# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 19:45:39*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525141.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_SRR10525141 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525141.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 19:45:39 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525141.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 987,493 |
| Mapped reads | 878,614 / 88.97% |
| Unmapped reads | 108,879 / 11.03% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 25,072 / 2.54% |
| Read min/max/mean length | 30 / 101 / 101.94 |
| Duplicated reads (estimated) | 23,114 / 2.34% |
| Duplication rate | 1.52% |
| Clipped reads | 903,524 / 91.5% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 17,460,040 / 25.75% |
| Number/percentage of C's | 13,531,031 / 19.95% |
| Number/percentage of T's | 20,562,299 / 30.32% |
| Number/percentage of G's | 16,256,046 / 23.97% |
| Number/percentage of N's | 2,634 / 0% |
| GC Percentage | 43.93% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0219 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2826 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.15 |

## 2.5. Mismatches and indels

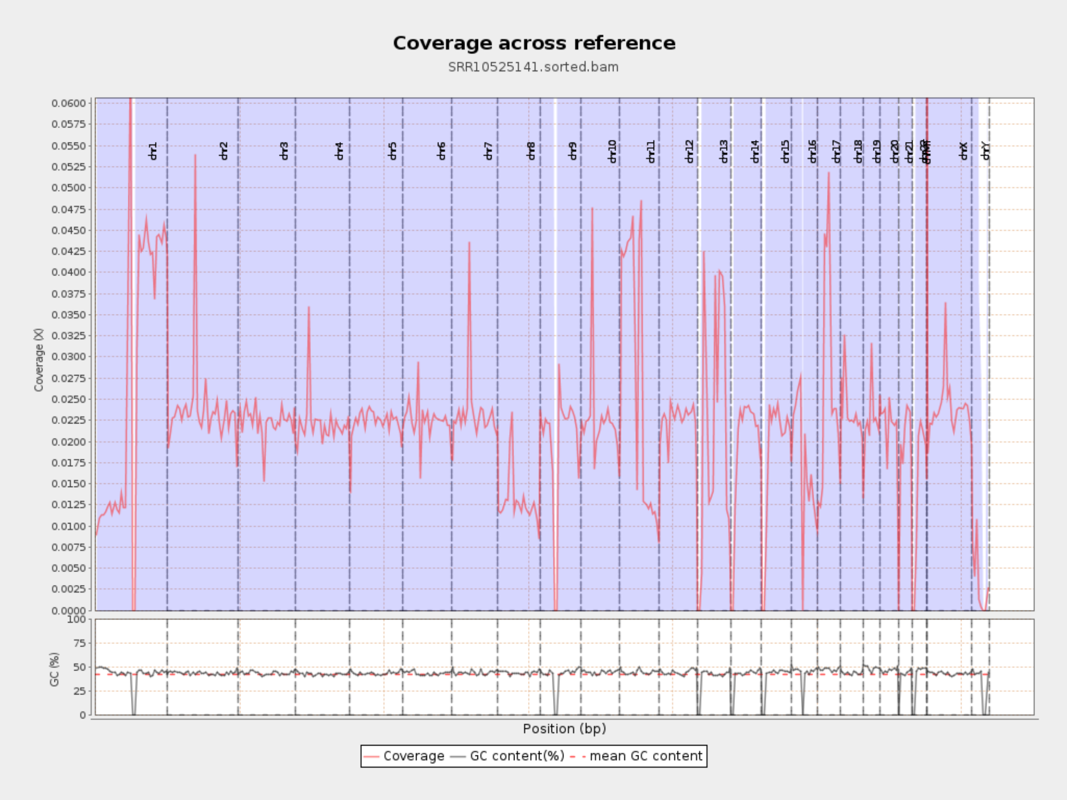
| | |
|---|---|
| General error rate | 0.79% |
| Mismatches | 527,150 |
| Insertions | 5,607 |
| Mapped reads with at least one insertion | 0.63% |
| Deletions | 17,301 |
| Mapped reads with at least one deletion | 1.94% |
| Homopolymer indels | 42.55% |

## 2.6. Chromosome stats

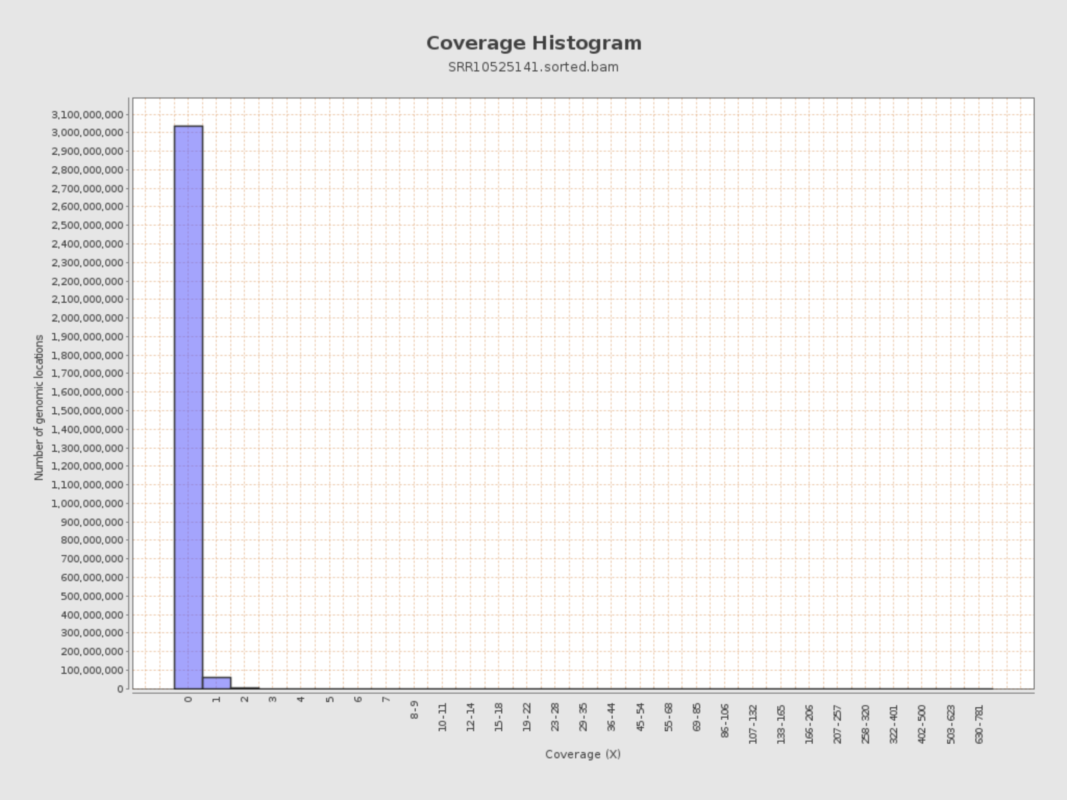
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6728473 | 0.027 | 0.6261 |
| chr2 | 243199373 | 5826762 | 0.024 | 0.3076 |
| chr3 | 198022430 | 4423827 | 0.0223 | 0.1589 |
| chr4 | 191154276 | 4241402 | 0.0222 | 0.1692 |
| chr5 | 180915260 | 4072407 | 0.0225 | 0.1603 |
| chr6 | 171115067 | 3853769 | 0.0225 | 0.1792 |
| chr7 | 159138663 | 3756577 | 0.0236 | 0.3489 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1911236 | 0.0131 | 0.2677 |
| chr9 | 141213431 | 2800987 | 0.0198 | 0.225 |
| chr10 | 135534747 | 3108497 | 0.0229 | 0.272 |
| chr11 | 135006516 | 3818309 | 0.0283 | 0.2799 |
| chr12 | 133851895 | 3029098 | 0.0226 | 0.1596 |
| chr13 | 115169878 | 2458908 | 0.0214 | 0.1542 |
| chr14 | 107349540 | 2040335 | 0.019 | 0.1595 |
| chr15 | 102531392 | 1891585 | 0.0184 | 0.1427 |
| chr16 | 90354753 | 1553634 | 0.0172 | 0.1535 |
| chr17 | 81195210 | 2158488 | 0.0266 | 0.1922 |
| chr18 | 78077248 | 1845338 | 0.0236 | 0.3825 |
| chr19 | 59128983 | 1350030 | 0.0228 | 0.4177 |
| chr20 | 63025520 | 1382432 | 0.0219 | 0.1616 |
| chr21 | 48129895 | 913271 | 0.019 | 0.1534 |
| chr22 | 51304566 | 742531 | 0.0145 | 0.1259 |
| chrMT | 16571 | 2027 | 0.1223 | 0.3807 |
| chrX | 155270560 | 3741640 | 0.0241 | 0.2009 |
| chrY | 59373566 | 190705 | 0.0032 | 0.0951 |

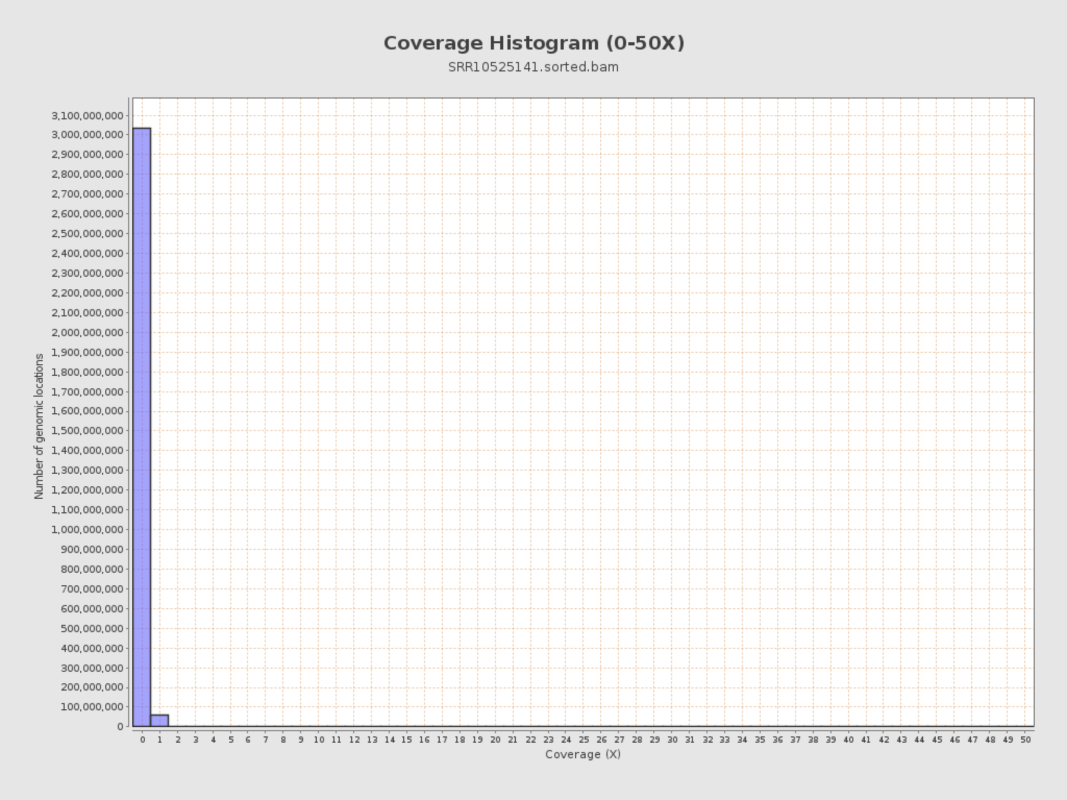
# 3. Results : Coverage across reference



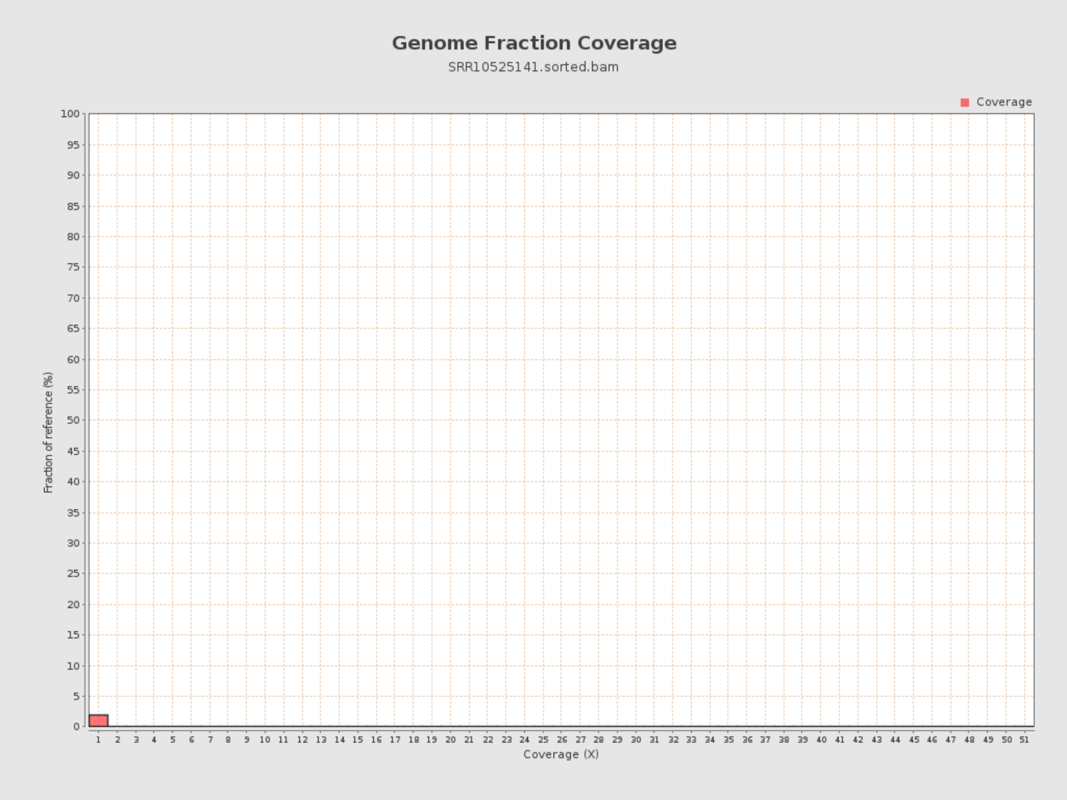
# 4. Results : Coverage Histogram



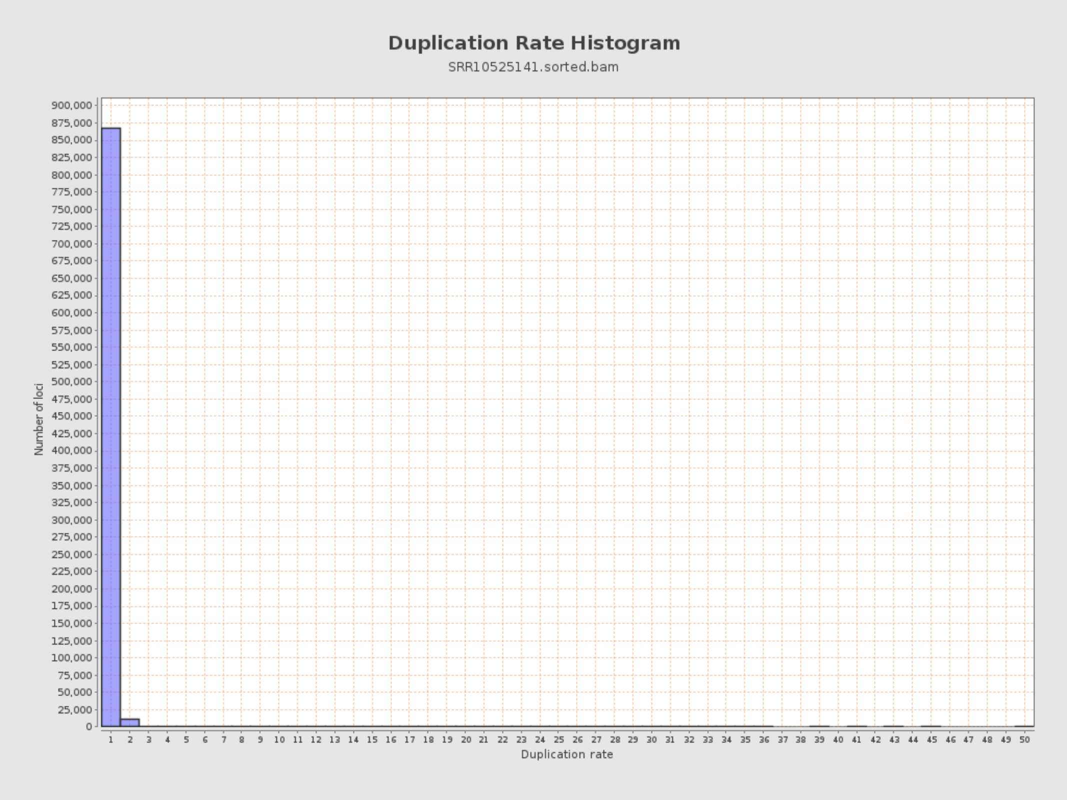
# 5. Results : Coverage Histogram (0-50X)



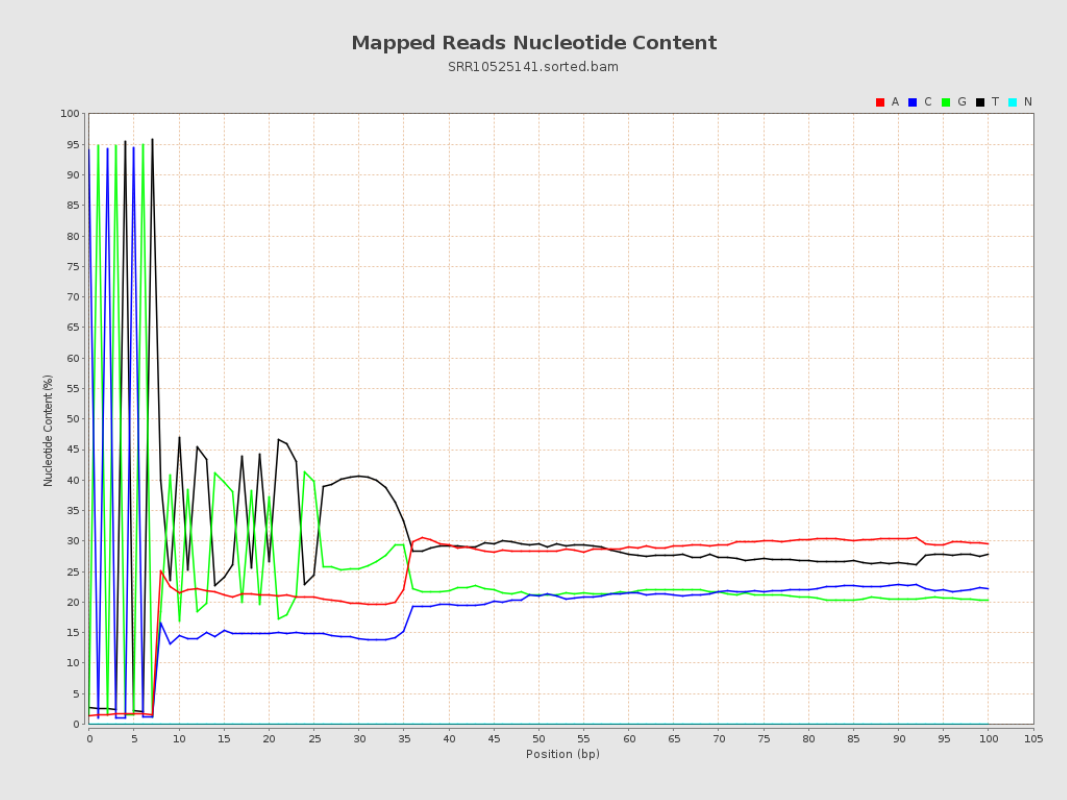
# 6. Results : Genome Fraction Coverage



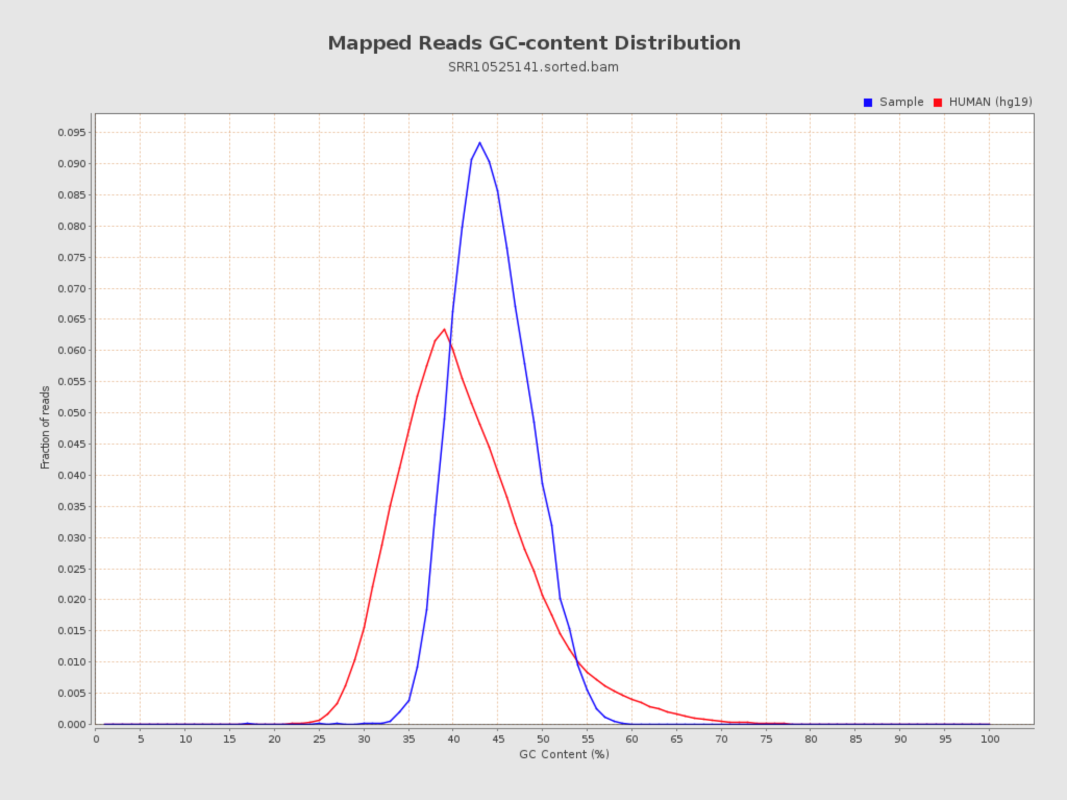
# 7. Results : Duplication Rate Histogram



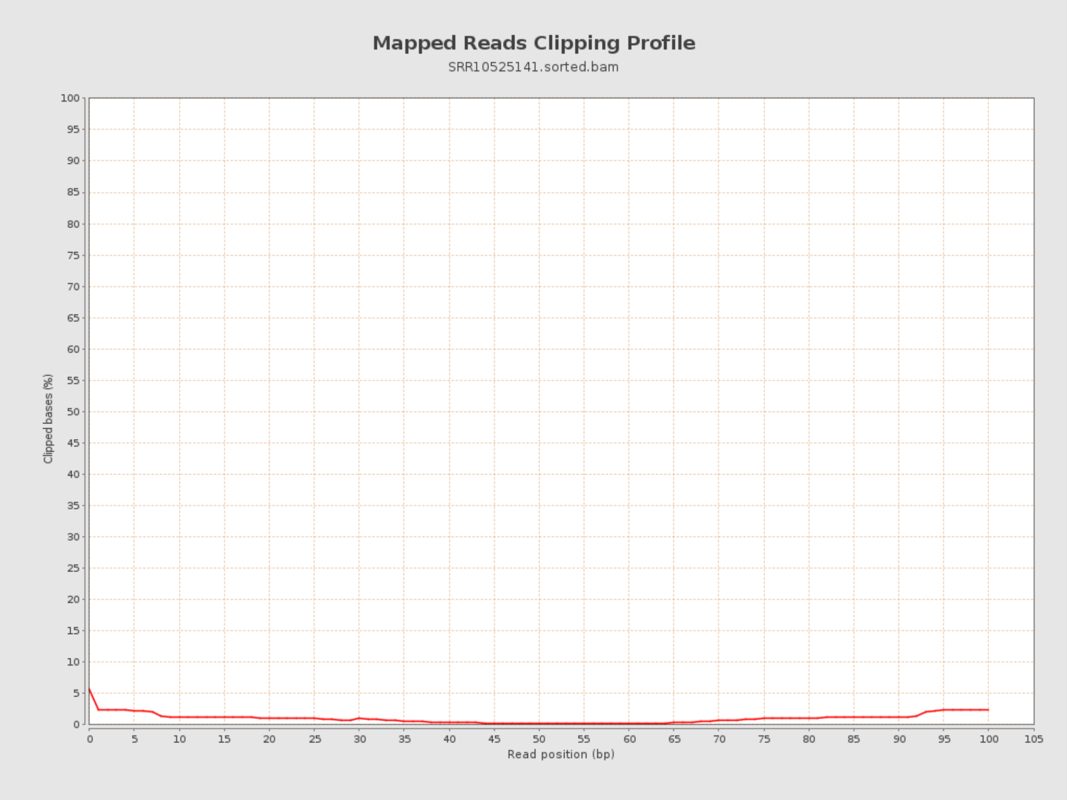
# 8. Results : Mapped Reads Nucleotide Content



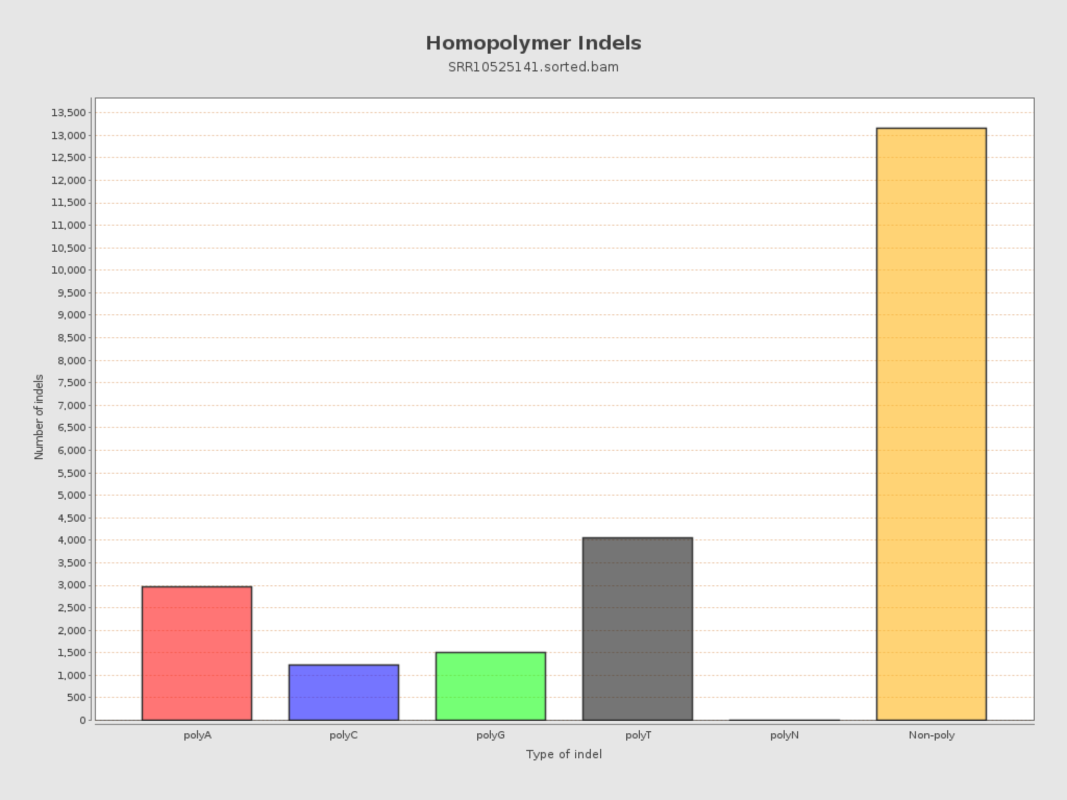
# 9. Results : Mapped Reads GC-content Distribution



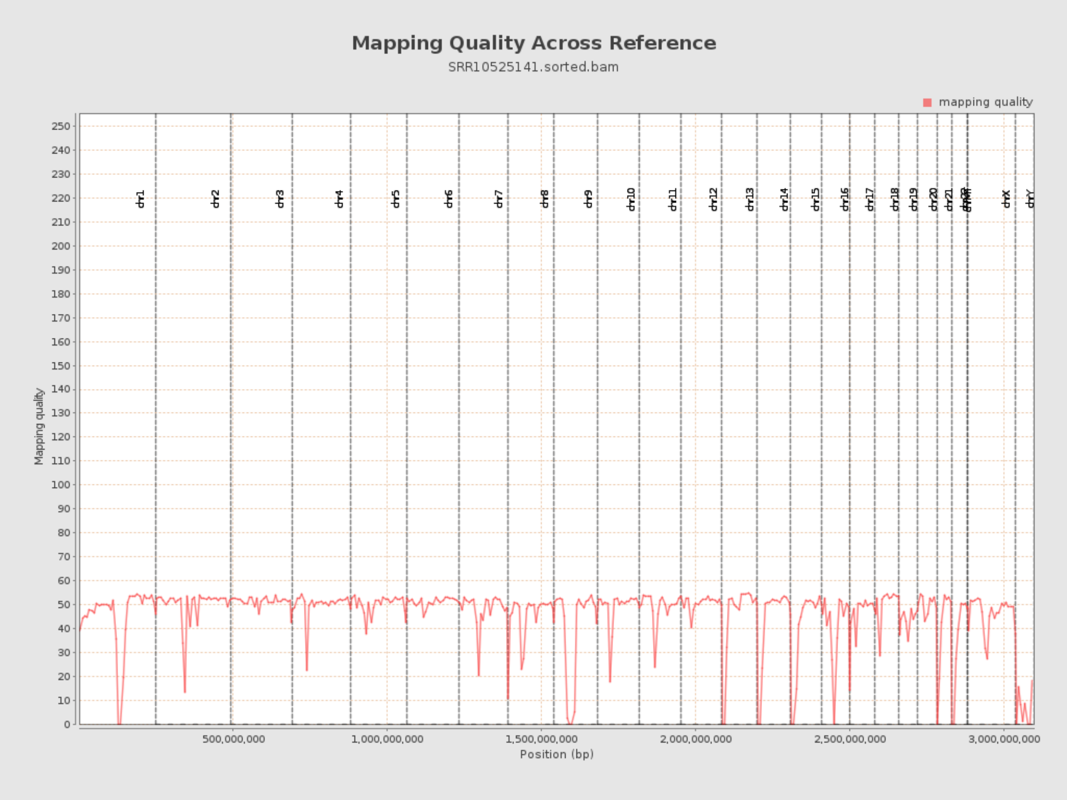
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram