# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 04:42:42*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237593.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_SRR6237593 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237593.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 17 04:42:41 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6237593.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,333,507 |
| Mapped reads | 1,018,282 / 76.36% |
| Unmapped reads | 315,225 / 23.64% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 5,189 / 0.39% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 48,066 / 3.6% |
| Duplication rate | 3.41% |
| Clipped reads | 621,725 / 46.62% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 17,038,329 / 26.87% |
| Number/percentage of C's | 11,091,156 / 17.49% |
| Number/percentage of T's | 20,034,735 / 31.59% |
| Number/percentage of G's | 15,141,116 / 23.87% |
| Number/percentage of N's | 114,842 / 0.18% |
| GC Percentage | 41.36% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0205 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2321 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 42.95 |

## 2.5. Mismatches and indels

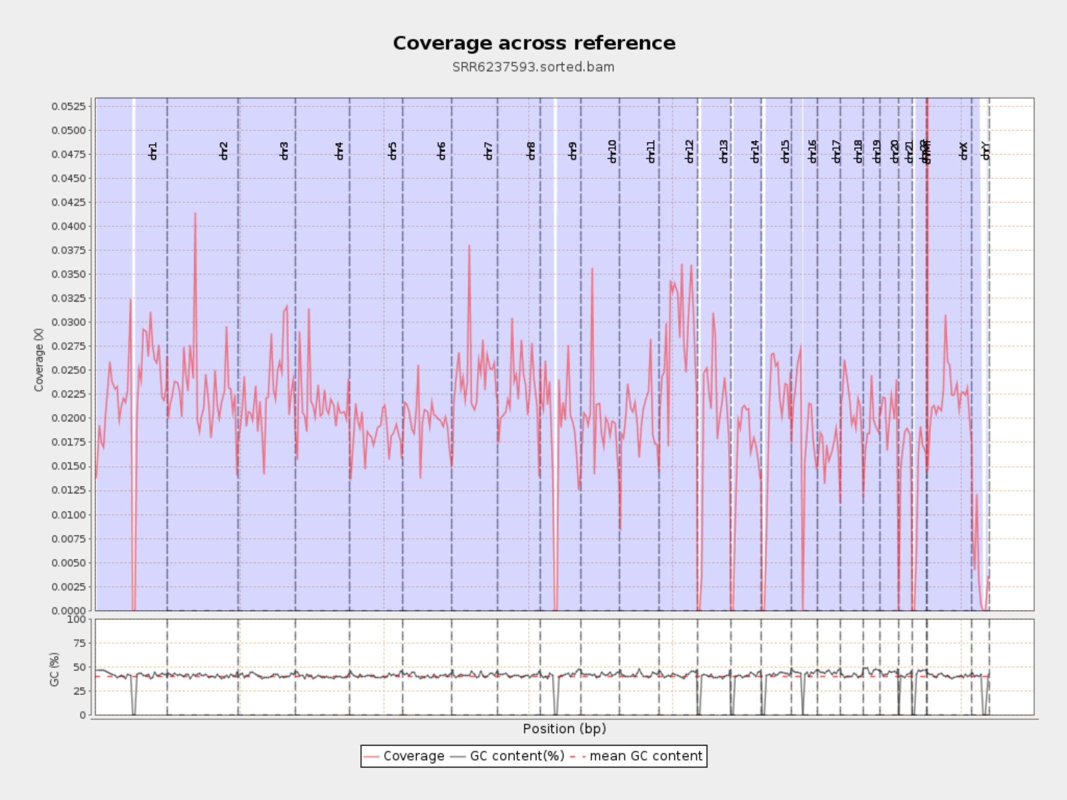
| | |
|---|---|
| General error rate | 1.02% |
| Mismatches | 633,141 |
| Insertions | 6,211 |
| Mapped reads with at least one insertion | 0.6% |
| Deletions | 23,594 |
| Mapped reads with at least one deletion | 2.29% |
| Homopolymer indels | 48.29% |

## 2.6. Chromosome stats

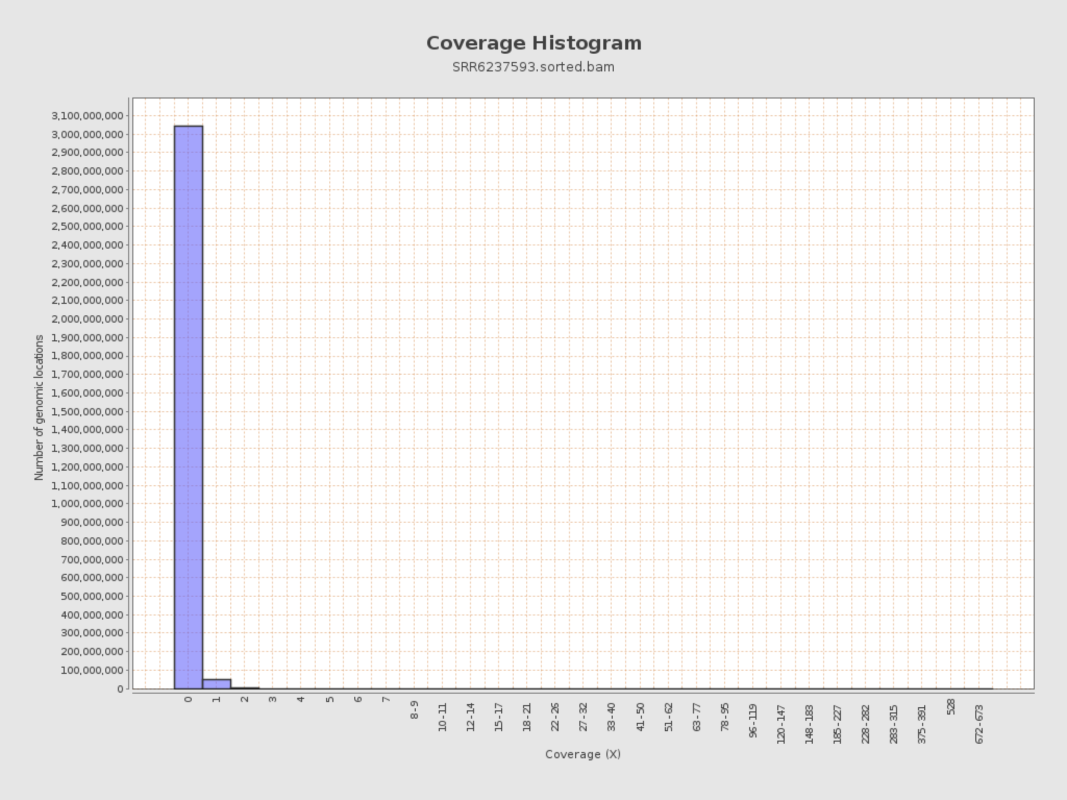
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5516058 | 0.0221 | 0.2954 |
| chr2 | 243199373 | 5585211 | 0.023 | 0.3643 |
| chr3 | 198022430 | 4460315 | 0.0225 | 0.1805 |
| chr4 | 191154276 | 4101556 | 0.0215 | 0.1803 |
| chr5 | 180915260 | 3347302 | 0.0185 | 0.157 |
| chr6 | 171115067 | 3385921 | 0.0198 | 0.1988 |
| chr7 | 159138663 | 3896381 | 0.0245 | 0.3308 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3313044 | 0.0226 | 0.223 |
| chr9 | 141213431 | 2581046 | 0.0183 | 0.2283 |
| chr10 | 135534747 | 2670395 | 0.0197 | 0.2141 |
| chr11 | 135006516 | 2706123 | 0.02 | 0.2132 |
| chr12 | 133851895 | 3856187 | 0.0288 | 0.2073 |
| chr13 | 115169878 | 2199170 | 0.0191 | 0.1709 |
| chr14 | 107349540 | 1663419 | 0.0155 | 0.1612 |
| chr15 | 102531392 | 1954679 | 0.0191 | 0.1678 |
| chr16 | 90354753 | 1693176 | 0.0187 | 0.1787 |
| chr17 | 81195210 | 1344095 | 0.0166 | 0.1586 |
| chr18 | 78077248 | 1679056 | 0.0215 | 0.3885 |
| chr19 | 59128983 | 1126444 | 0.0191 | 0.2164 |
| chr20 | 63025520 | 1297516 | 0.0206 | 0.1727 |
| chr21 | 48129895 | 743896 | 0.0155 | 0.1558 |
| chr22 | 51304566 | 612057 | 0.0119 | 0.1275 |
| chrMT | 16571 | 49956 | 3.0147 | 2.4482 |
| chrX | 155270560 | 3453966 | 0.0222 | 0.1861 |
| chrY | 59373566 | 222229 | 0.0037 | 0.0987 |

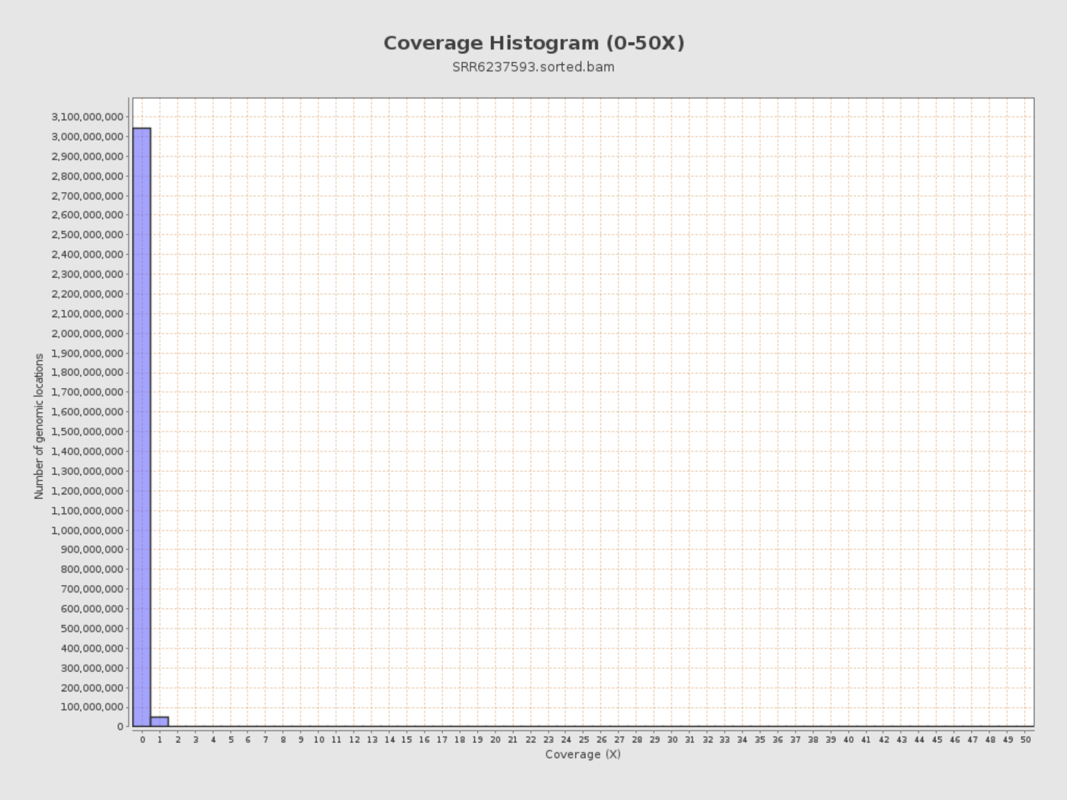
# 3. Results : Coverage across reference



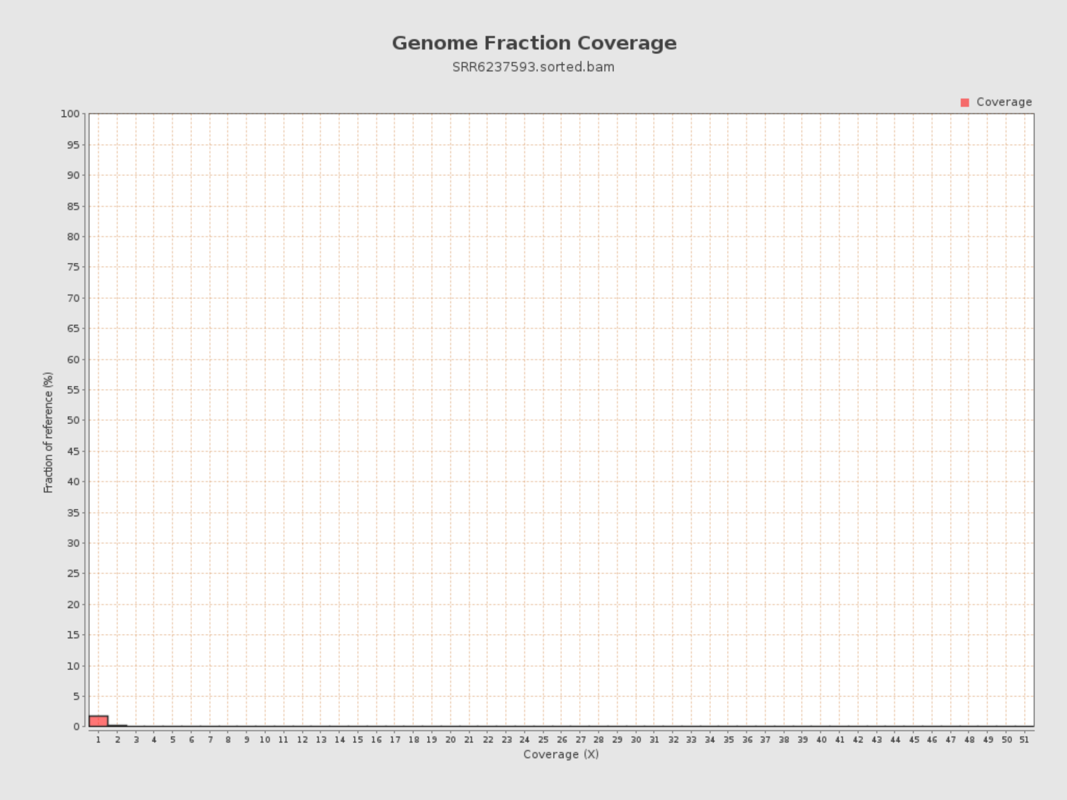
# 4. Results : Coverage Histogram



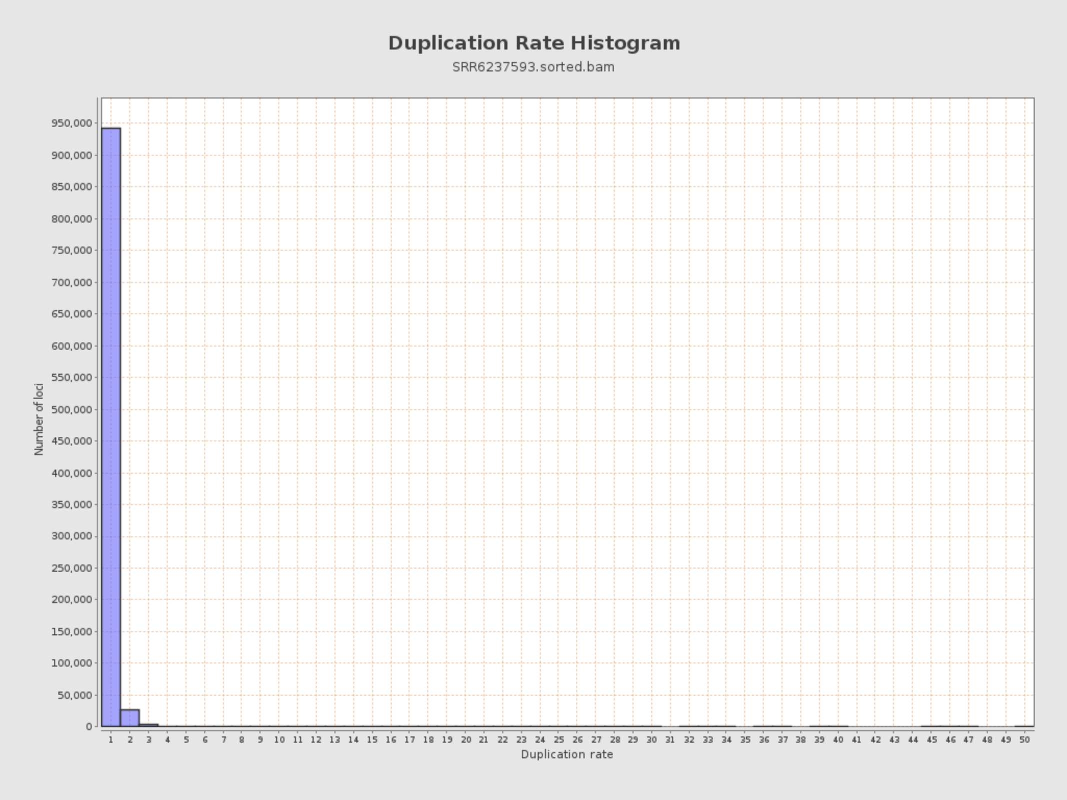
# 5. Results : Coverage Histogram (0-50X)



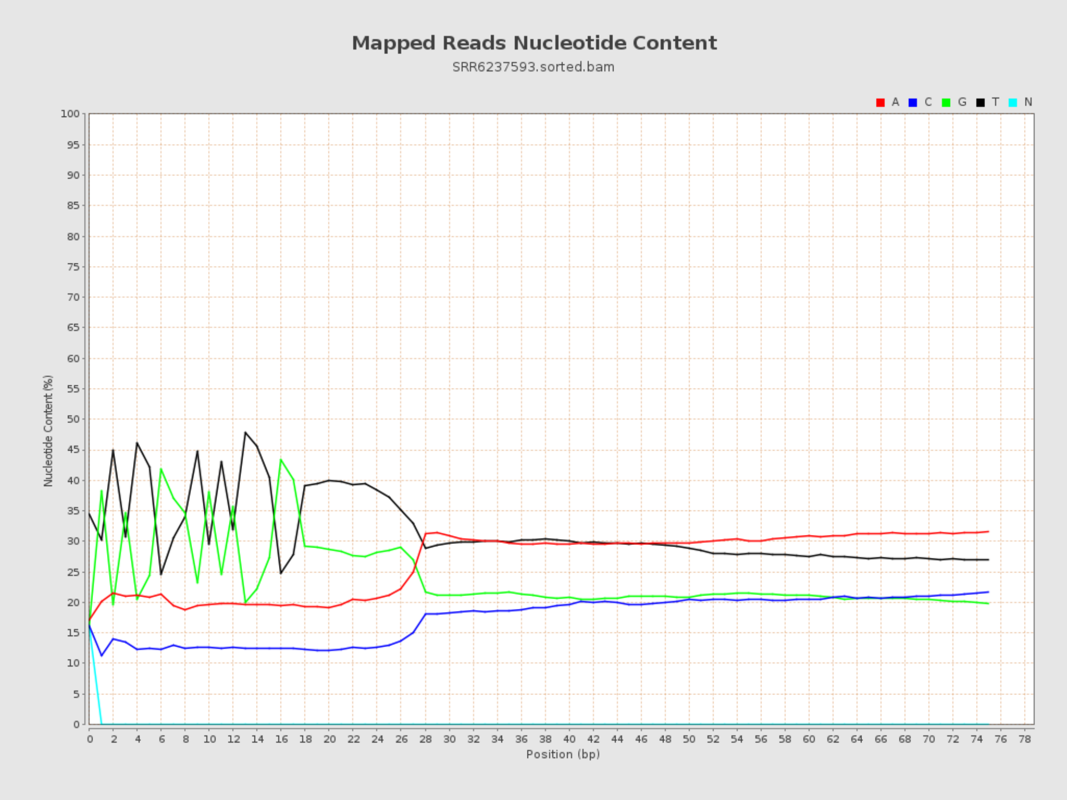
# 6. Results : Genome Fraction Coverage



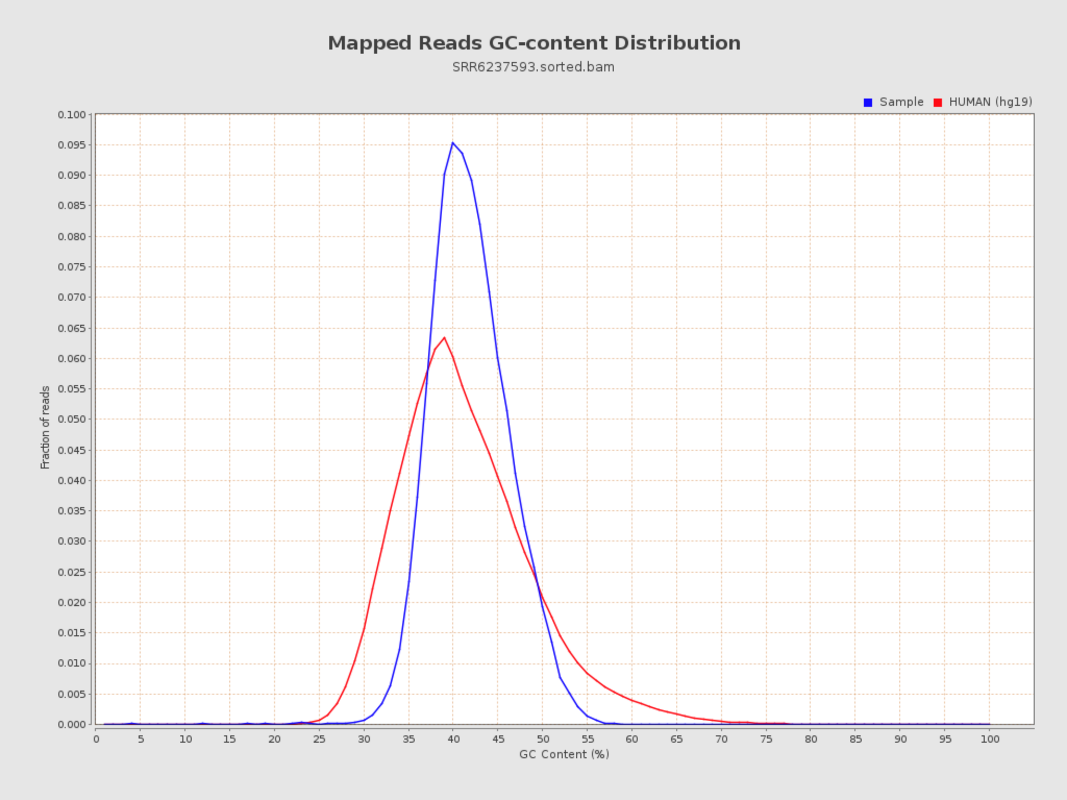
# 7. Results : Duplication Rate Histogram



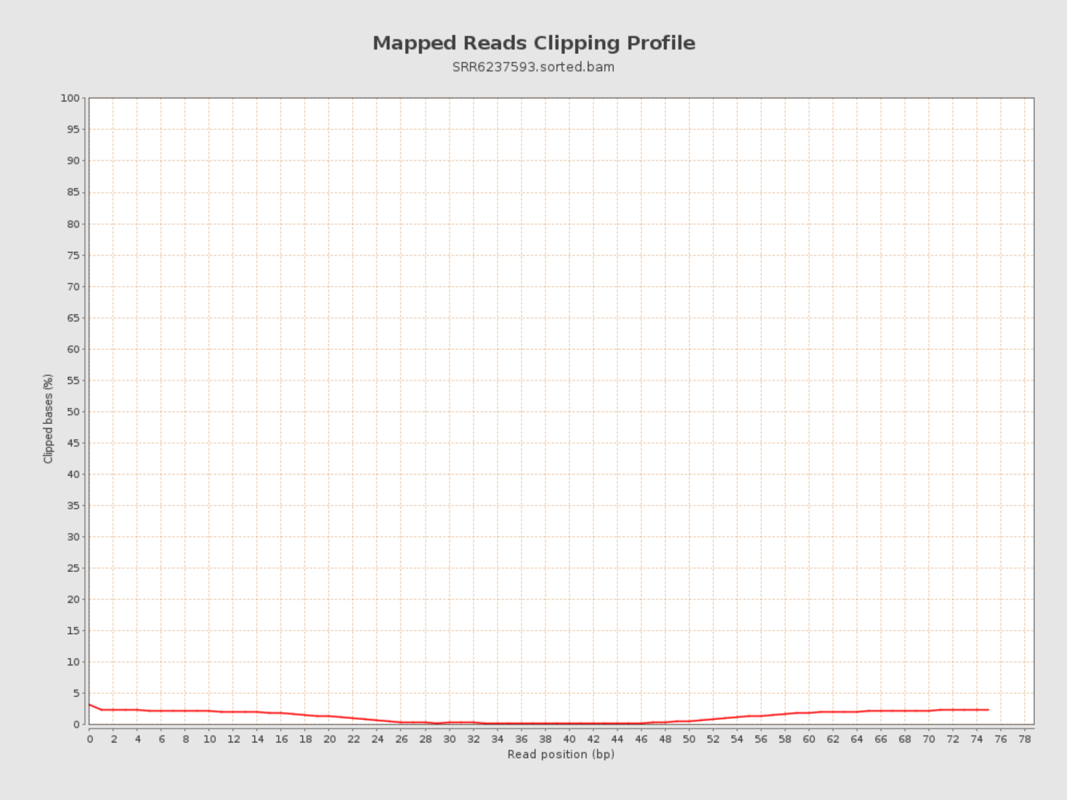
# 8. Results : Mapped Reads Nucleotide Content



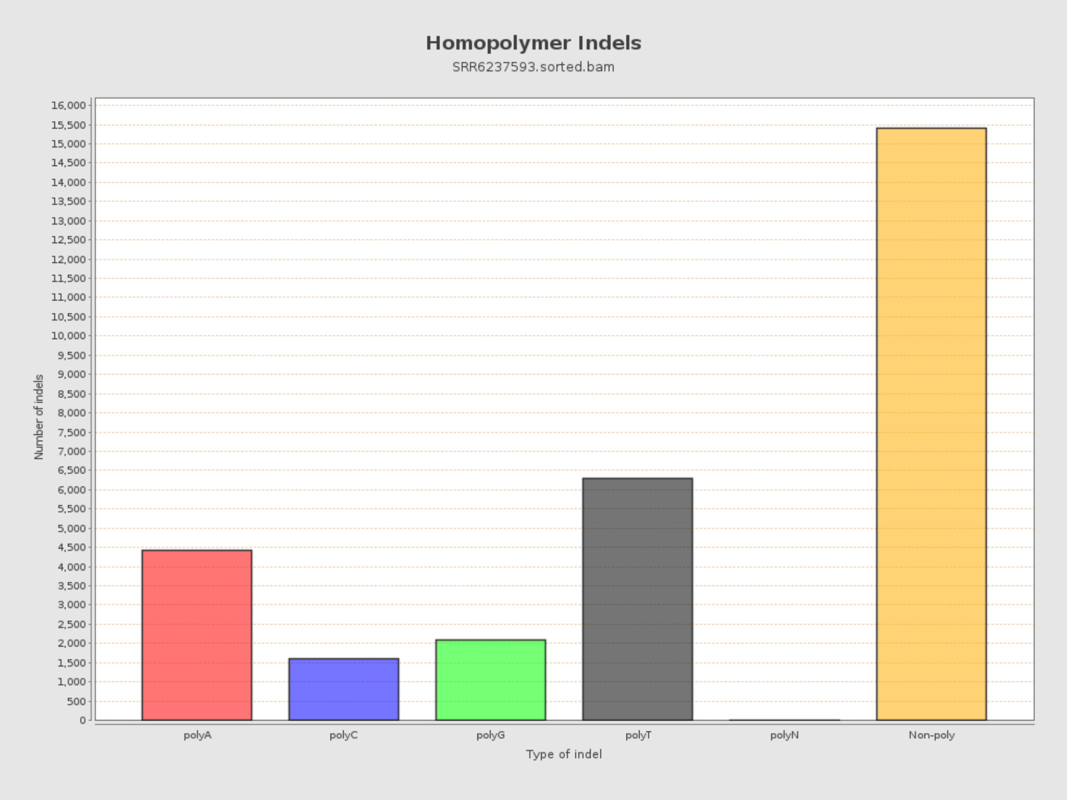
# 9. Results : Mapped Reads GC-content Distribution



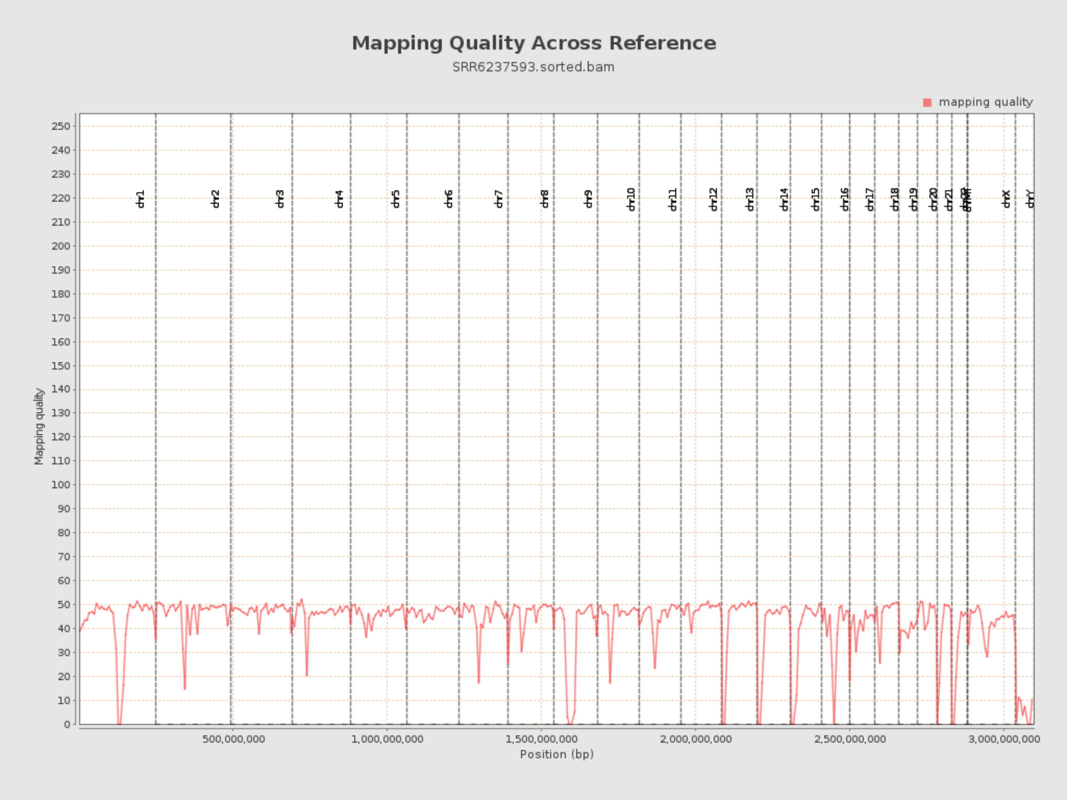
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram