# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 13:59:47*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525029.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_SRR10525029 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525029.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 13:59:44 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525029.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 871,415 |
| Mapped reads | 776,602 / 89.12% |
| Unmapped reads | 94,813 / 10.88% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 2,756 / 0.32% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 19,322 / 2.22% |
| Duplication rate | 1.85% |
| Clipped reads | 777,391 / 89.21% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 11,377,445 / 25.4% |
| Number/percentage of C's | 8,300,969 / 18.53% |
| Number/percentage of T's | 14,442,534 / 32.24% |
| Number/percentage of G's | 10,676,206 / 23.83% |
| Number/percentage of N's | 400 / 0% |
| GC Percentage | 42.36% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0145 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1562 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.28 |

## 2.5. Mismatches and indels

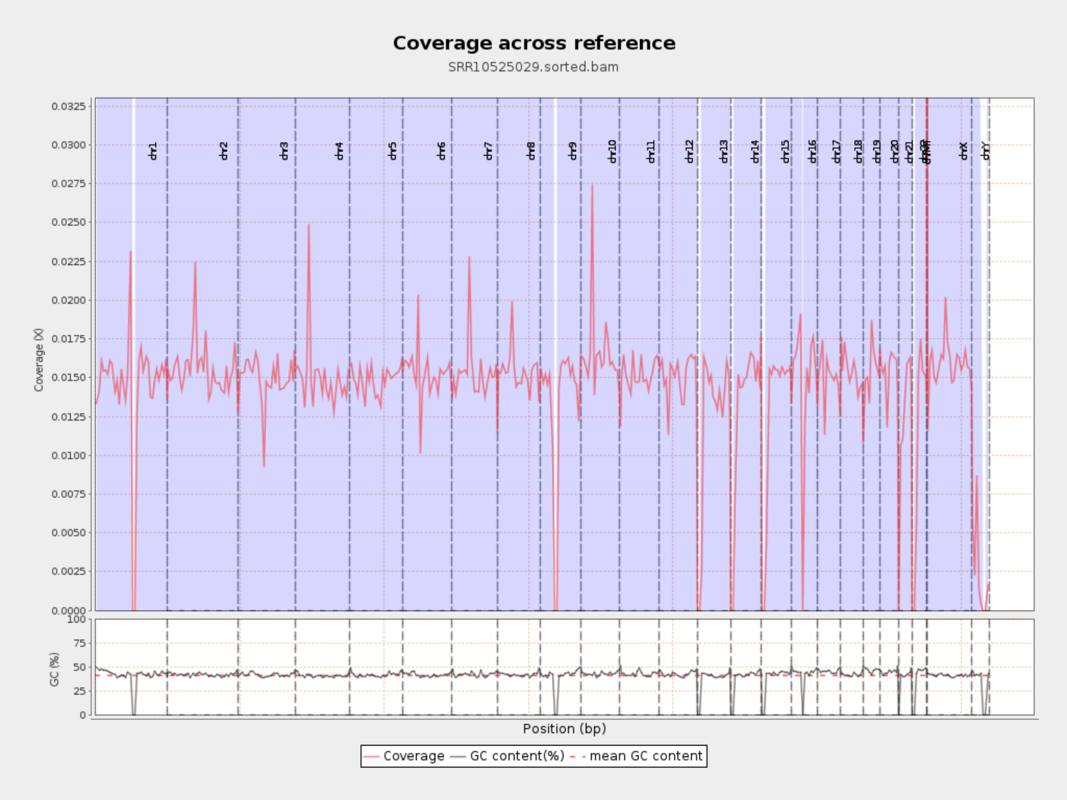
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 228,855 |
| Insertions | 2,942 |
| Mapped reads with at least one insertion | 0.38% |
| Deletions | 8,927 |
| Mapped reads with at least one deletion | 1.14% |
| Homopolymer indels | 42.3% |

## 2.6. Chromosome stats

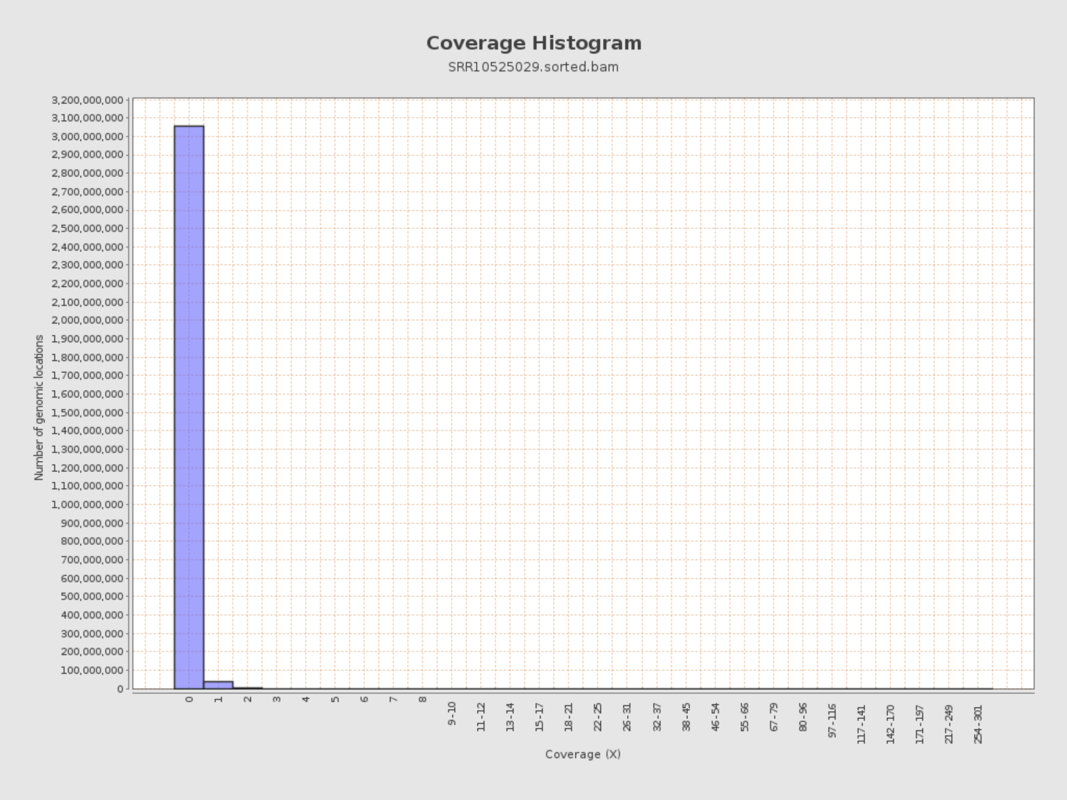
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3577780 | 0.0144 | 0.2402 |
| chr2 | 243199373 | 3791857 | 0.0156 | 0.1843 |
| chr3 | 198022430 | 2950514 | 0.0149 | 0.1278 |
| chr4 | 191154276 | 2873891 | 0.015 | 0.1387 |
| chr5 | 180915260 | 2691586 | 0.0149 | 0.1281 |
| chr6 | 171115067 | 2606700 | 0.0152 | 0.1463 |
| chr7 | 159138663 | 2443648 | 0.0154 | 0.1787 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2257407 | 0.0154 | 0.1617 |
| chr9 | 141213431 | 1861861 | 0.0132 | 0.1373 |
| chr10 | 135534747 | 2258813 | 0.0167 | 0.1688 |
| chr11 | 135006516 | 2051259 | 0.0152 | 0.1542 |
| chr12 | 133851895 | 2019976 | 0.0151 | 0.1298 |
| chr13 | 115169878 | 1393383 | 0.0121 | 0.1155 |
| chr14 | 107349540 | 1372748 | 0.0128 | 0.1208 |
| chr15 | 102531392 | 1273879 | 0.0124 | 0.1177 |
| chr16 | 90354753 | 1310110 | 0.0145 | 0.1305 |
| chr17 | 81195210 | 1218048 | 0.015 | 0.1363 |
| chr18 | 78077248 | 1201211 | 0.0154 | 0.1978 |
| chr19 | 59128983 | 916553 | 0.0155 | 0.1801 |
| chr20 | 63025520 | 969945 | 0.0154 | 0.1313 |
| chr21 | 48129895 | 595226 | 0.0124 | 0.1229 |
| chr22 | 51304566 | 559260 | 0.0109 | 0.1093 |
| chrMT | 16571 | 2420 | 0.146 | 0.3937 |
| chrX | 155270560 | 2473809 | 0.0159 | 0.1395 |
| chrY | 59373566 | 140771 | 0.0024 | 0.0821 |

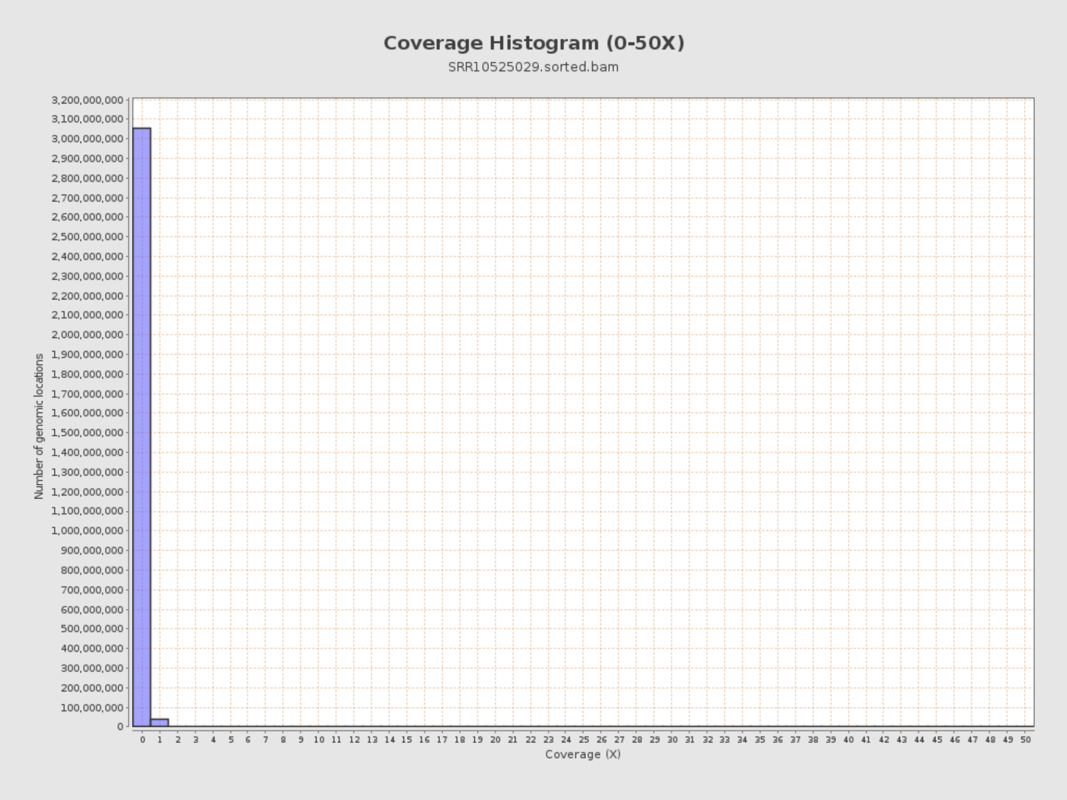
# 3. Results : Coverage across reference



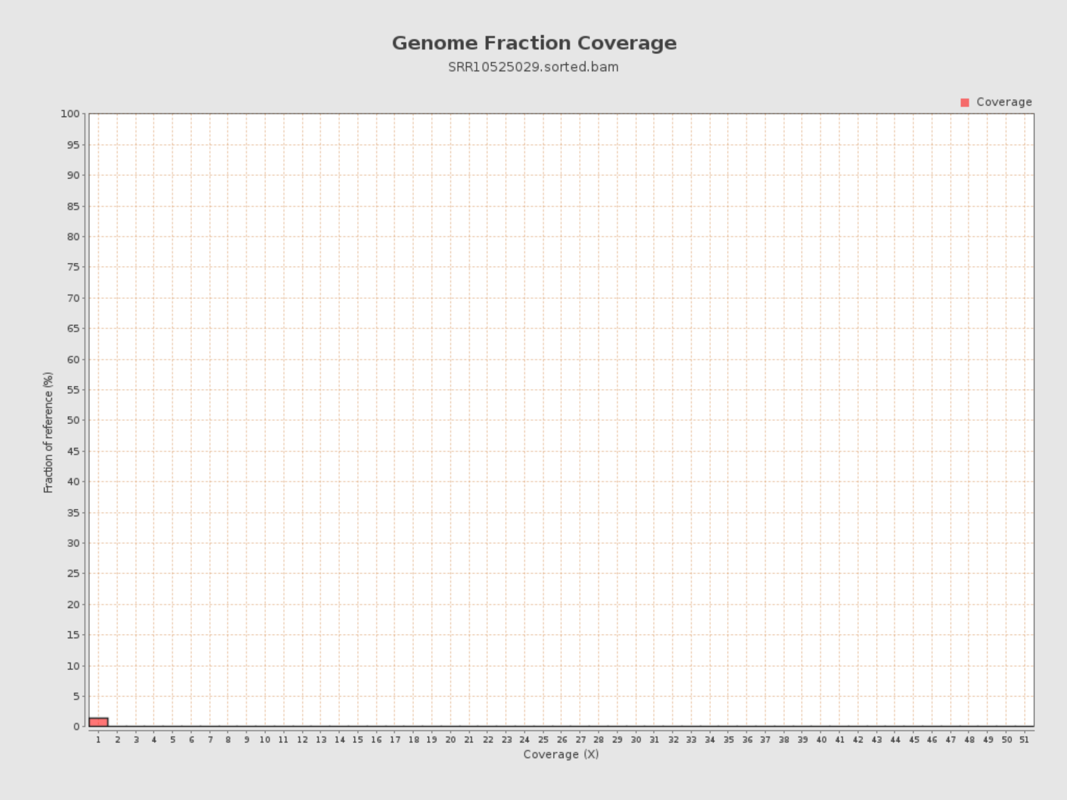
# 4. Results : Coverage Histogram



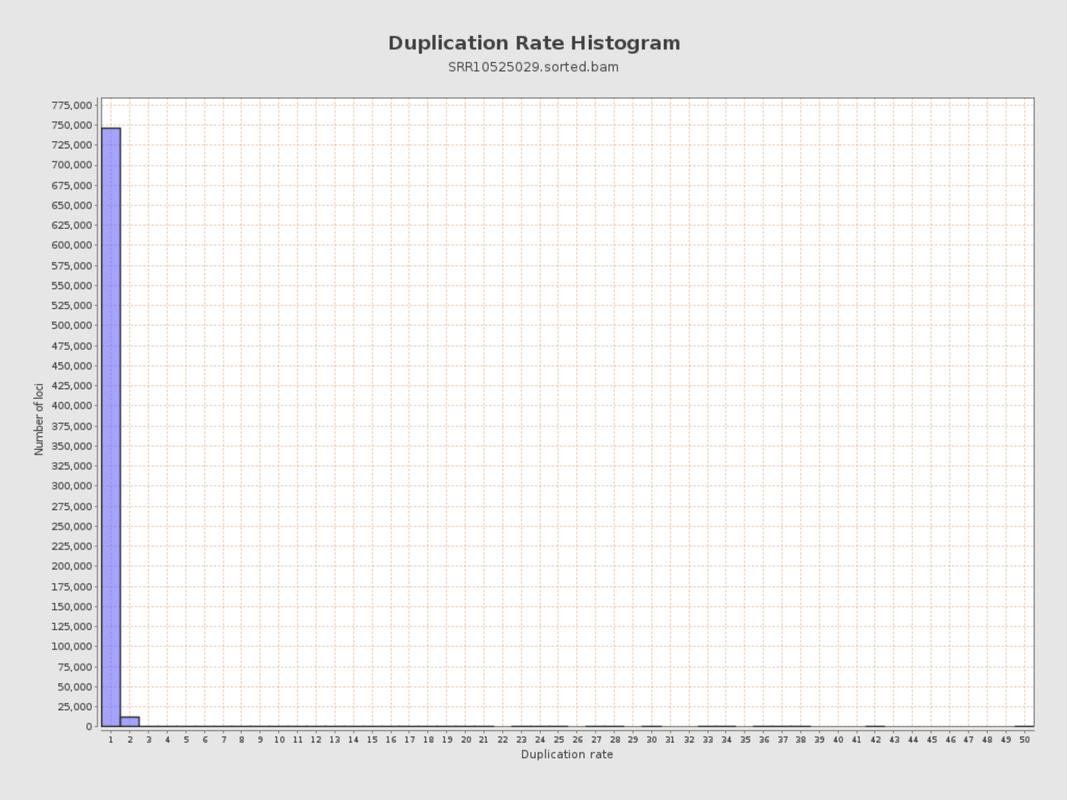
# 5. Results : Coverage Histogram (0-50X)



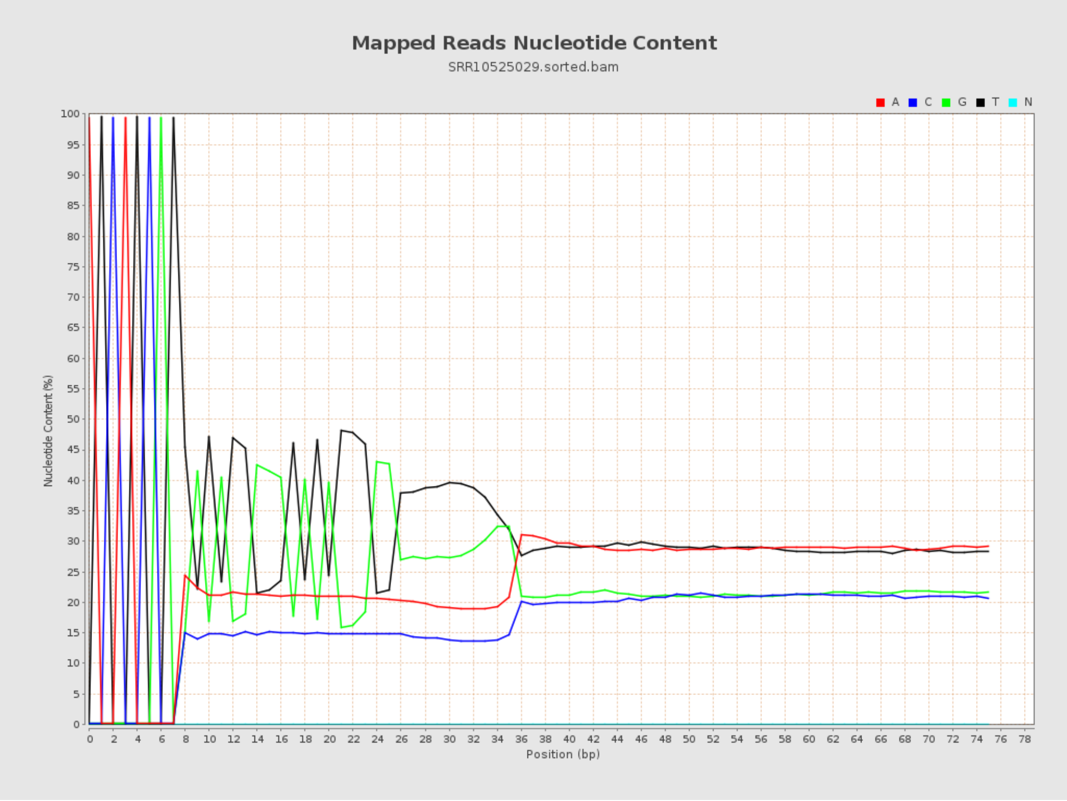
# 6. Results : Genome Fraction Coverage



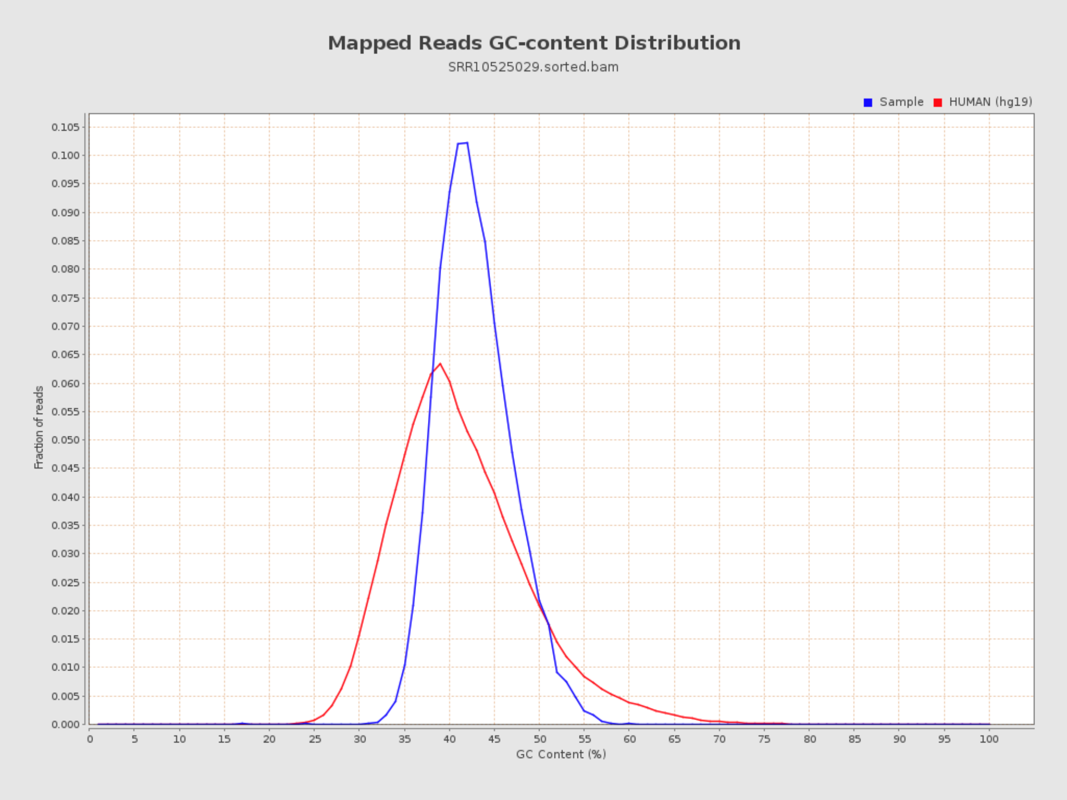
# 7. Results : Duplication Rate Histogram



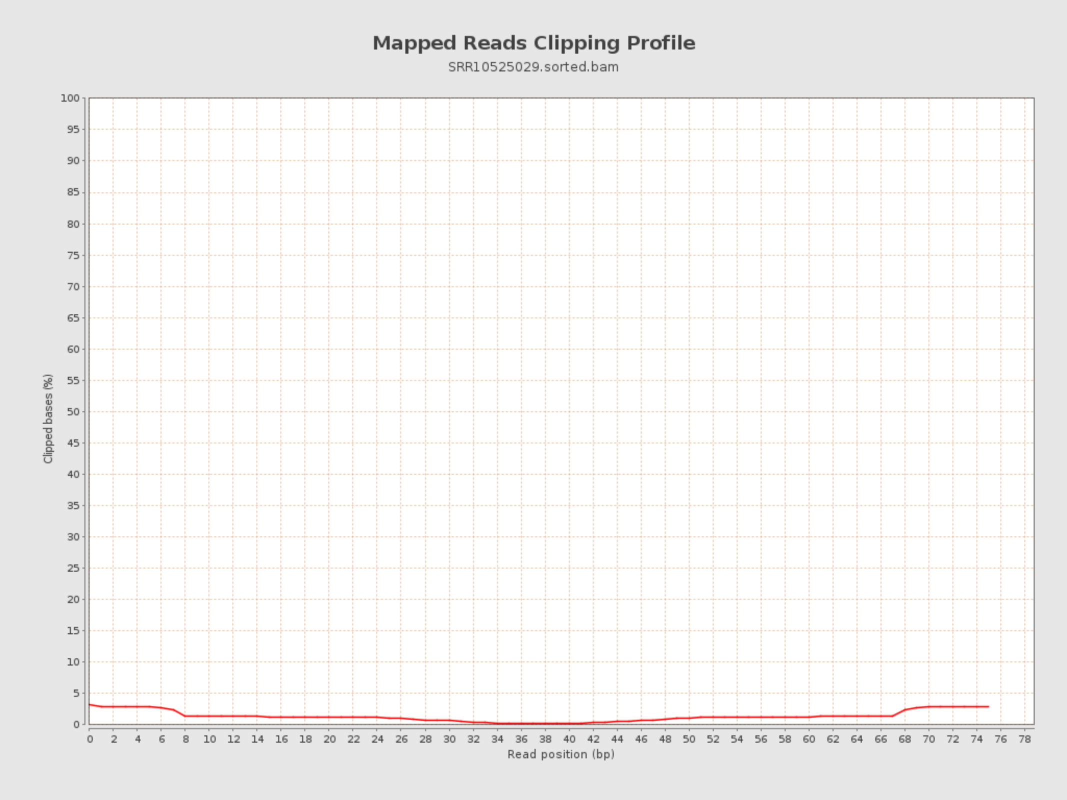
# 8. Results : Mapped Reads Nucleotide Content



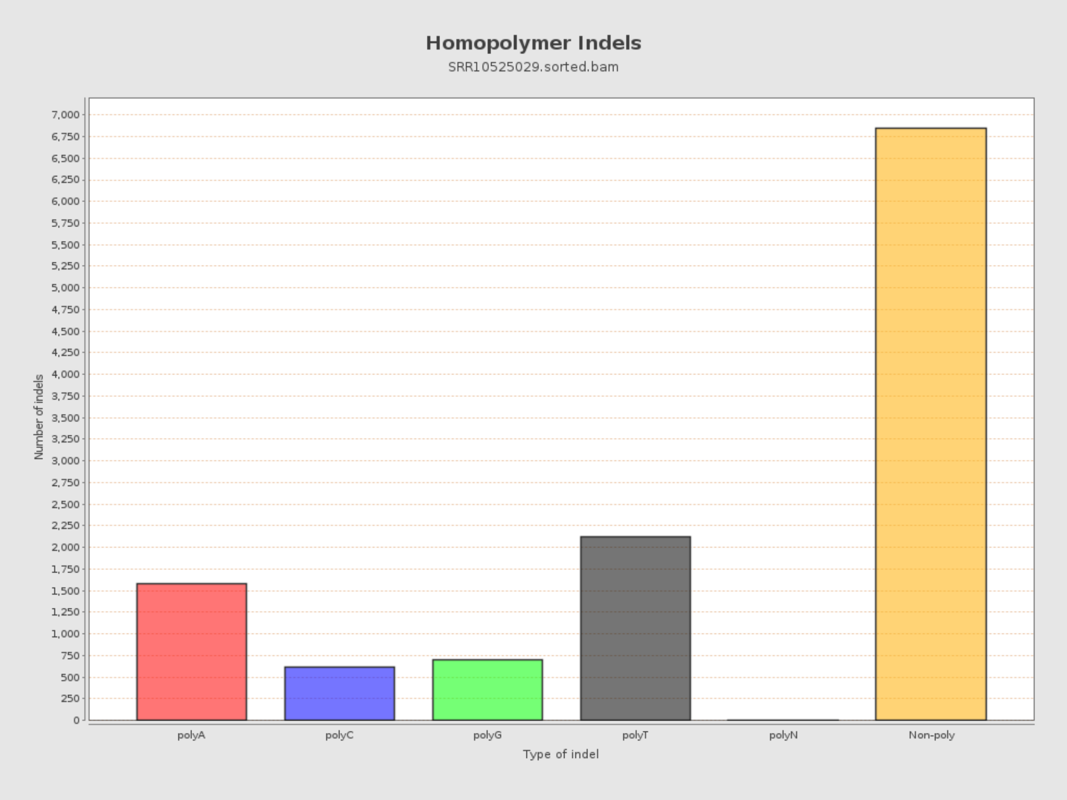
# 9. Results : Mapped Reads GC-content Distribution



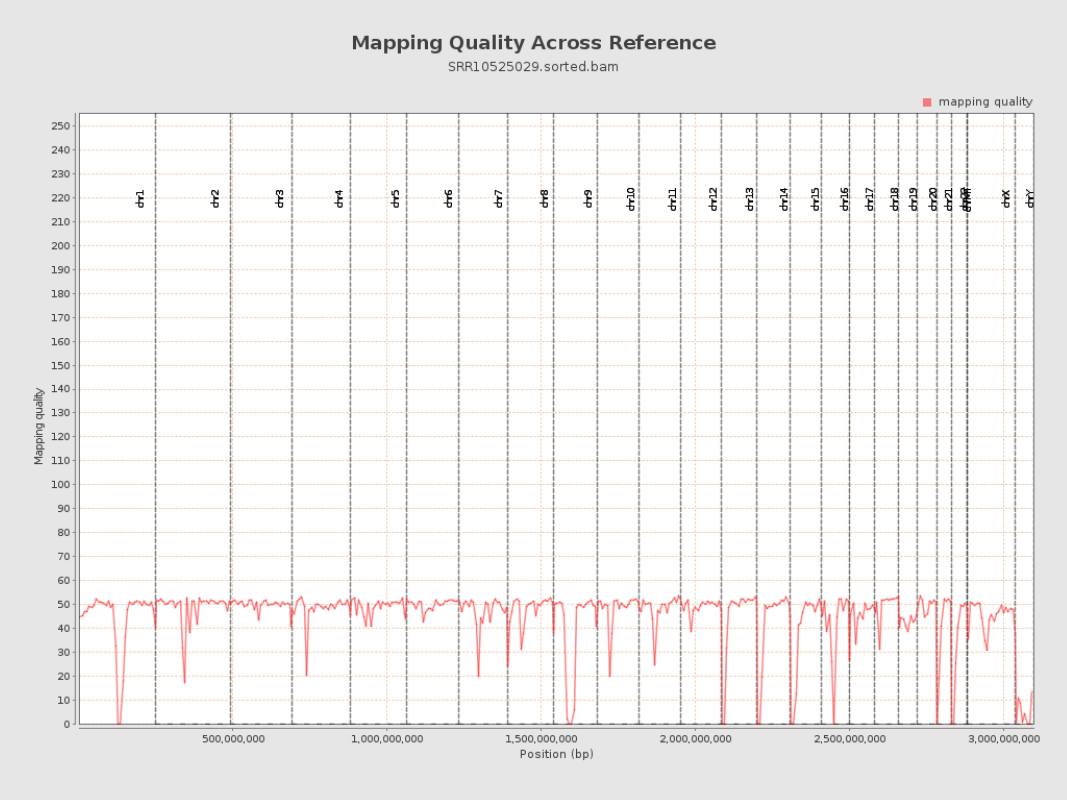
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram