# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 00:39:33*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524364.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_SRR10524364 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524364.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 00:39:32 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524364.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,655,216 |
| Mapped reads | 2,439,644 / 91.88% |
| Unmapped reads | 215,572 / 8.12% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 11,332 / 0.43% |
| Read min/max/mean length | 30 / 76 / 76.14 |
| Duplicated reads (estimated) | 158,304 / 5.96% |
| Duplication rate | 4.73% |
| Clipped reads | 2,443,651 / 92.03% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 35,289,856 / 24.67% |
| Number/percentage of C's | 27,321,355 / 19.1% |
| Number/percentage of T's | 45,558,498 / 31.85% |
| Number/percentage of G's | 34,864,694 / 24.37% |
| Number/percentage of N's | 20,534 / 0.01% |
| GC Percentage | 43.47% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0462 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4551 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.11 |

## 2.5. Mismatches and indels

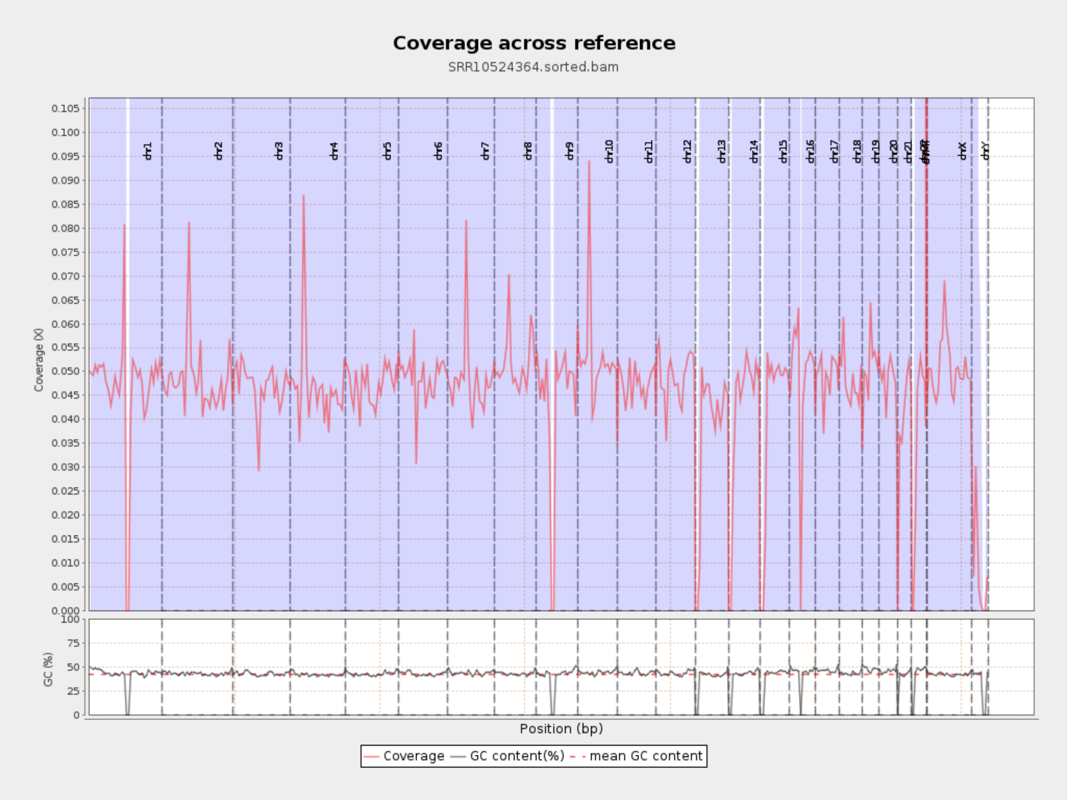
| | |
|---|---|
| General error rate | 0.53% |
| Mismatches | 745,123 |
| Insertions | 9,971 |
| Mapped reads with at least one insertion | 0.41% |
| Deletions | 26,024 |
| Mapped reads with at least one deletion | 1.06% |
| Homopolymer indels | 42.94% |

## 2.6. Chromosome stats

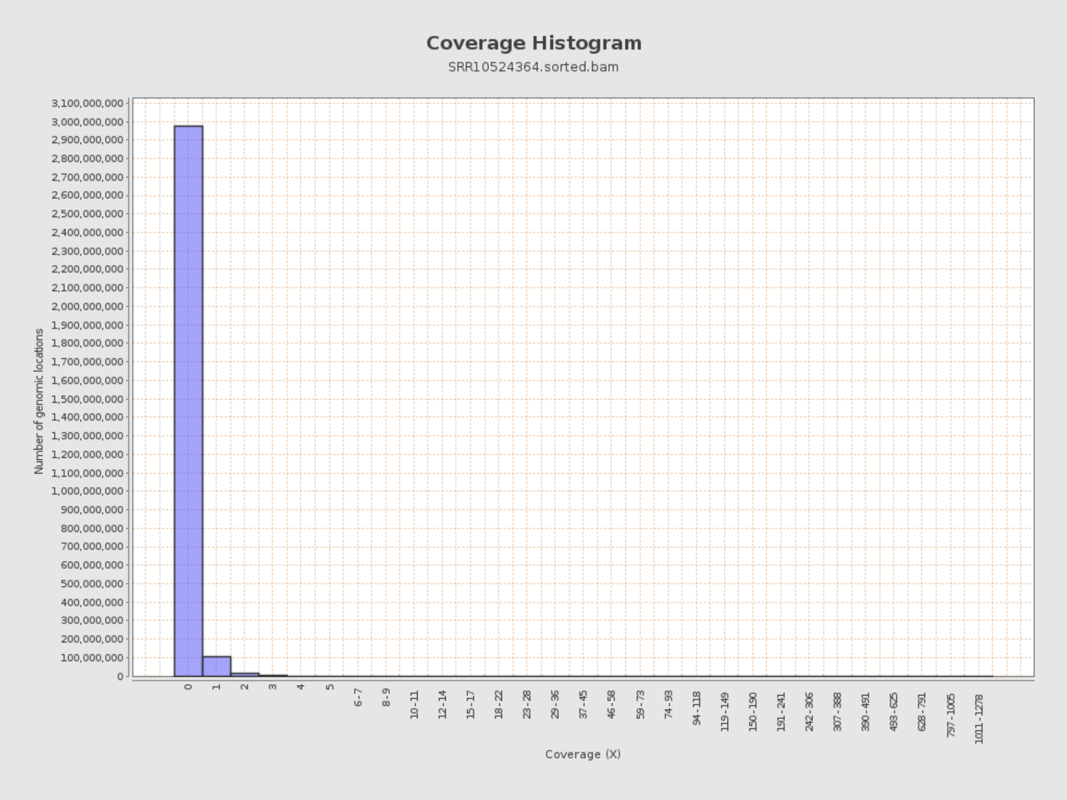
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 11542708 | 0.0463 | 0.9395 |
| chr2 | 243199373 | 11779027 | 0.0484 | 0.592 |
| chr3 | 198022430 | 9287598 | 0.0469 | 0.2518 |
| chr4 | 191154276 | 8943276 | 0.0468 | 0.3201 |
| chr5 | 180915260 | 8539656 | 0.0472 | 0.257 |
| chr6 | 171115067 | 8342178 | 0.0488 | 0.2952 |
| chr7 | 159138663 | 7676287 | 0.0482 | 0.5684 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7584682 | 0.0518 | 0.3938 |
| chr9 | 141213431 | 6072834 | 0.043 | 0.3741 |
| chr10 | 135534747 | 7155582 | 0.0528 | 0.4403 |
| chr11 | 135006516 | 6402577 | 0.0474 | 0.3734 |
| chr12 | 133851895 | 6555041 | 0.049 | 0.2685 |
| chr13 | 115169878 | 4267669 | 0.0371 | 0.2232 |
| chr14 | 107349540 | 4411858 | 0.0411 | 0.258 |
| chr15 | 102531392 | 4139406 | 0.0404 | 0.2331 |
| chr16 | 90354753 | 4416834 | 0.0489 | 0.2912 |
| chr17 | 81195210 | 3971501 | 0.0489 | 0.2876 |
| chr18 | 78077248 | 3779425 | 0.0484 | 0.739 |
| chr19 | 59128983 | 3036613 | 0.0514 | 0.5935 |
| chr20 | 63025520 | 3042587 | 0.0483 | 0.2679 |
| chr21 | 48129895 | 1890915 | 0.0393 | 0.2874 |
| chr22 | 51304566 | 1740738 | 0.0339 | 0.2177 |
| chrMT | 16571 | 146182 | 8.8216 | 5.8914 |
| chrX | 155270560 | 7876896 | 0.0507 | 0.3141 |
| chrY | 59373566 | 494415 | 0.0083 | 0.2482 |

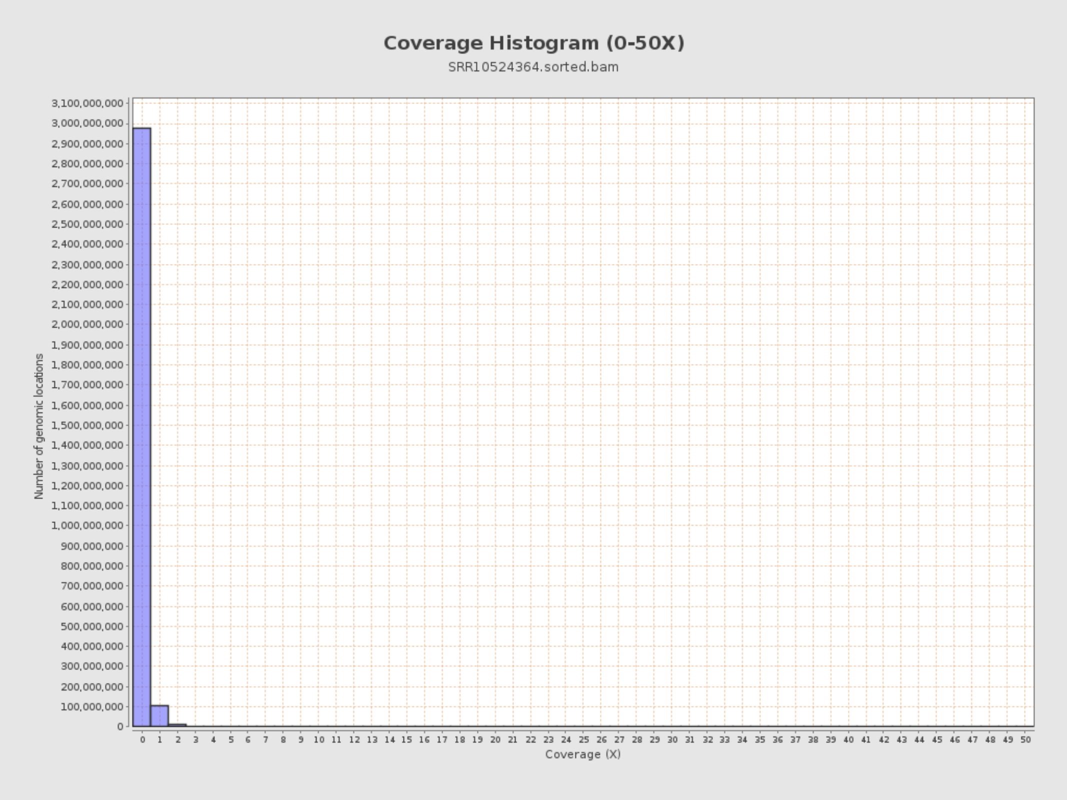
# 3. Results : Coverage across reference



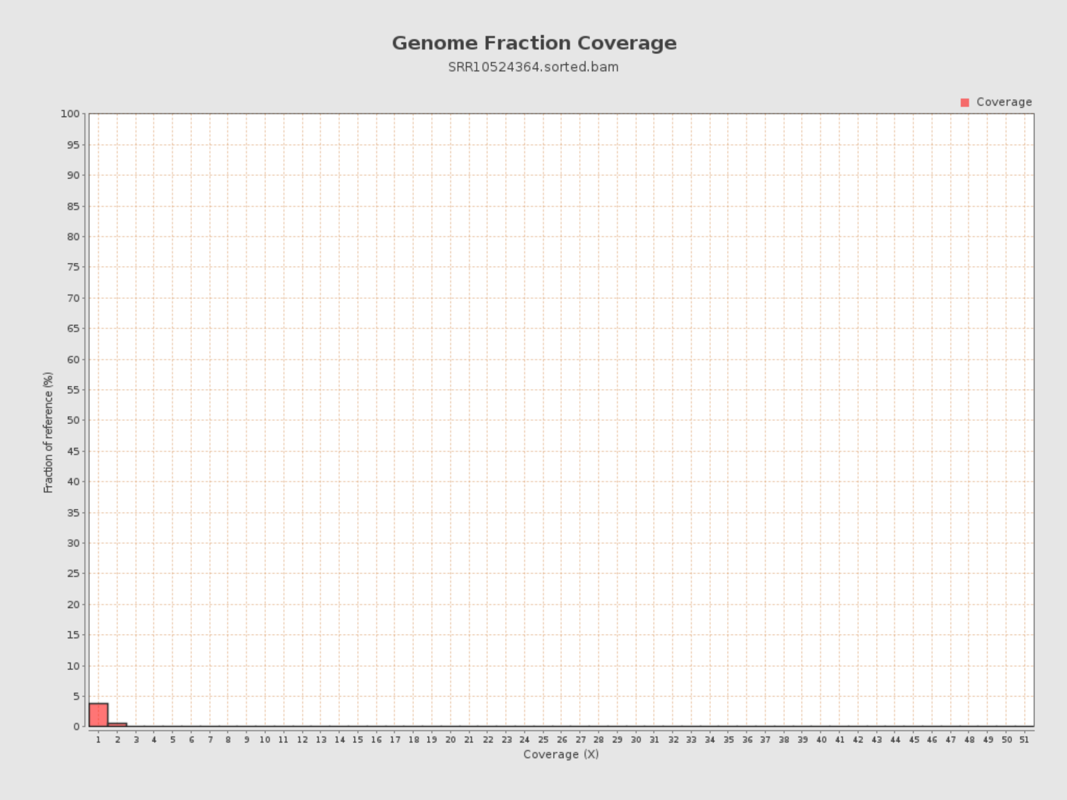
# 4. Results : Coverage Histogram



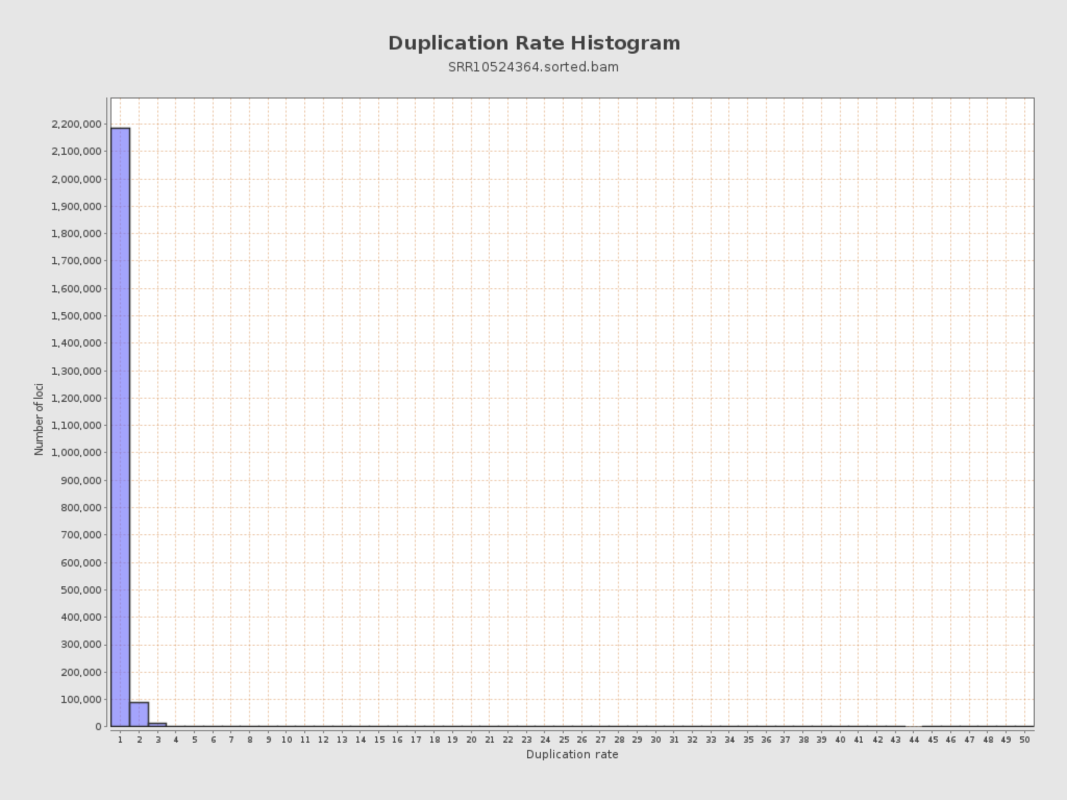
# 5. Results : Coverage Histogram (0-50X)



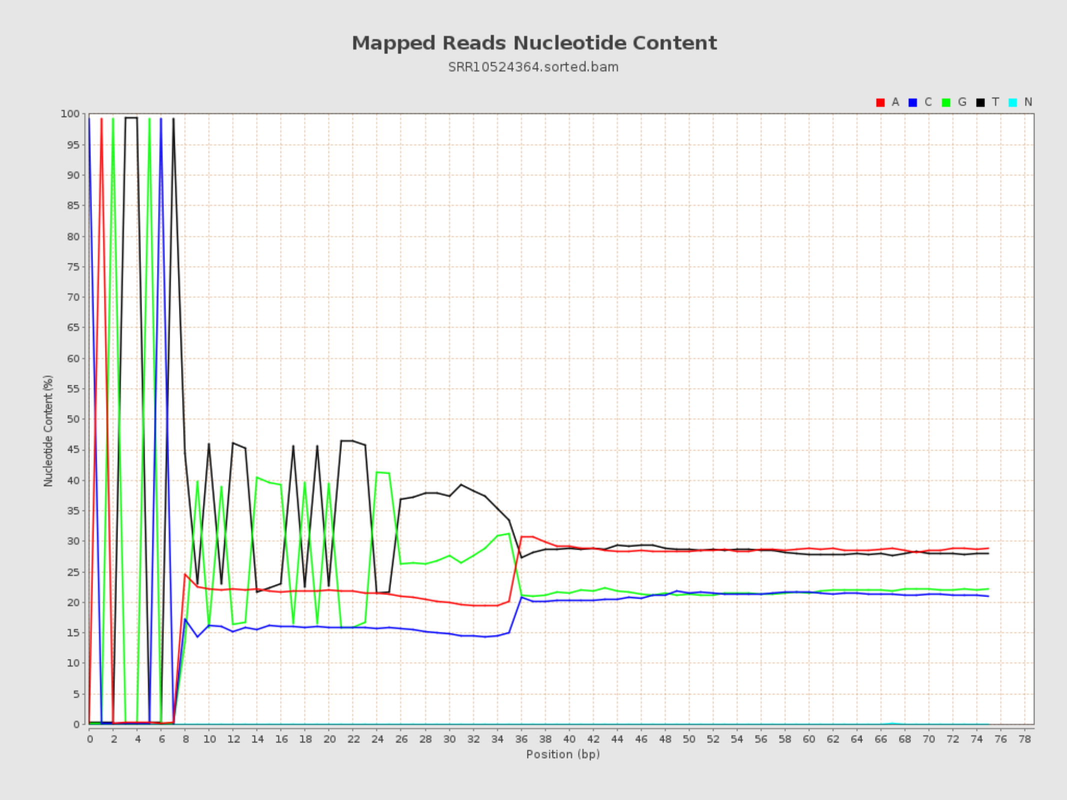
# 6. Results : Genome Fraction Coverage



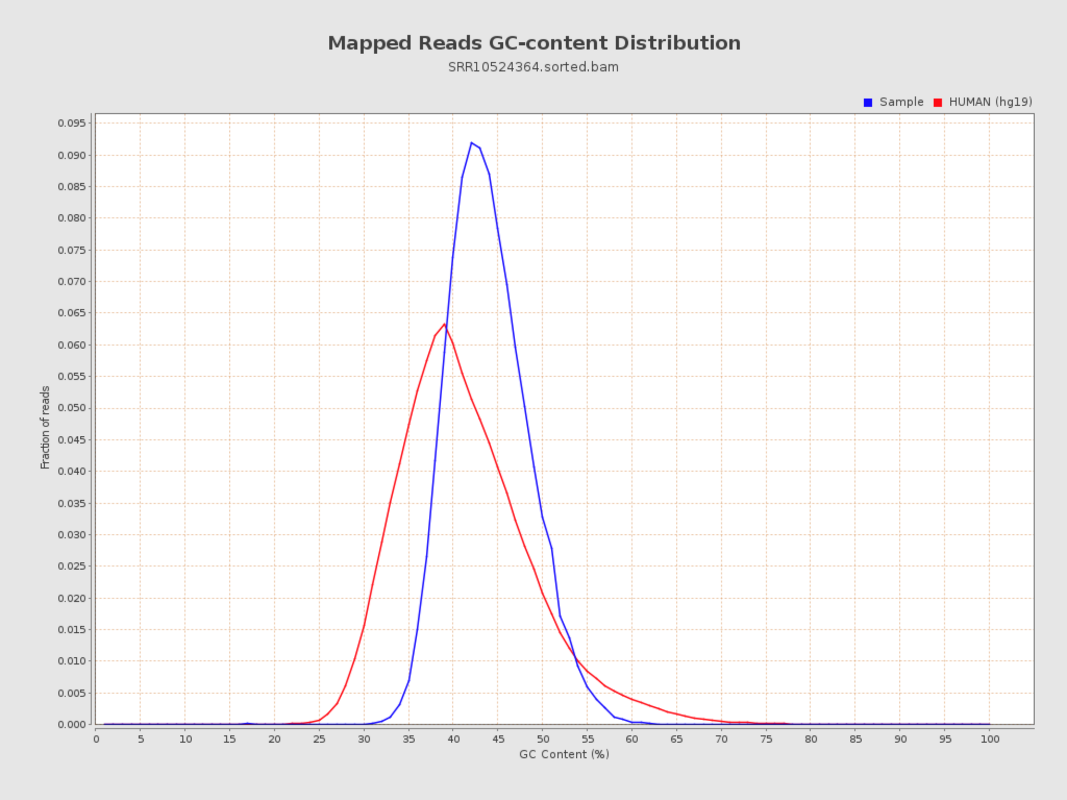
# 7. Results : Duplication Rate Histogram



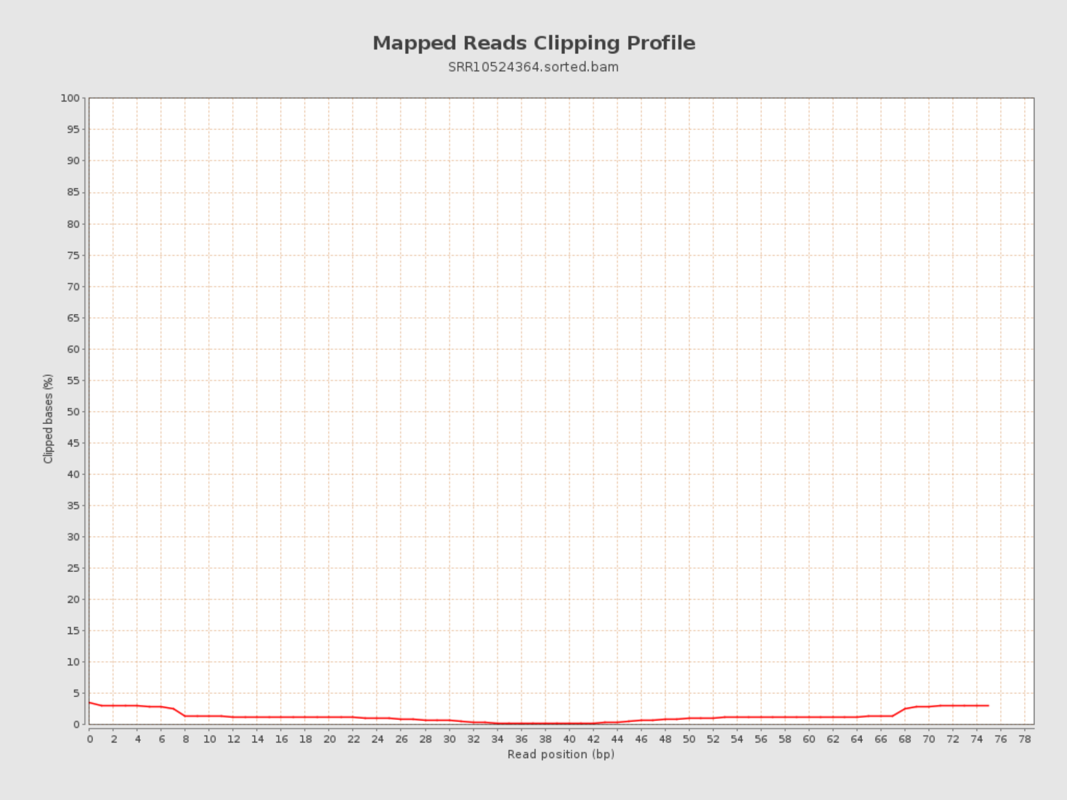
# 8. Results : Mapped Reads Nucleotide Content



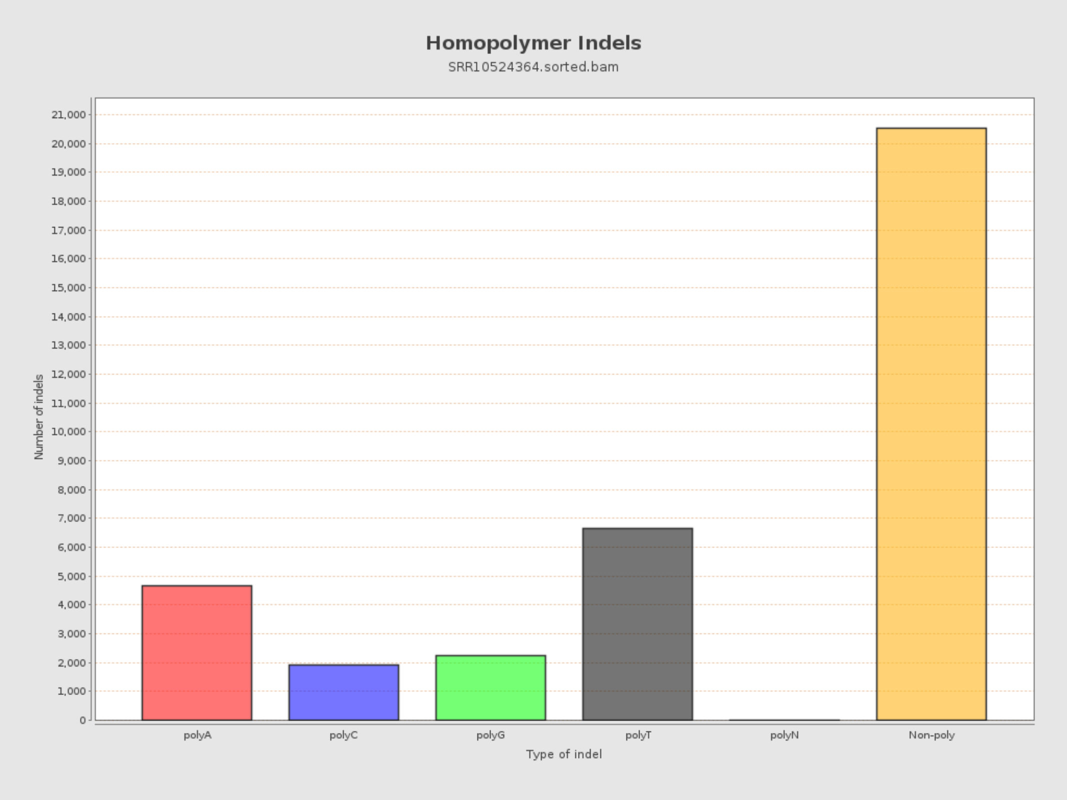
# 9. Results : Mapped Reads GC-content Distribution



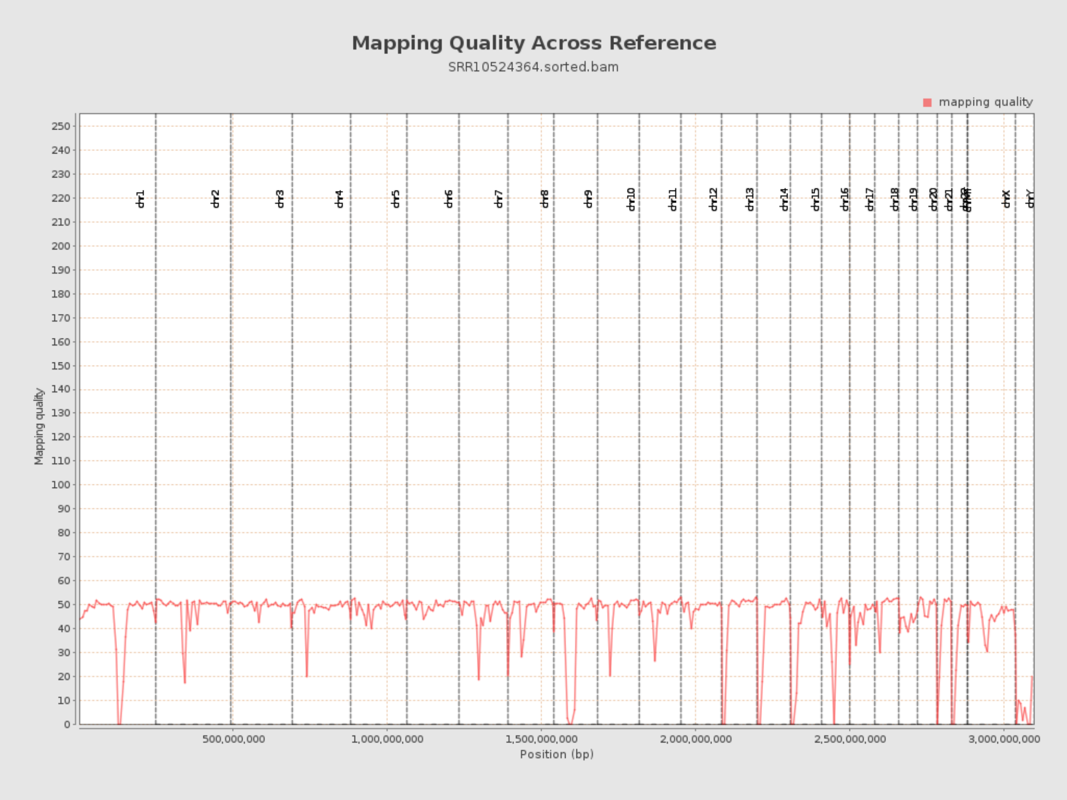
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram