# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 19:12:34*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525129.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_SRR10525129 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525129.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 19:12:32 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525129.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,412,516 |
| Mapped reads | 1,267,189 / 89.71% |
| Unmapped reads | 145,327 / 10.29% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 30,727 / 2.18% |
| Read min/max/mean length | 30 / 101 / 101.79 |
| Duplicated reads (estimated) | 37,744 / 2.67% |
| Duplication rate | 1.76% |
| Clipped reads | 1,296,572 / 91.79% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 25,166,162 / 26.15% |
| Number/percentage of C's | 18,373,653 / 19.1% |
| Number/percentage of T's | 30,083,191 / 31.27% |
| Number/percentage of G's | 22,593,353 / 23.48% |
| Number/percentage of N's | 3,550 / 0% |
| GC Percentage | 42.58% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0311 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3477 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.98 |

## 2.5. Mismatches and indels

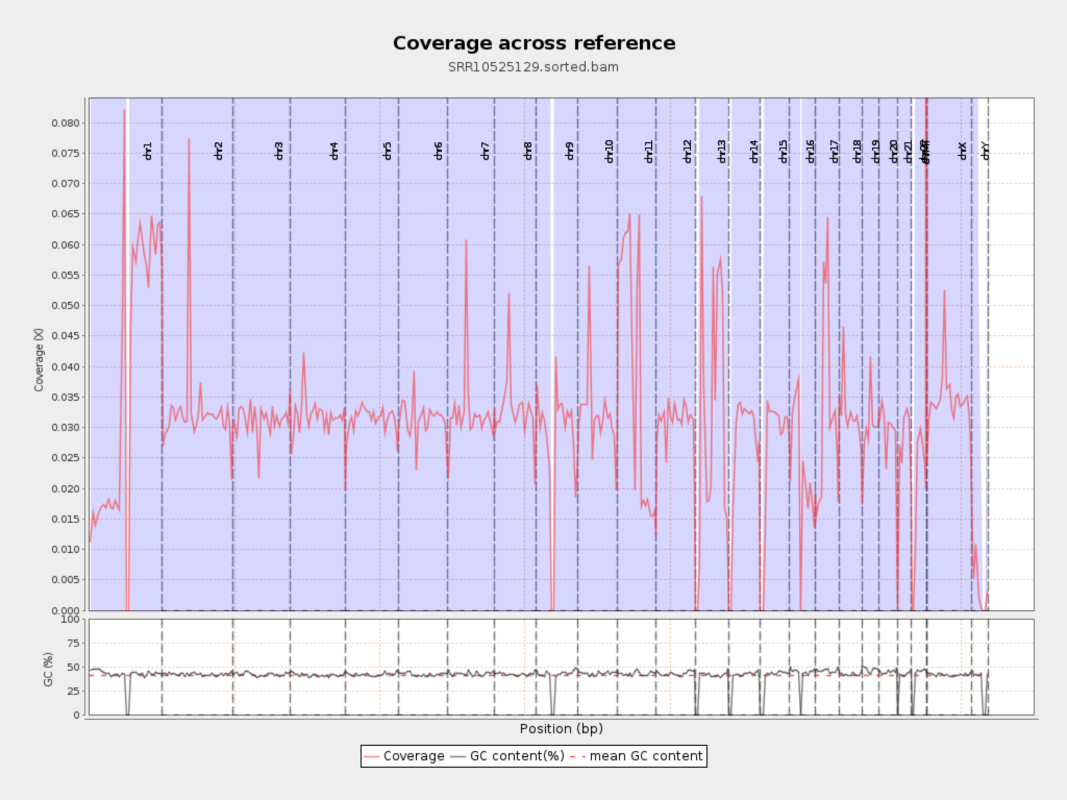
| | |
|---|---|
| General error rate | 0.77% |
| Mismatches | 726,902 |
| Insertions | 8,243 |
| Mapped reads with at least one insertion | 0.64% |
| Deletions | 22,604 |
| Mapped reads with at least one deletion | 1.76% |
| Homopolymer indels | 42.19% |

## 2.6. Chromosome stats

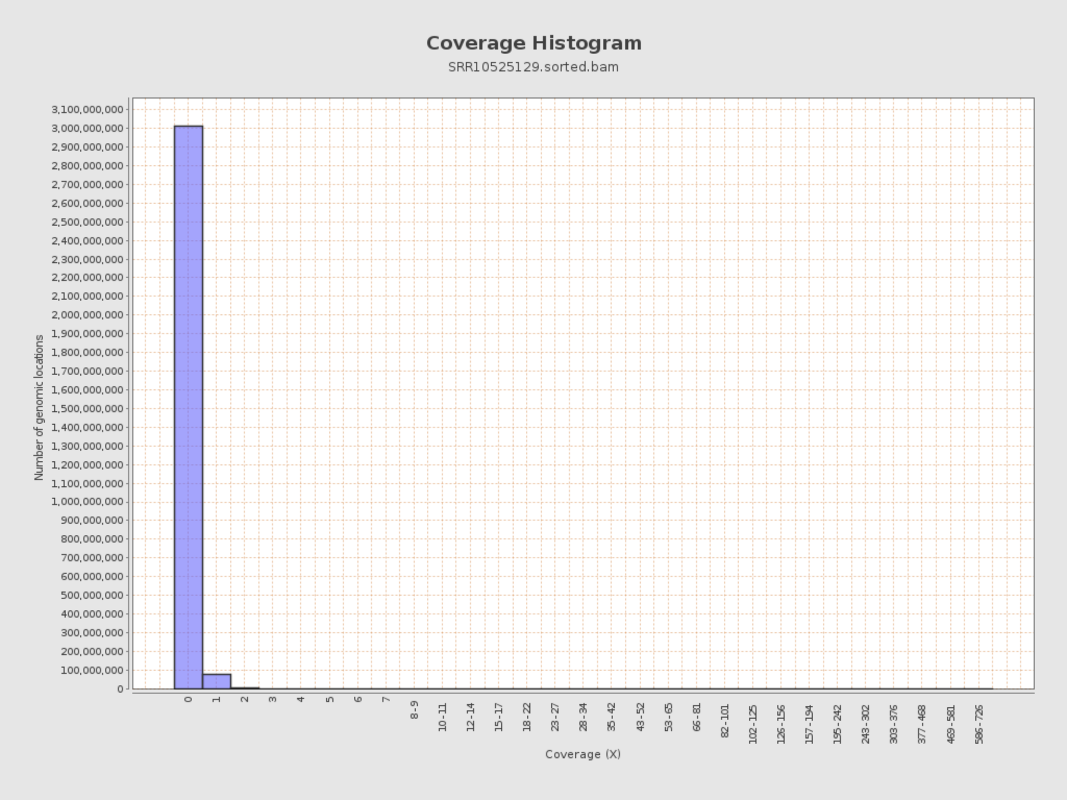
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 9270463 | 0.0372 | 0.6268 |
| chr2 | 243199373 | 7993396 | 0.0329 | 0.481 |
| chr3 | 198022430 | 6161085 | 0.0311 | 0.1914 |
| chr4 | 191154276 | 6105076 | 0.0319 | 0.2026 |
| chr5 | 180915260 | 5694327 | 0.0315 | 0.1952 |
| chr6 | 171115067 | 5381778 | 0.0315 | 0.2216 |
| chr7 | 159138663 | 5212665 | 0.0328 | 0.4735 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4833264 | 0.033 | 0.4493 |
| chr9 | 141213431 | 3897675 | 0.0276 | 0.2999 |
| chr10 | 135534747 | 4391522 | 0.0324 | 0.3473 |
| chr11 | 135006516 | 5236475 | 0.0388 | 0.3741 |
| chr12 | 133851895 | 4183098 | 0.0313 | 0.1928 |
| chr13 | 115169878 | 3544820 | 0.0308 | 0.1908 |
| chr14 | 107349540 | 2831957 | 0.0264 | 0.2073 |
| chr15 | 102531392 | 2648079 | 0.0258 | 0.1735 |
| chr16 | 90354753 | 2086234 | 0.0231 | 0.1827 |
| chr17 | 81195210 | 2754615 | 0.0339 | 0.2339 |
| chr18 | 78077248 | 2554697 | 0.0327 | 0.5452 |
| chr19 | 59128983 | 1800577 | 0.0305 | 0.4421 |
| chr20 | 63025520 | 1855556 | 0.0294 | 0.1914 |
| chr21 | 48129895 | 1239892 | 0.0258 | 0.1888 |
| chr22 | 51304566 | 957425 | 0.0187 | 0.1481 |
| chrMT | 16571 | 20397 | 1.2309 | 1.663 |
| chrX | 155270560 | 5378769 | 0.0346 | 0.2721 |
| chrY | 59373566 | 224485 | 0.0038 | 0.0932 |

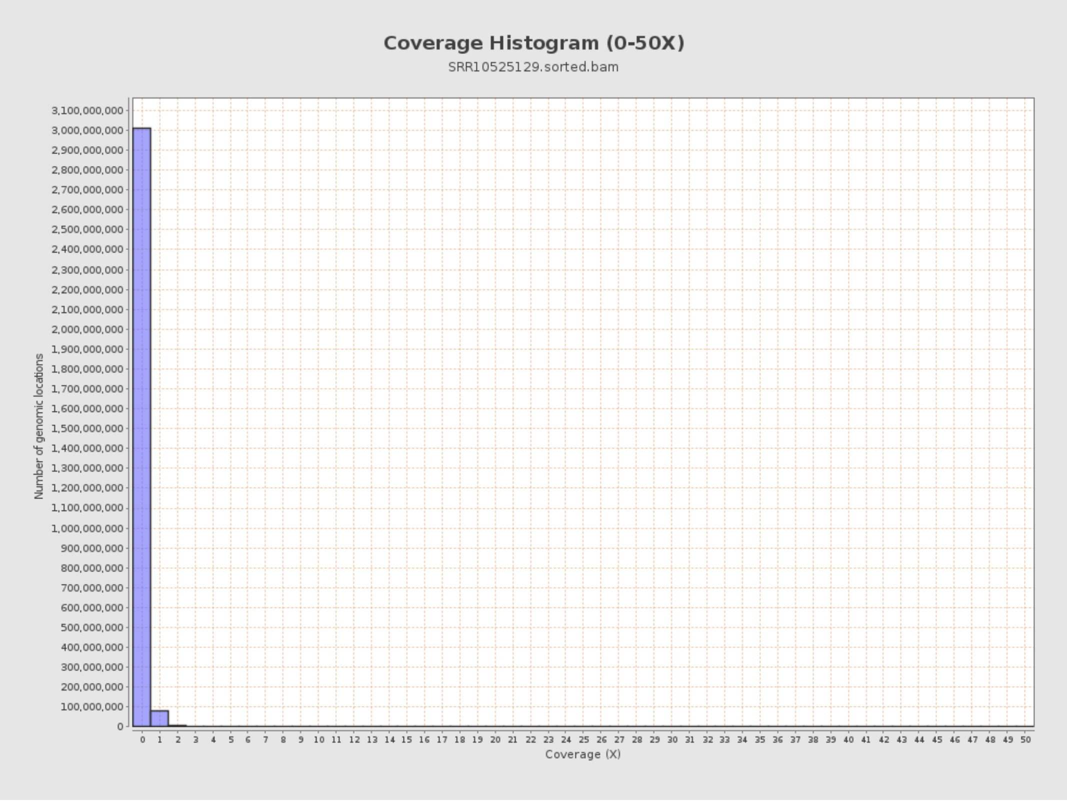
# 3. Results : Coverage across reference



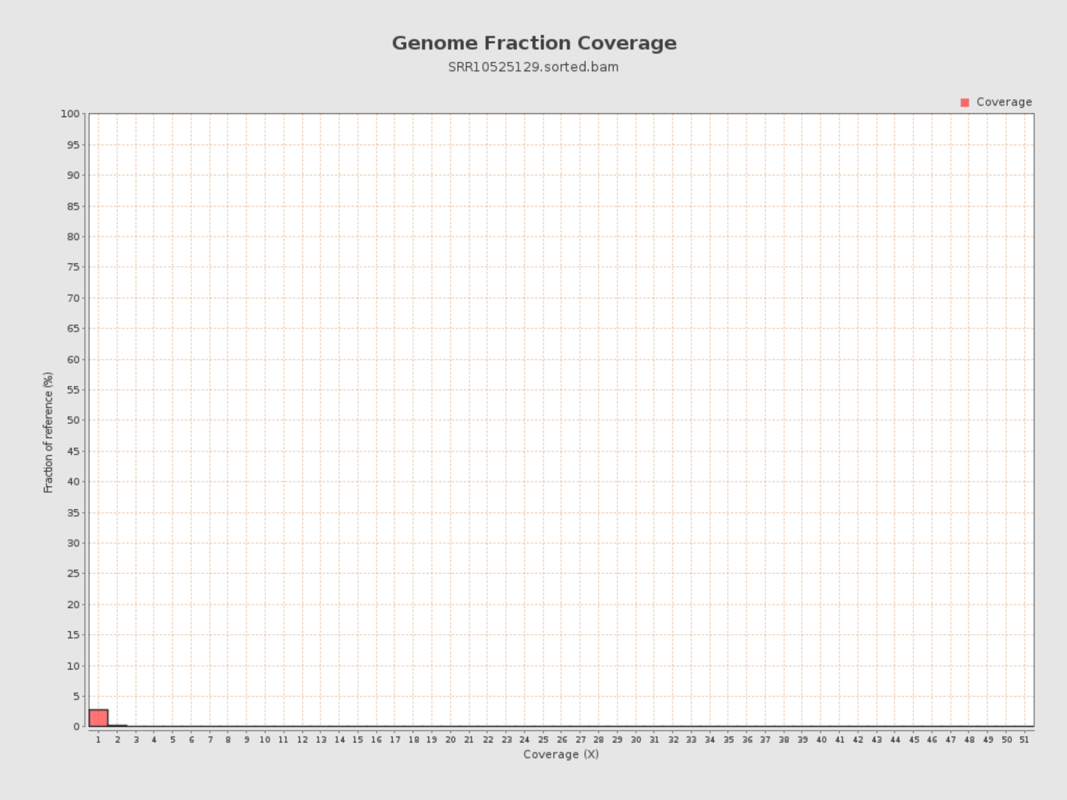
# 4. Results : Coverage Histogram



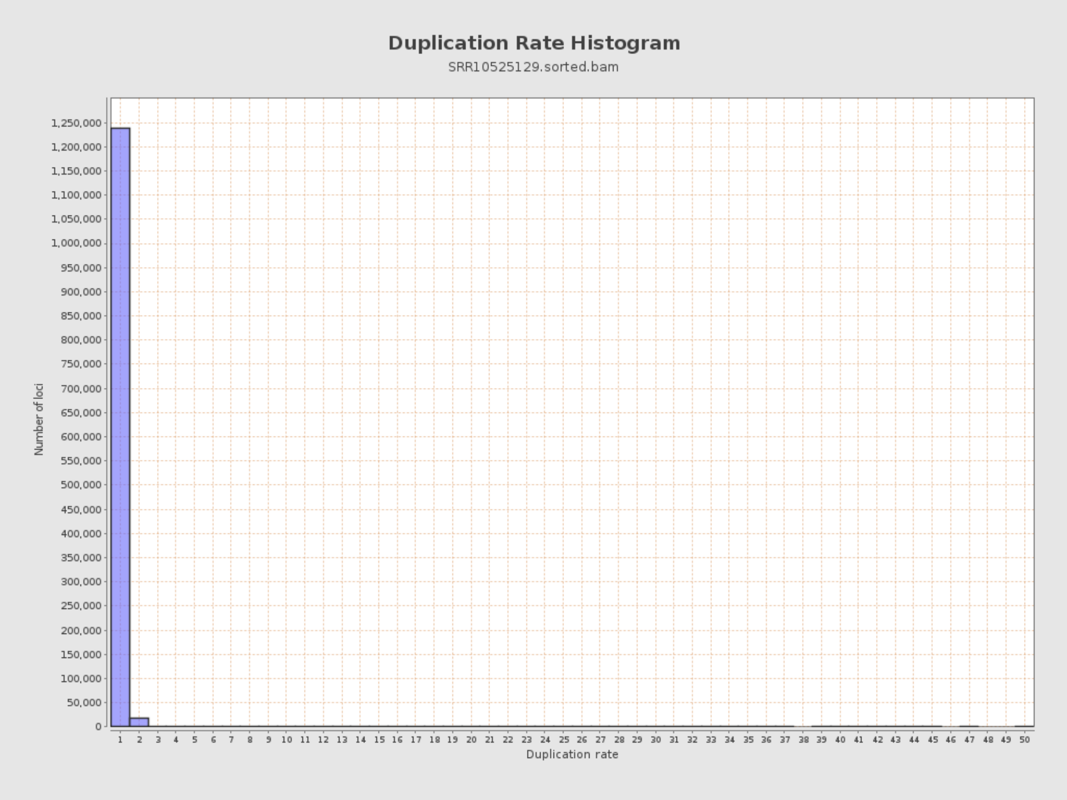
# 5. Results : Coverage Histogram (0-50X)



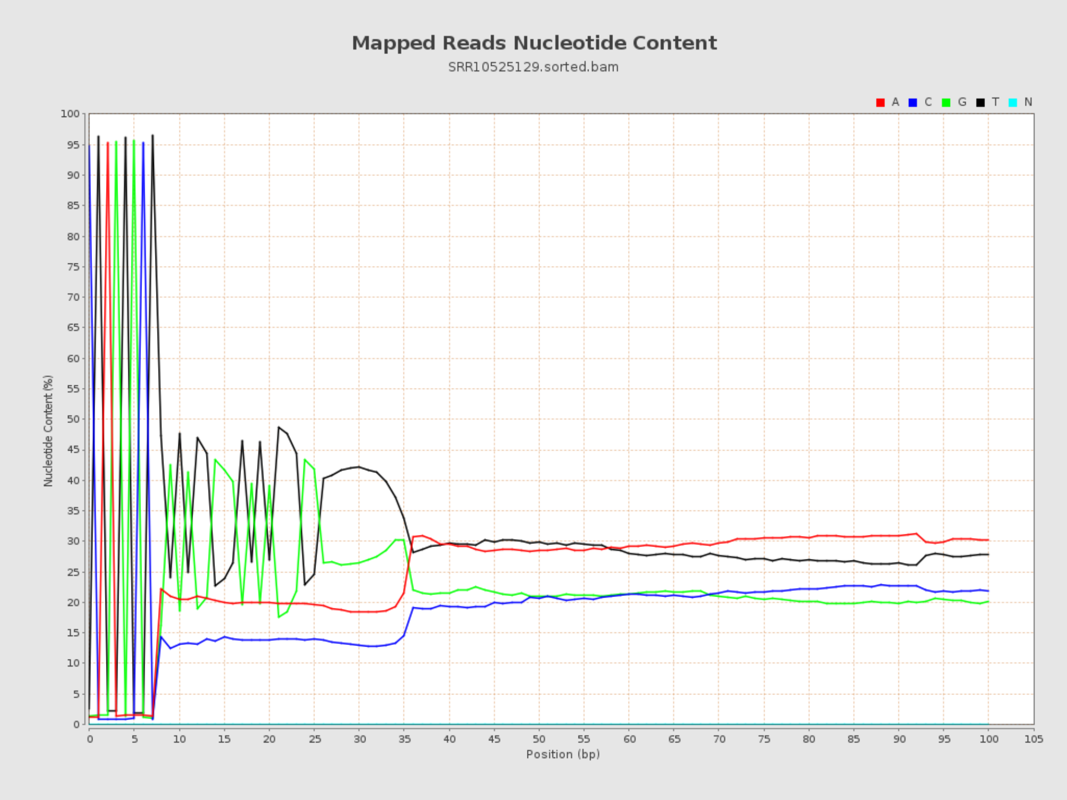
# 6. Results : Genome Fraction Coverage



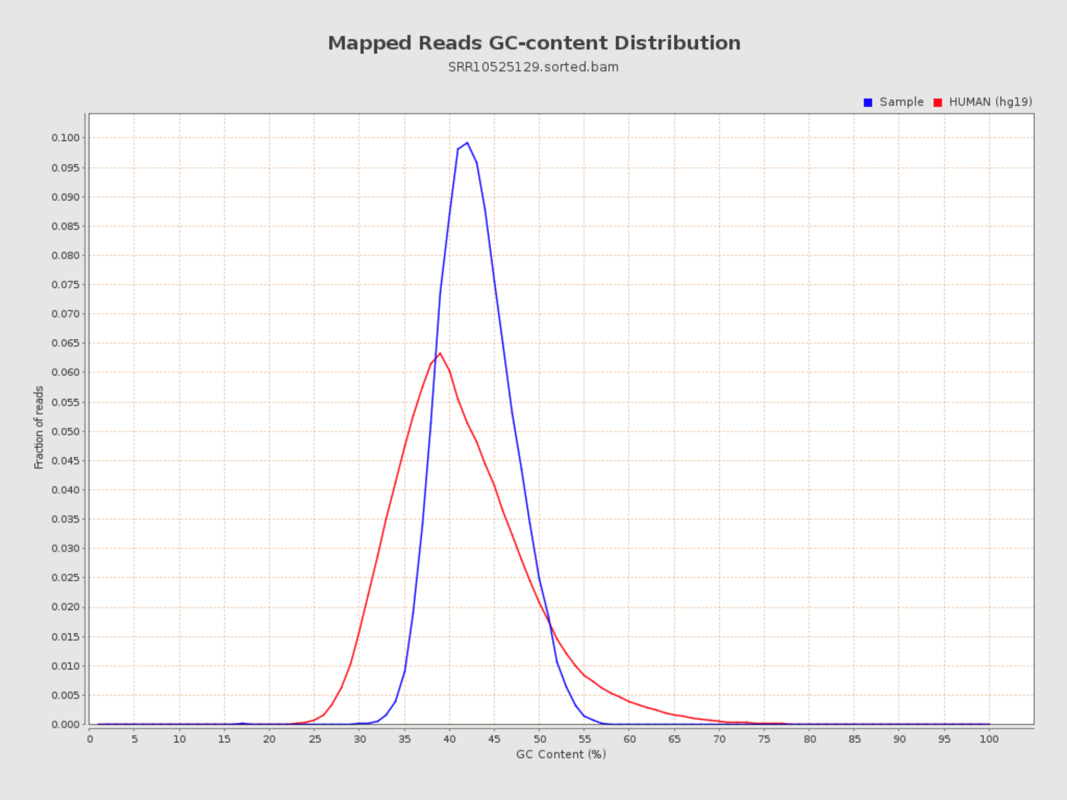
# 7. Results : Duplication Rate Histogram



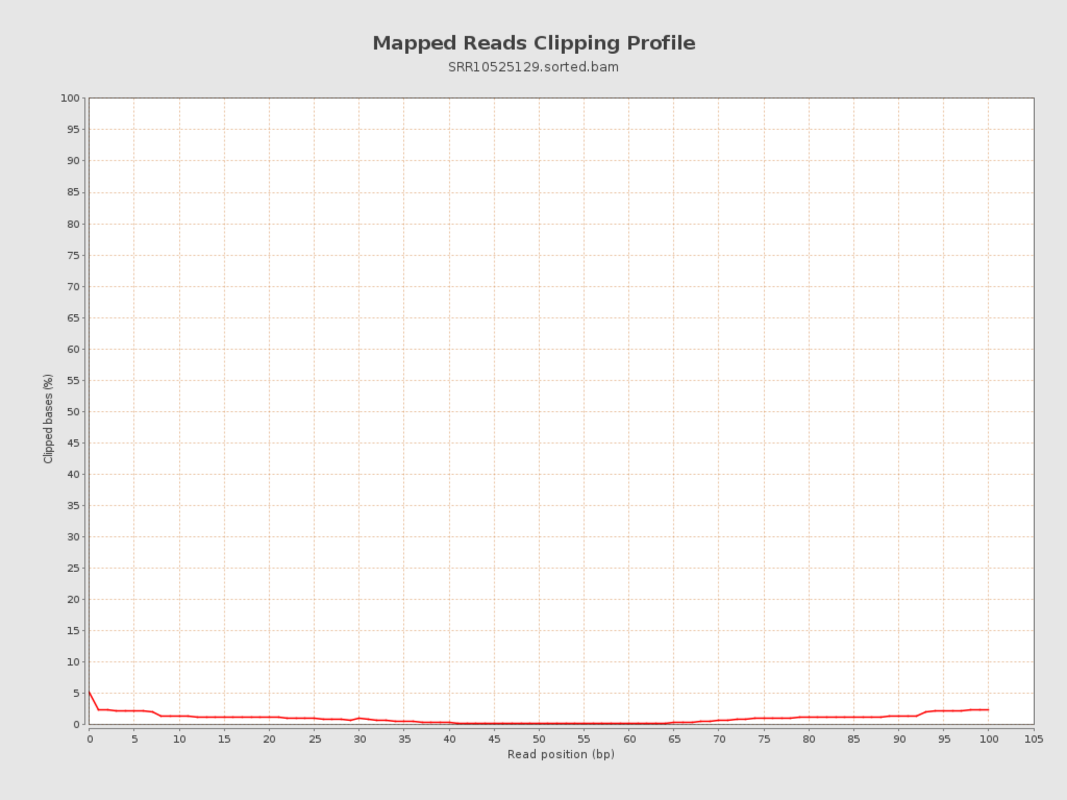
# 8. Results : Mapped Reads Nucleotide Content



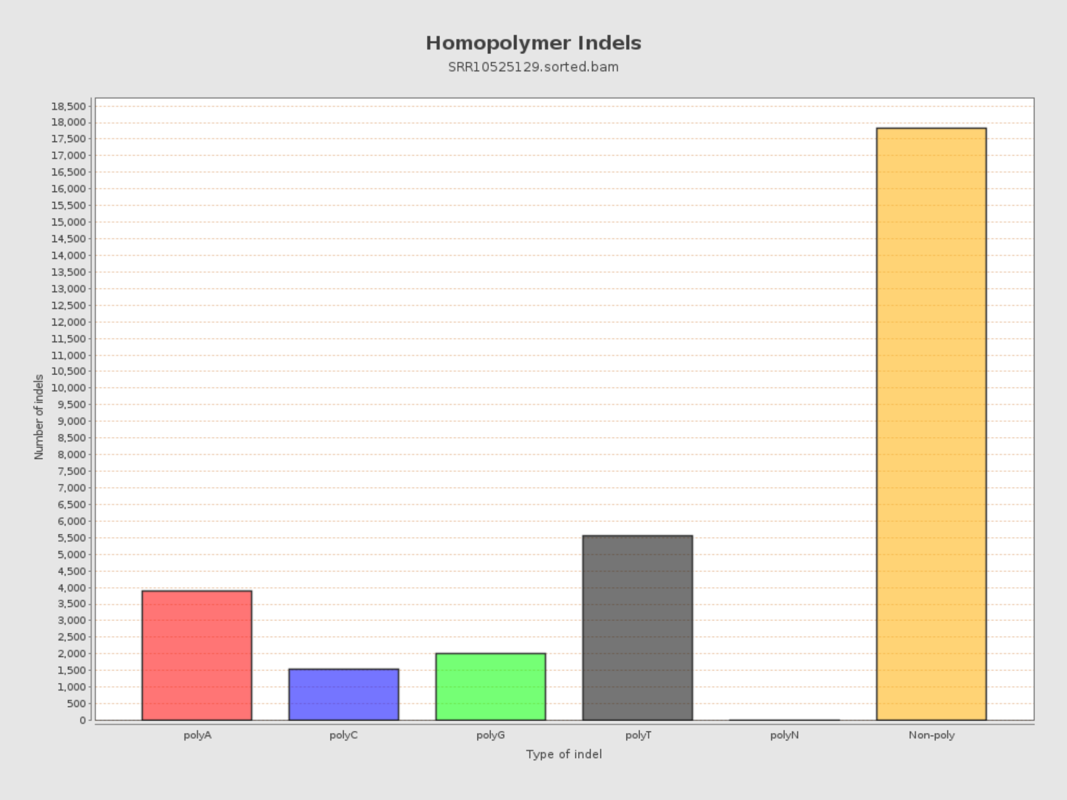
# 9. Results : Mapped Reads GC-content Distribution



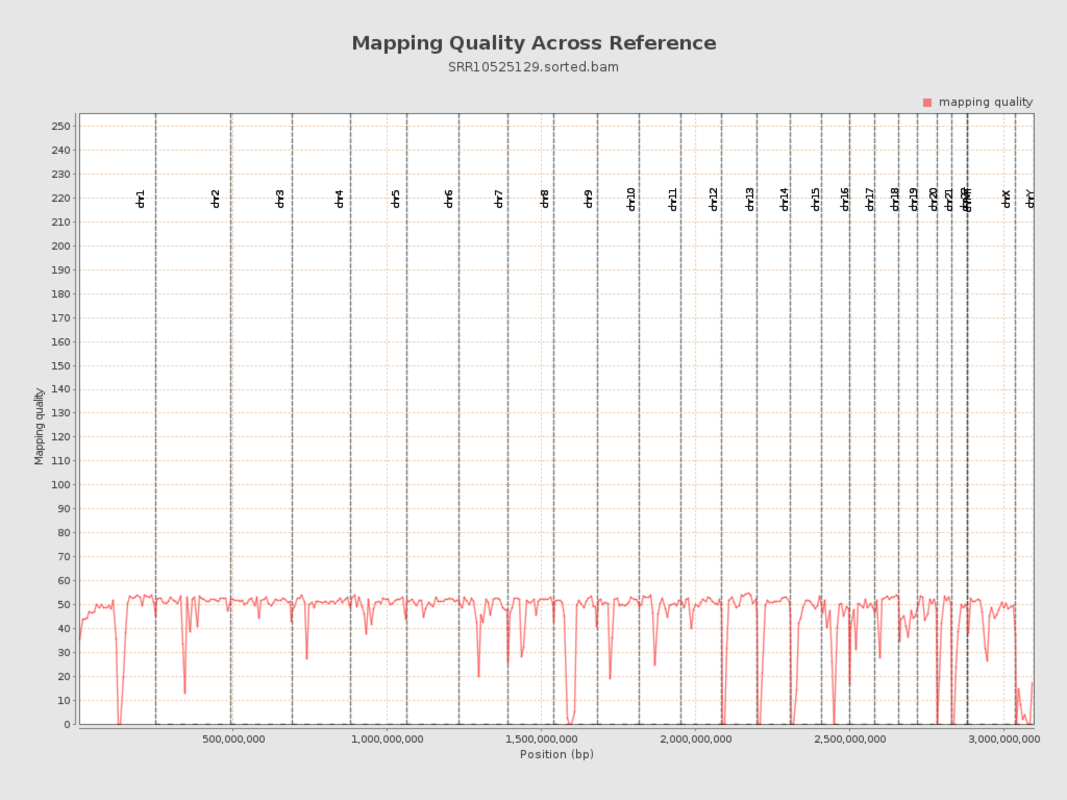
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram