# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/30 02:03:01*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525267.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_SRR10525267 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525267.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 30 02:03:01 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525267.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 973,198 |
| Mapped reads | 897,496 / 92.22% |
| Unmapped reads | 75,702 / 7.78% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,906 / 0.4% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 23,215 / 2.39% |
| Duplication rate | 1.83% |
| Clipped reads | 899,449 / 92.42% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 13,242,752 / 25.29% |
| Number/percentage of C's | 10,365,050 / 19.79% |
| Number/percentage of T's | 16,316,309 / 31.16% |
| Number/percentage of G's | 12,439,948 / 23.76% |
| Number/percentage of N's | 1,087 / 0% |
| GC Percentage | 43.55% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0169 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1927 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.19 |

## 2.5. Mismatches and indels

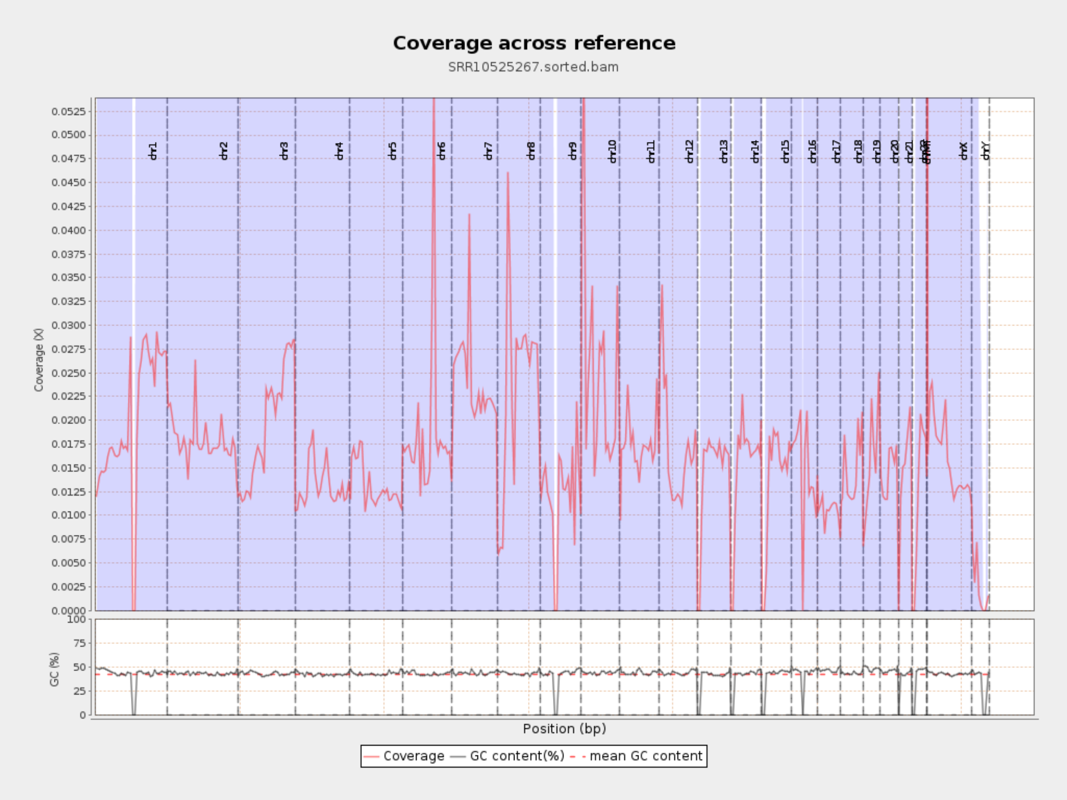
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 261,701 |
| Insertions | 3,789 |
| Mapped reads with at least one insertion | 0.42% |
| Deletions | 11,060 |
| Mapped reads with at least one deletion | 1.22% |
| Homopolymer indels | 43.36% |

## 2.6. Chromosome stats

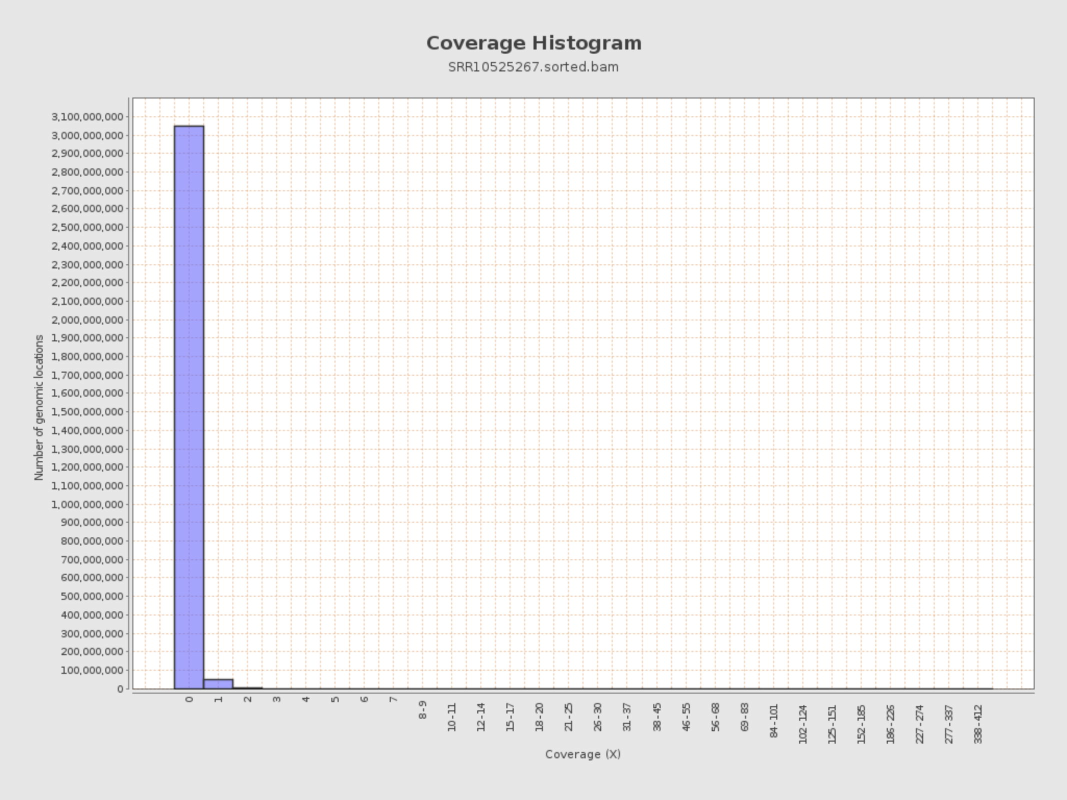
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 4952793 | 0.0199 | 0.3149 |
| chr2 | 243199373 | 4351347 | 0.0179 | 0.2278 |
| chr3 | 198022430 | 3849136 | 0.0194 | 0.1474 |
| chr4 | 191154276 | 2537470 | 0.0133 | 0.1242 |
| chr5 | 180915260 | 2388702 | 0.0132 | 0.121 |
| chr6 | 171115067 | 3242833 | 0.019 | 0.1559 |
| chr7 | 159138663 | 3856507 | 0.0242 | 0.3453 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3504174 | 0.0239 | 0.2021 |
| chr9 | 141213431 | 1713178 | 0.0121 | 0.1408 |
| chr10 | 135534747 | 3468315 | 0.0256 | 0.2173 |
| chr11 | 135006516 | 2350491 | 0.0174 | 0.1692 |
| chr12 | 133851895 | 2317450 | 0.0173 | 0.1395 |
| chr13 | 115169878 | 1667916 | 0.0145 | 0.1266 |
| chr14 | 107349540 | 1605417 | 0.015 | 0.1311 |
| chr15 | 102531392 | 1390621 | 0.0136 | 0.1232 |
| chr16 | 90354753 | 1336535 | 0.0148 | 0.1365 |
| chr17 | 81195210 | 854304 | 0.0105 | 0.1104 |
| chr18 | 78077248 | 1130101 | 0.0145 | 0.272 |
| chr19 | 59128983 | 946075 | 0.016 | 0.2333 |
| chr20 | 63025520 | 904000 | 0.0143 | 0.1277 |
| chr21 | 48129895 | 716642 | 0.0149 | 0.1311 |
| chr22 | 51304566 | 628711 | 0.0123 | 0.1164 |
| chrMT | 16571 | 9424 | 0.5687 | 0.7941 |
| chrX | 155270560 | 2519316 | 0.0162 | 0.1428 |
| chrY | 59373566 | 141153 | 0.0024 | 0.0692 |

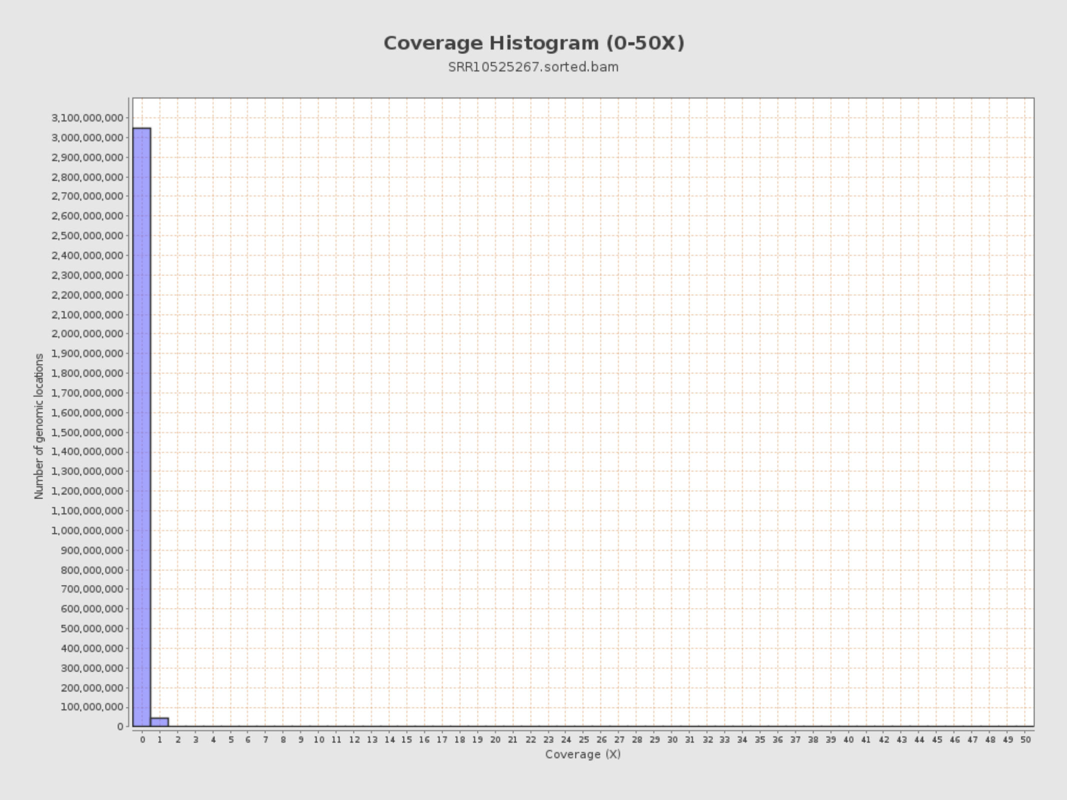
# 3. Results : Coverage across reference



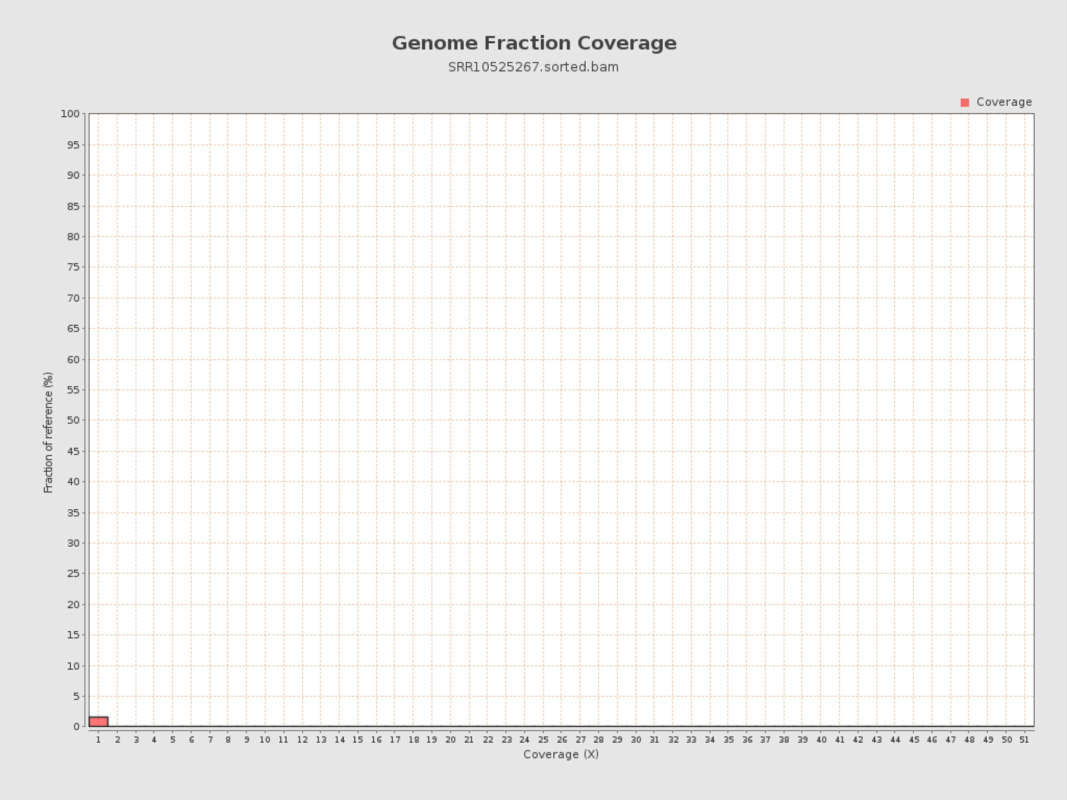
# 4. Results : Coverage Histogram



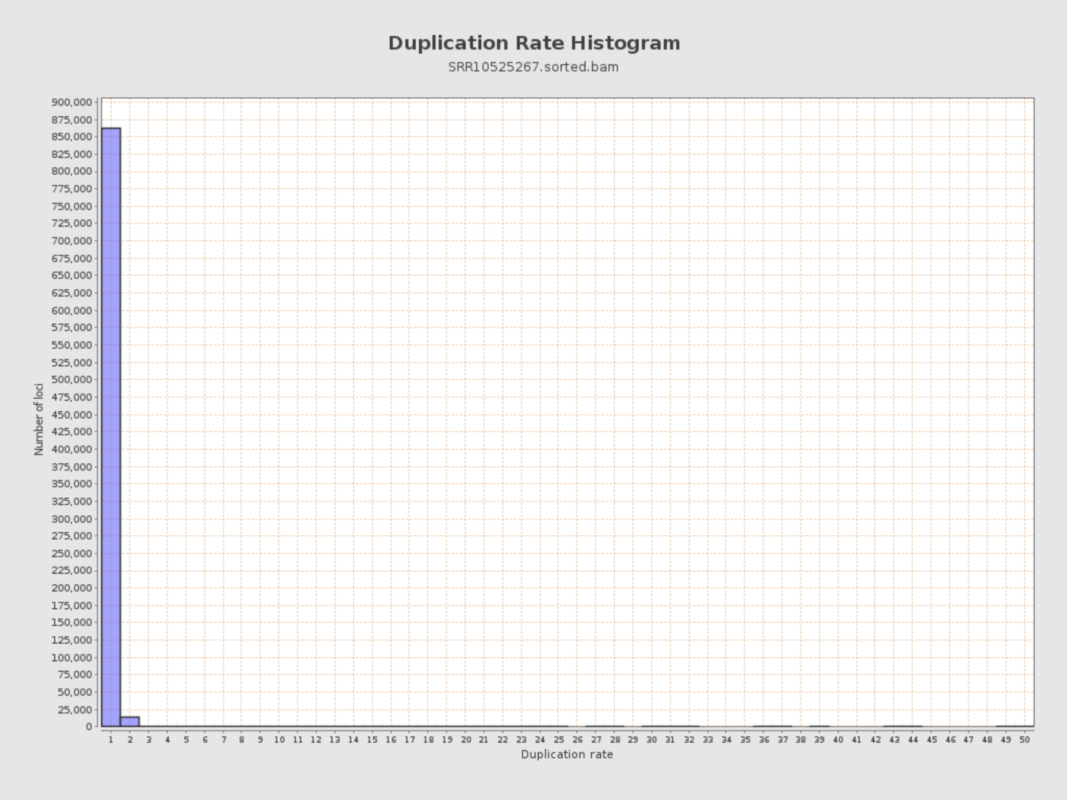
# 5. Results : Coverage Histogram (0-50X)



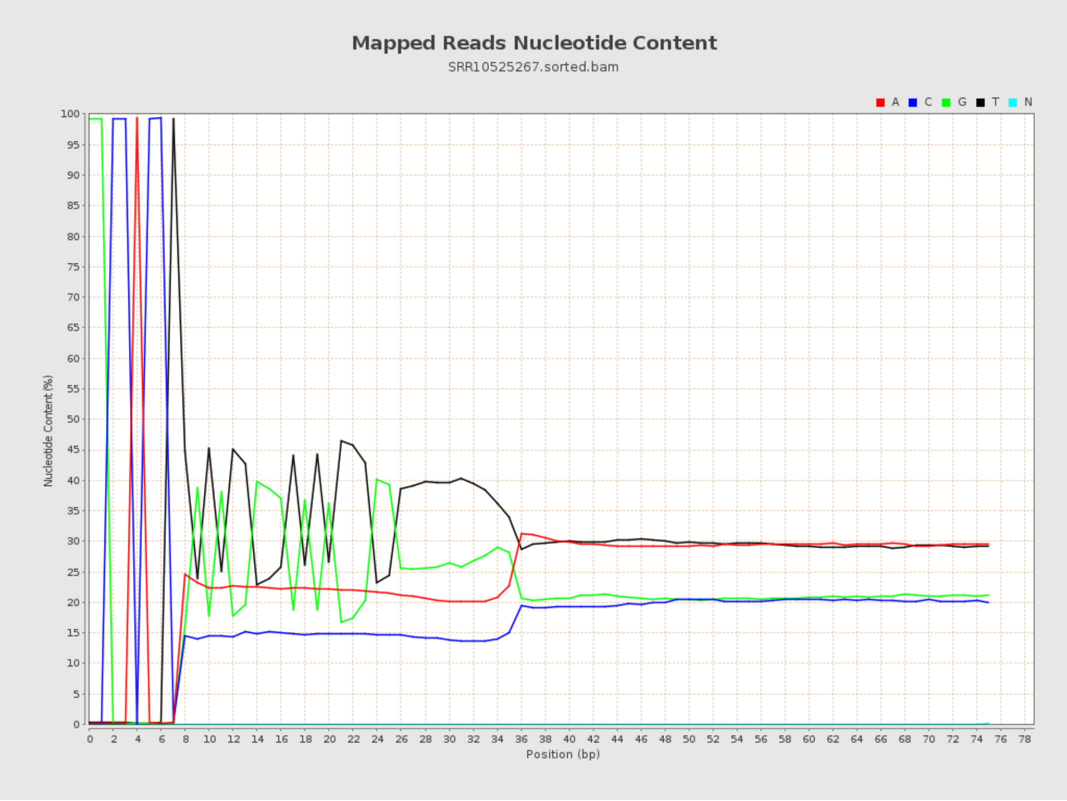
# 6. Results : Genome Fraction Coverage



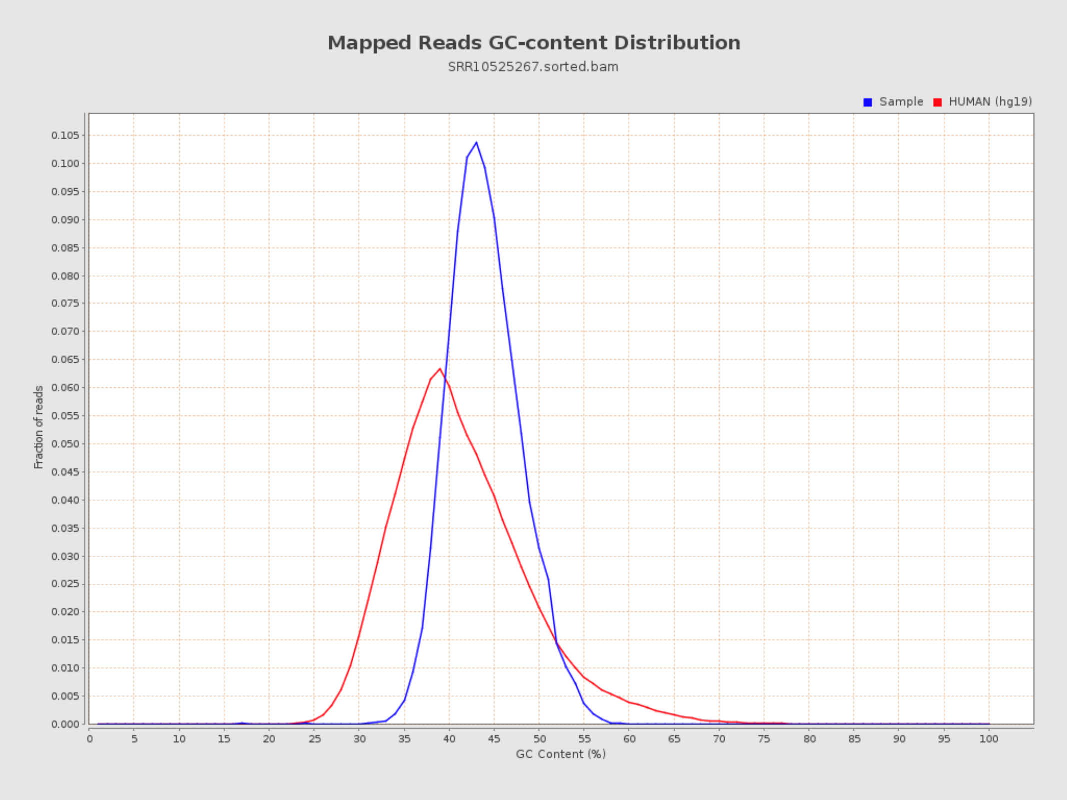
# 7. Results : Duplication Rate Histogram



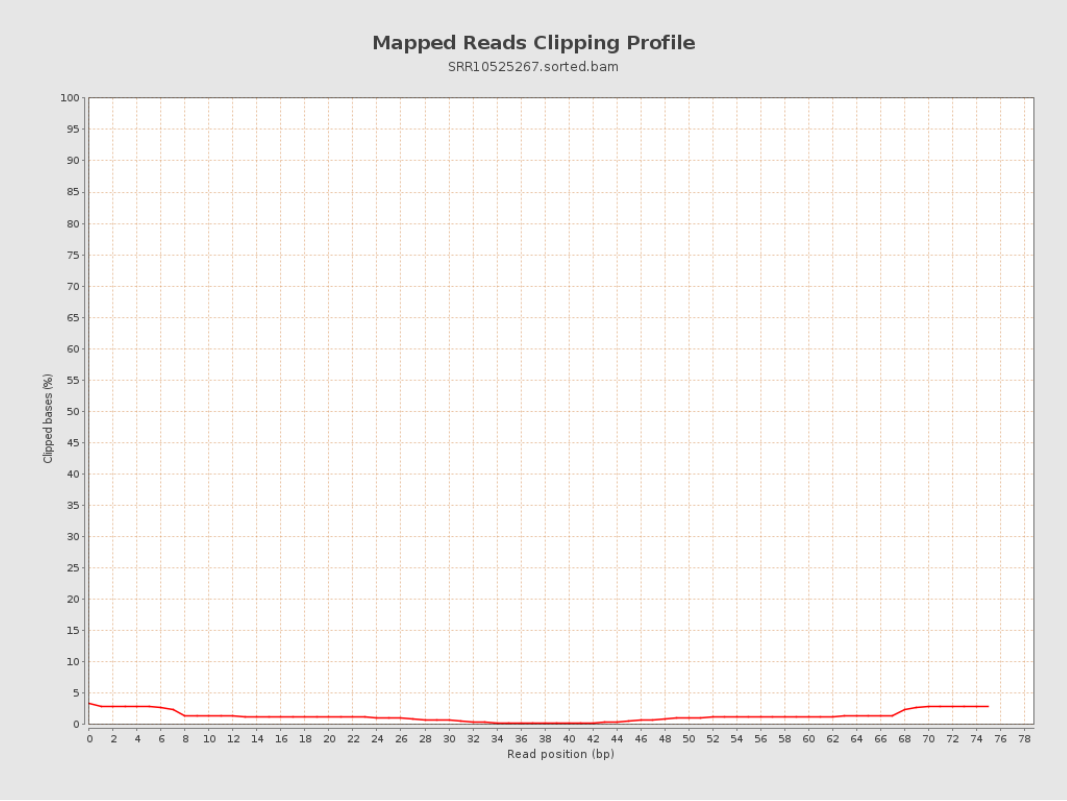
# 8. Results : Mapped Reads Nucleotide Content



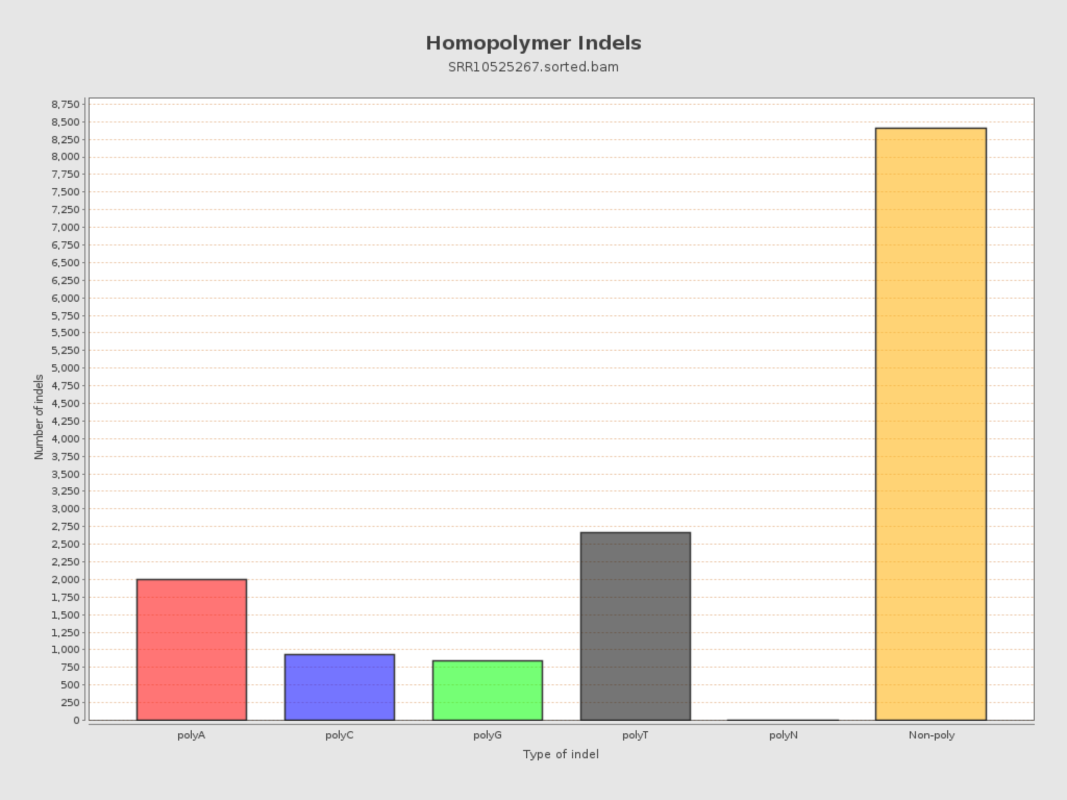
# 9. Results : Mapped Reads GC-content Distribution



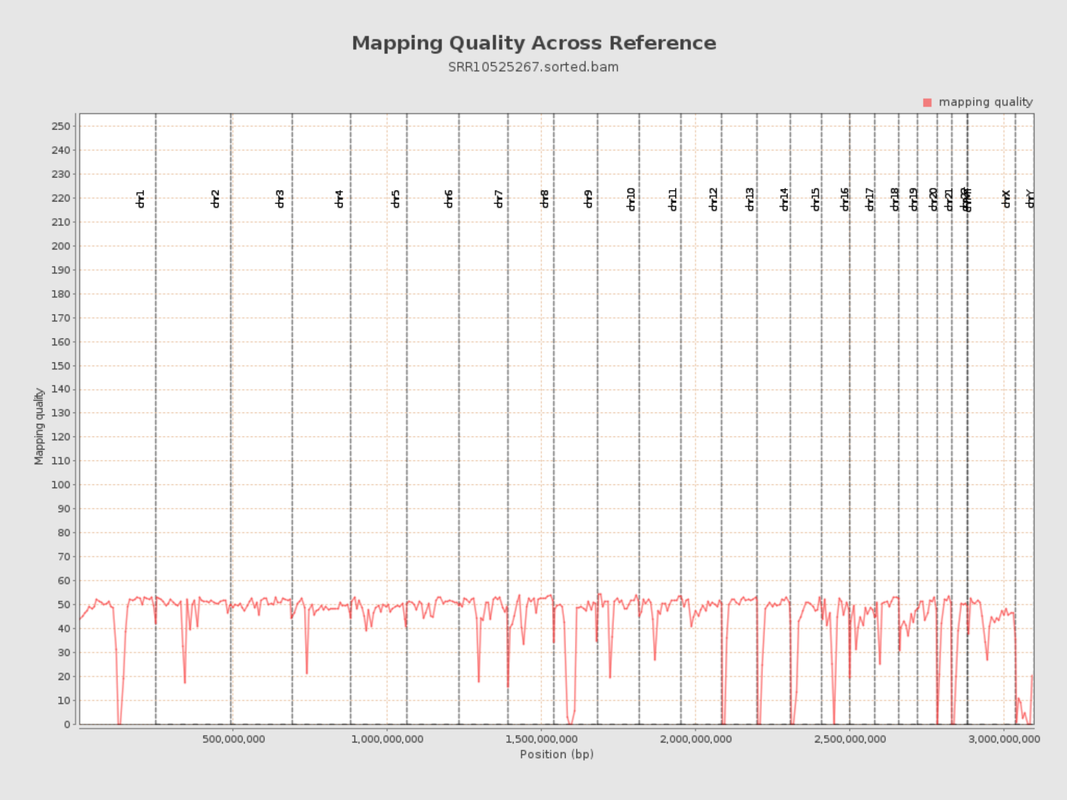
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram