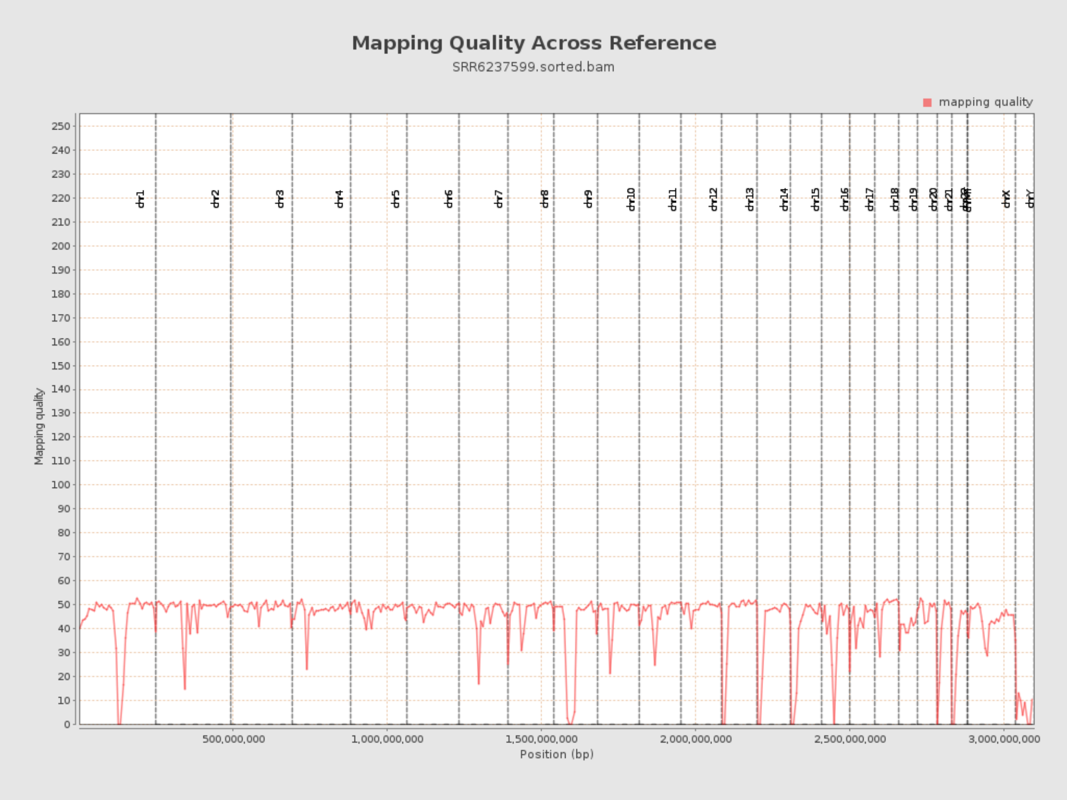
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram