# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/30 00:50:09*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525246.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_SRR10525246 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525246.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 30 00:50:08 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525246.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,395,187 |
| Mapped reads | 1,277,312 / 91.55% |
| Unmapped reads | 117,875 / 8.45% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,765 / 0.27% |
| Read min/max/mean length | 30 / 76 / 76.09 |
| Duplicated reads (estimated) | 42,102 / 3.02% |
| Duplication rate | 2.51% |
| Clipped reads | 1,275,806 / 91.44% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 19,758,906 / 26.69% |
| Number/percentage of C's | 12,706,729 / 17.16% |
| Number/percentage of T's | 23,721,153 / 32.04% |
| Number/percentage of G's | 17,838,929 / 24.1% |
| Number/percentage of N's | 1,581 / 0% |
| GC Percentage | 41.26% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0239 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2306 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.29 |

## 2.5. Mismatches and indels

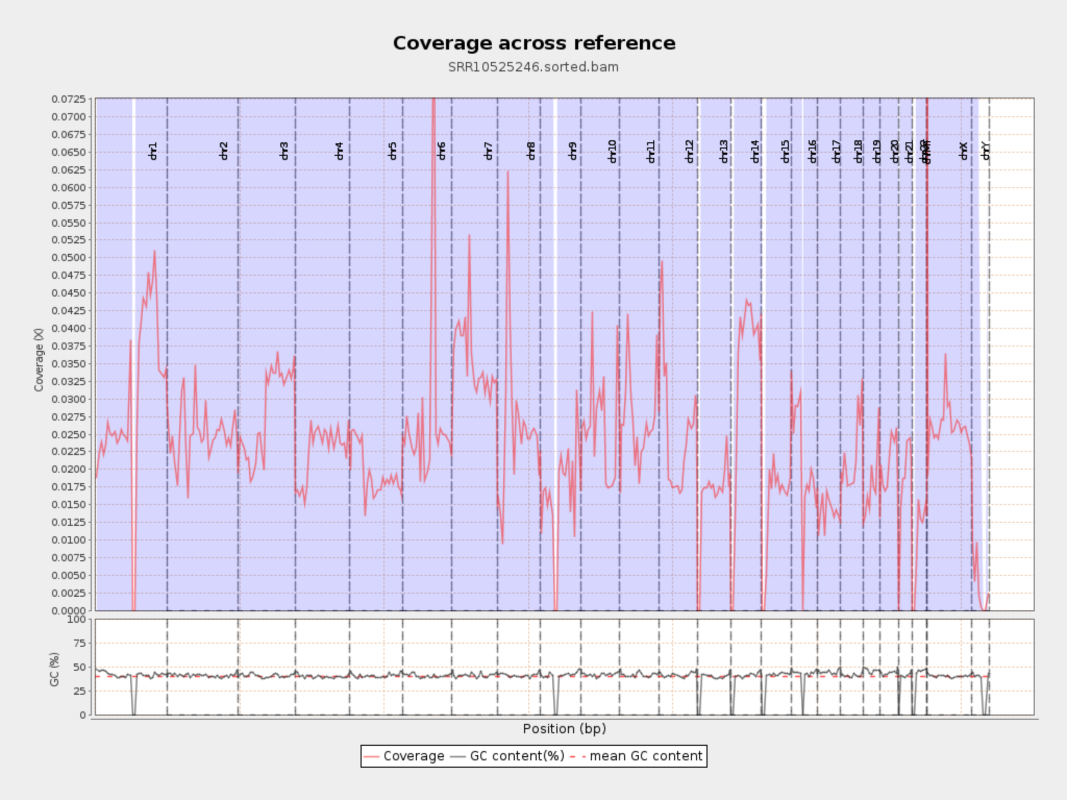
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 363,753 |
| Insertions | 6,511 |
| Mapped reads with at least one insertion | 0.51% |
| Deletions | 14,843 |
| Mapped reads with at least one deletion | 1.15% |
| Homopolymer indels | 42.9% |

## 2.6. Chromosome stats

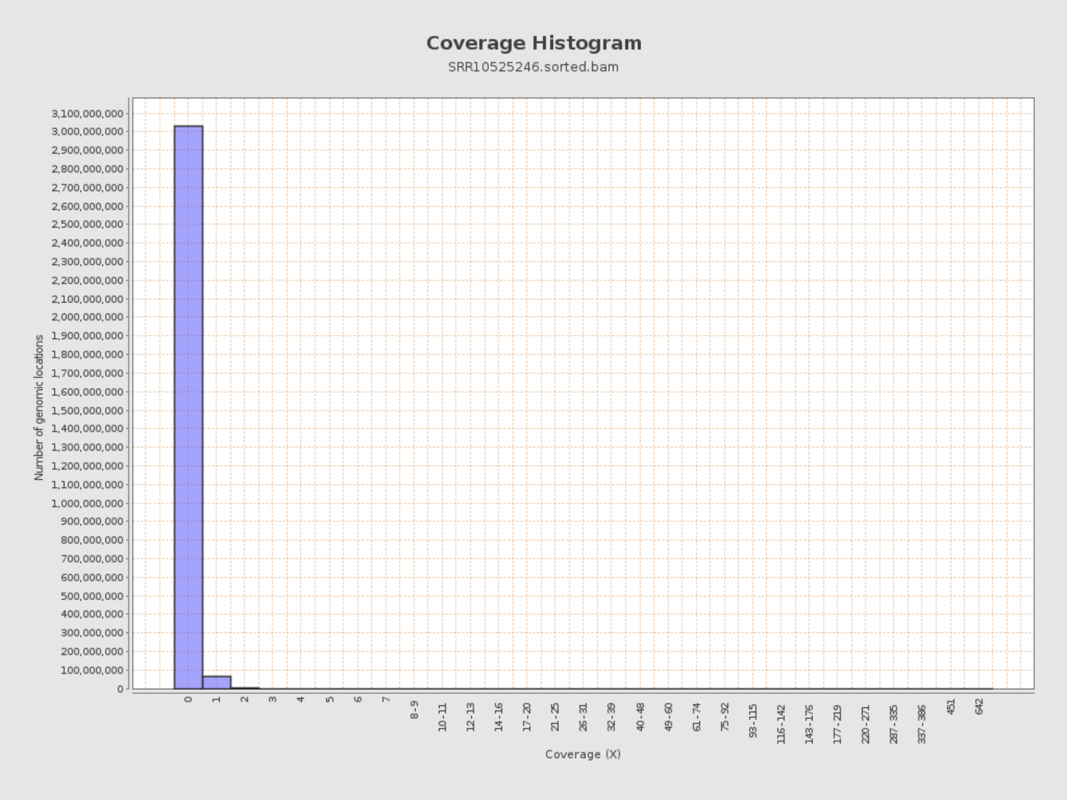
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7485270 | 0.03 | 0.3347 |
| chr2 | 243199373 | 6103129 | 0.0251 | 0.3102 |
| chr3 | 198022430 | 5556518 | 0.0281 | 0.1808 |
| chr4 | 191154276 | 4339264 | 0.0227 | 0.1662 |
| chr5 | 180915260 | 3533774 | 0.0195 | 0.1496 |
| chr6 | 171115067 | 4864377 | 0.0284 | 0.201 |
| chr7 | 159138663 | 5662234 | 0.0356 | 0.4298 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3852714 | 0.0263 | 0.2514 |
| chr9 | 141213431 | 2325103 | 0.0165 | 0.1635 |
| chr10 | 135534747 | 3550102 | 0.0262 | 0.2365 |
| chr11 | 135006516 | 3632355 | 0.0269 | 0.1995 |
| chr12 | 133851895 | 3465159 | 0.0259 | 0.174 |
| chr13 | 115169878 | 1851692 | 0.0161 | 0.1382 |
| chr14 | 107349540 | 3574365 | 0.0333 | 0.198 |
| chr15 | 102531392 | 1505754 | 0.0147 | 0.1377 |
| chr16 | 90354753 | 1862211 | 0.0206 | 0.1654 |
| chr17 | 81195210 | 1132515 | 0.0139 | 0.1312 |
| chr18 | 78077248 | 1700832 | 0.0218 | 0.2703 |
| chr19 | 59128983 | 1050001 | 0.0178 | 0.259 |
| chr20 | 63025520 | 1328944 | 0.0211 | 0.1584 |
| chr21 | 48129895 | 883120 | 0.0183 | 0.1493 |
| chr22 | 51304566 | 511589 | 0.01 | 0.1067 |
| chrMT | 16571 | 4598 | 0.2775 | 0.5534 |
| chrX | 155270560 | 4078937 | 0.0263 | 0.1862 |
| chrY | 59373566 | 196218 | 0.0033 | 0.0941 |

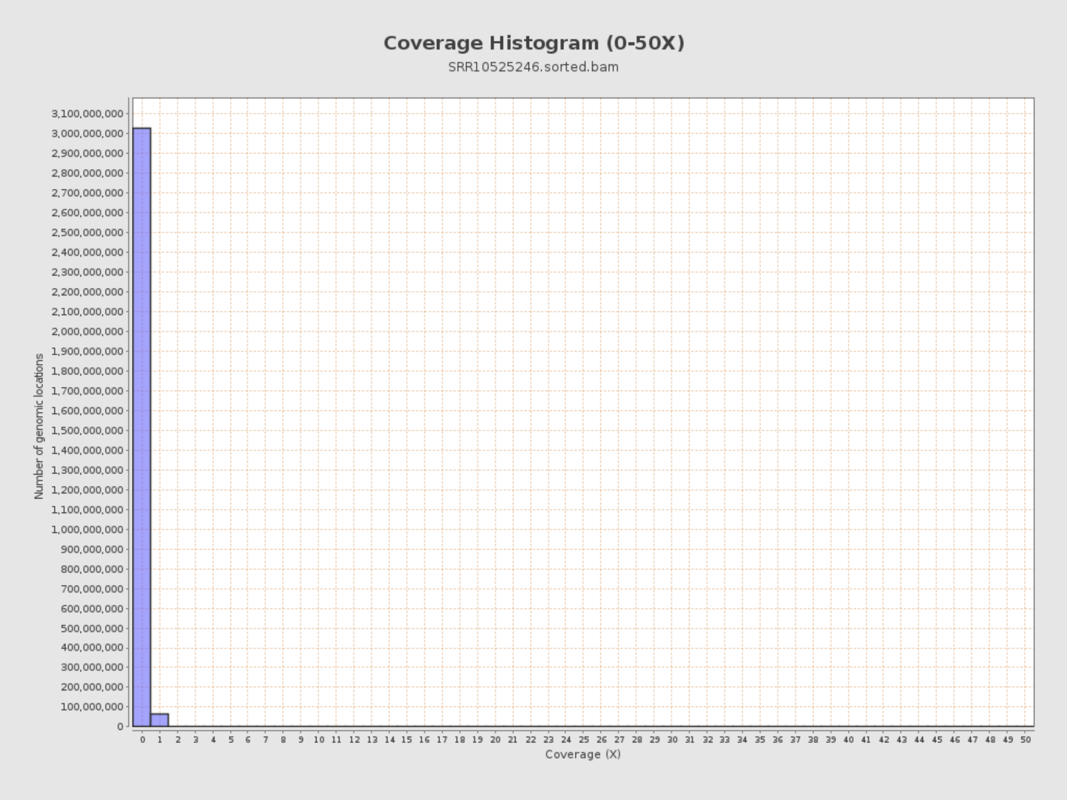
# 3. Results : Coverage across reference



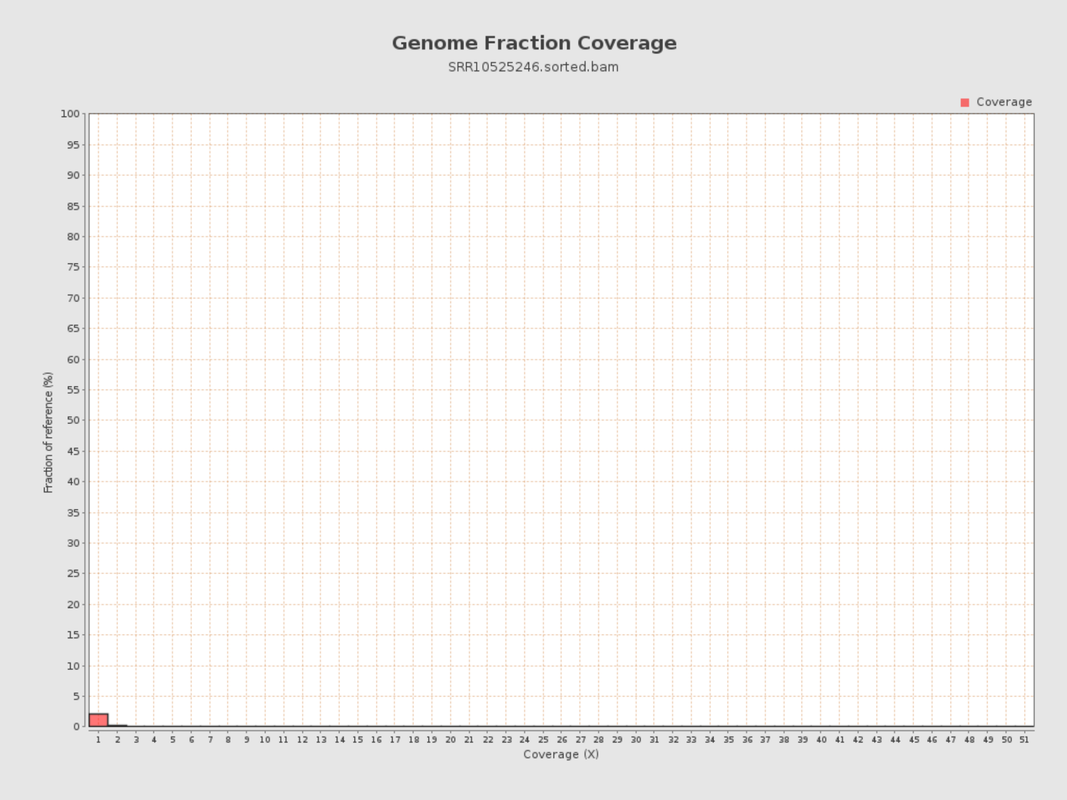
# 4. Results : Coverage Histogram



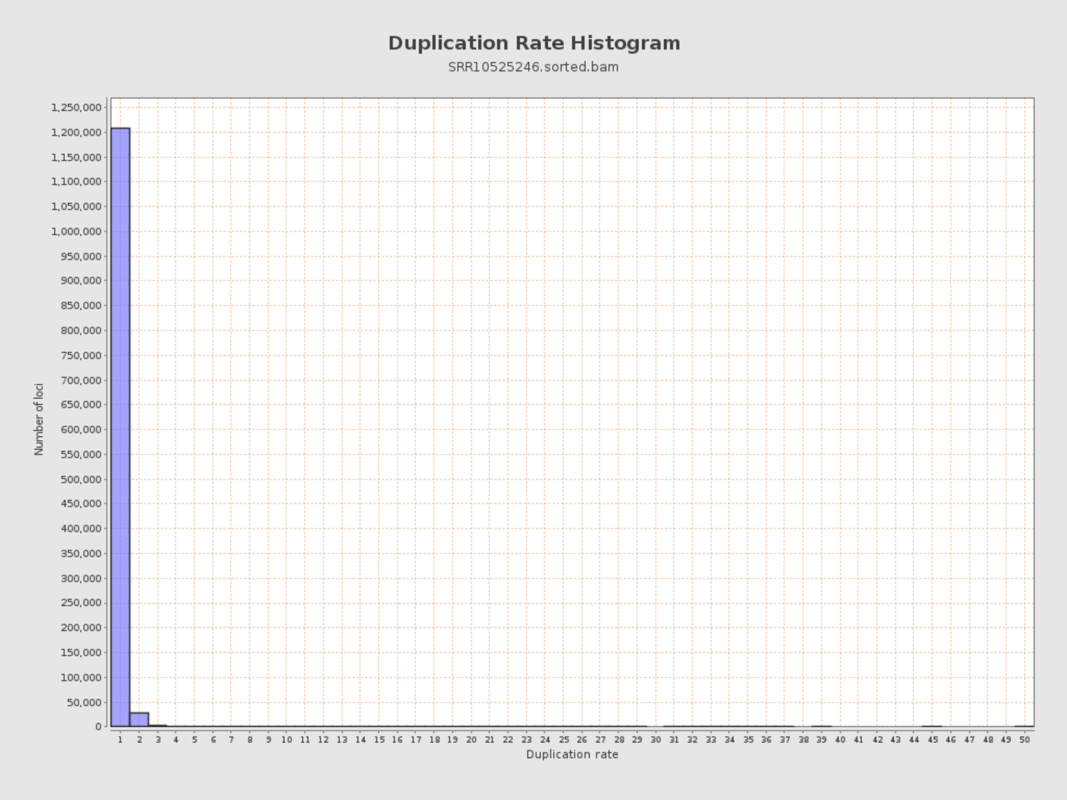
# 5. Results : Coverage Histogram (0-50X)



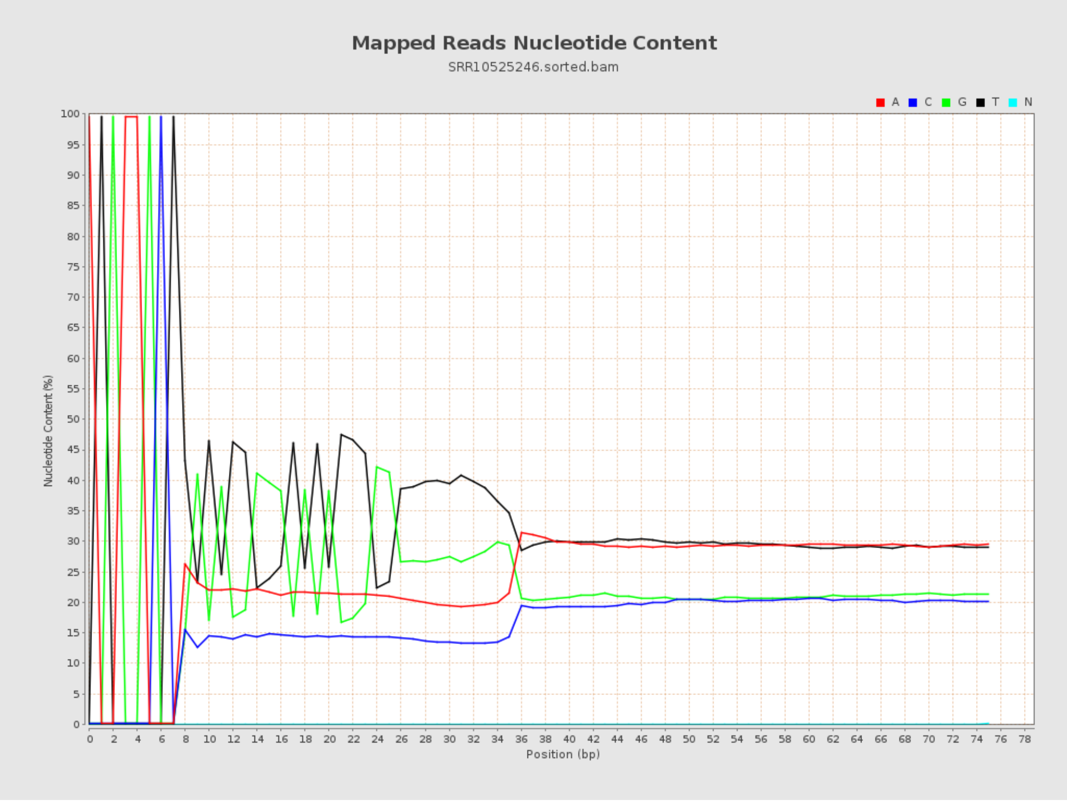
# 6. Results : Genome Fraction Coverage



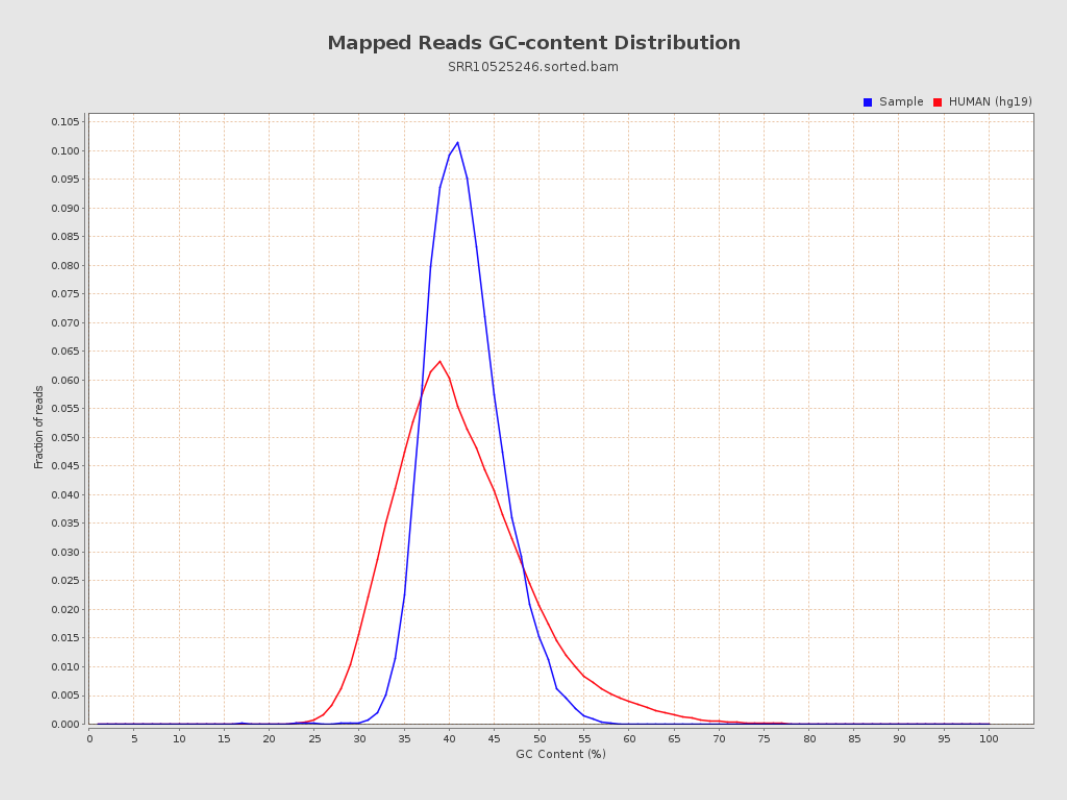
# 7. Results : Duplication Rate Histogram



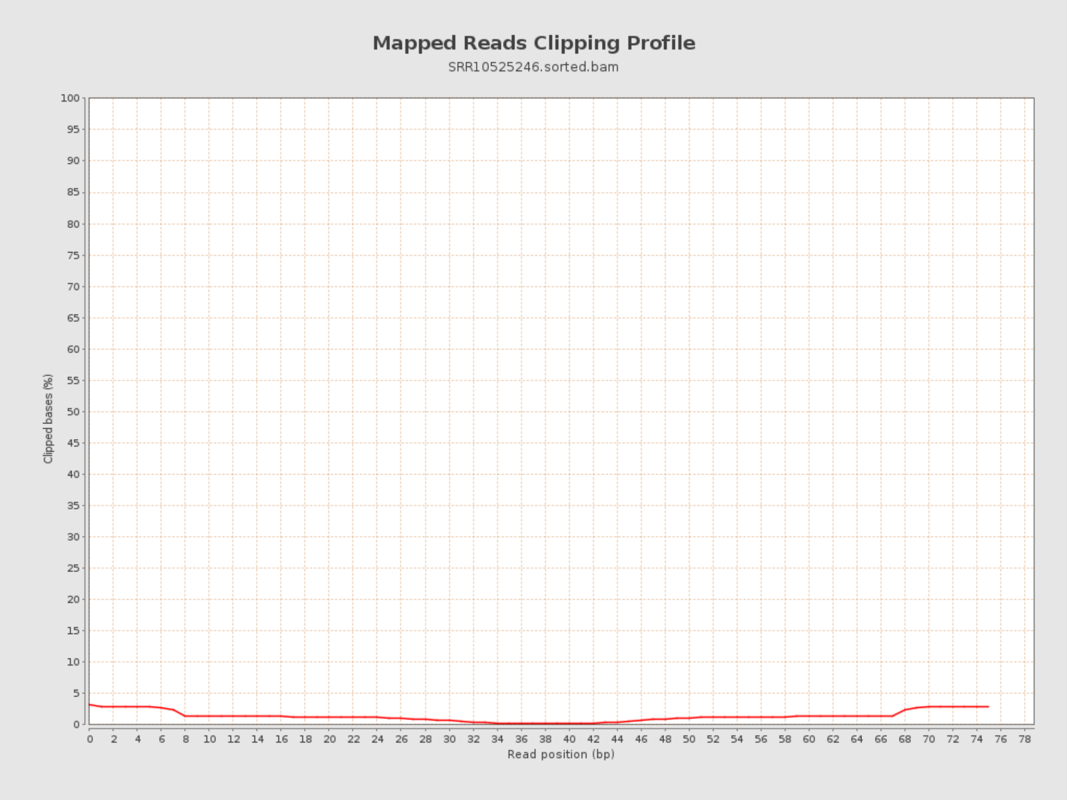
# 8. Results : Mapped Reads Nucleotide Content



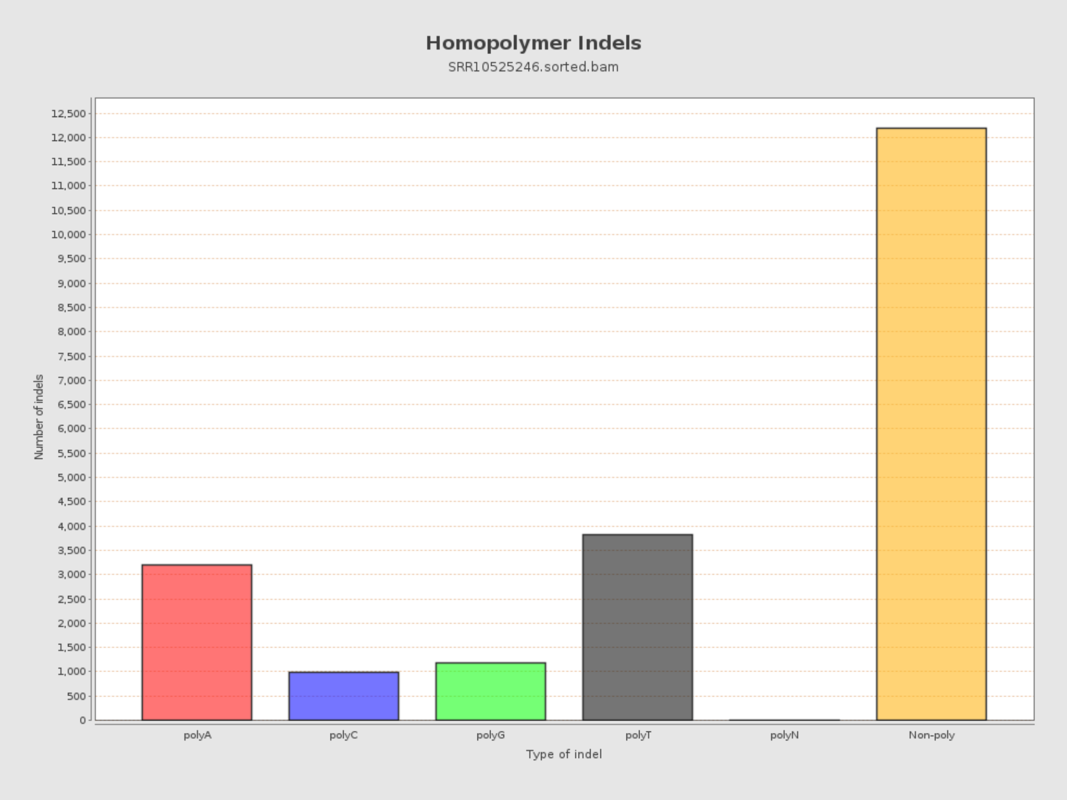
# 9. Results : Mapped Reads GC-content Distribution



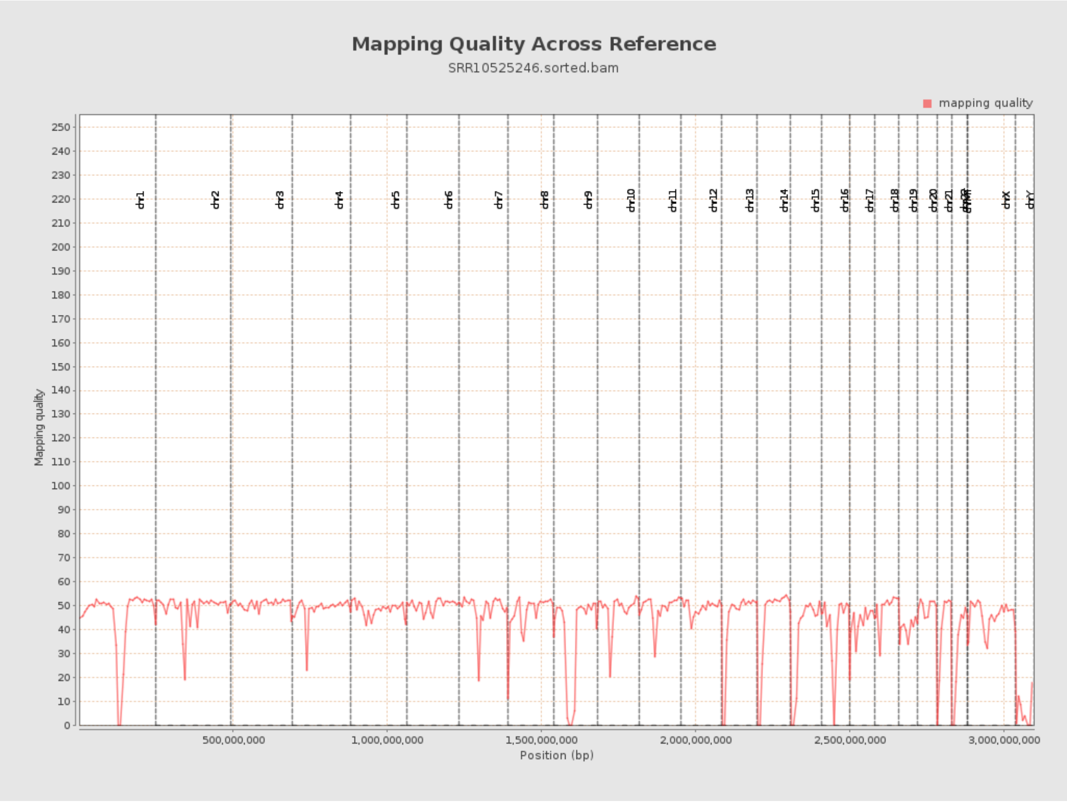
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram