# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 04:40:35*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524446.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_SRR10524446 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524446.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 04:40:34 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524446.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,918,833 |
| Mapped reads | 3,644,283 / 92.99% |
| Unmapped reads | 274,550 / 7.01% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 8,851 / 0.23% |
| Read min/max/mean length | 30 / 76 / 76.08 |
| Duplicated reads (estimated) | 288,549 / 7.36% |
| Duplication rate | 5.9% |
| Clipped reads | 3,638,804 / 92.85% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 53,475,568 / 25.02% |
| Number/percentage of C's | 39,848,444 / 18.65% |
| Number/percentage of T's | 68,478,610 / 32.04% |
| Number/percentage of G's | 51,895,064 / 24.28% |
| Number/percentage of N's | 4,476 / 0% |
| GC Percentage | 42.93% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0691 |
| | |

| | |
|---|---|
| Standard Deviation | 0.5788 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.65 |

## 2.5. Mismatches and indels

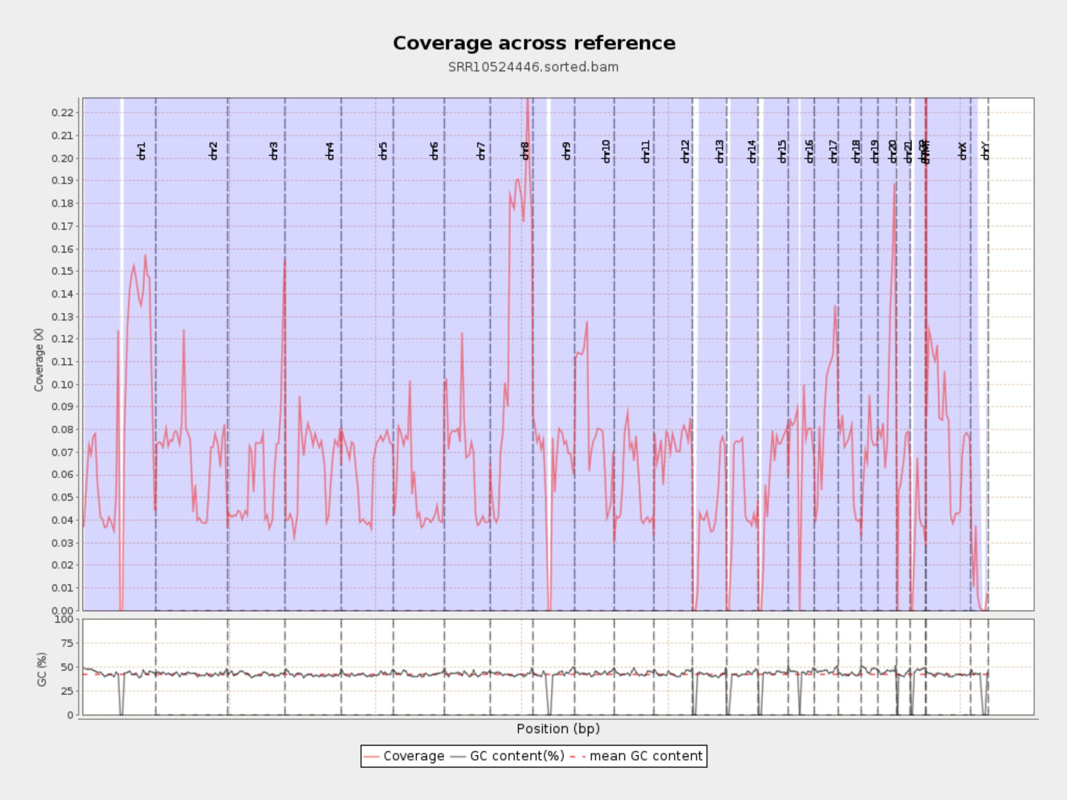
| | |
|---|---|
| General error rate | 0.48% |
| Mismatches | 984,446 |
| Insertions | 16,385 |
| Mapped reads with at least one insertion | 0.45% |
| Deletions | 40,725 |
| Mapped reads with at least one deletion | 1.11% |
| Homopolymer indels | 41.24% |

## 2.6. Chromosome stats

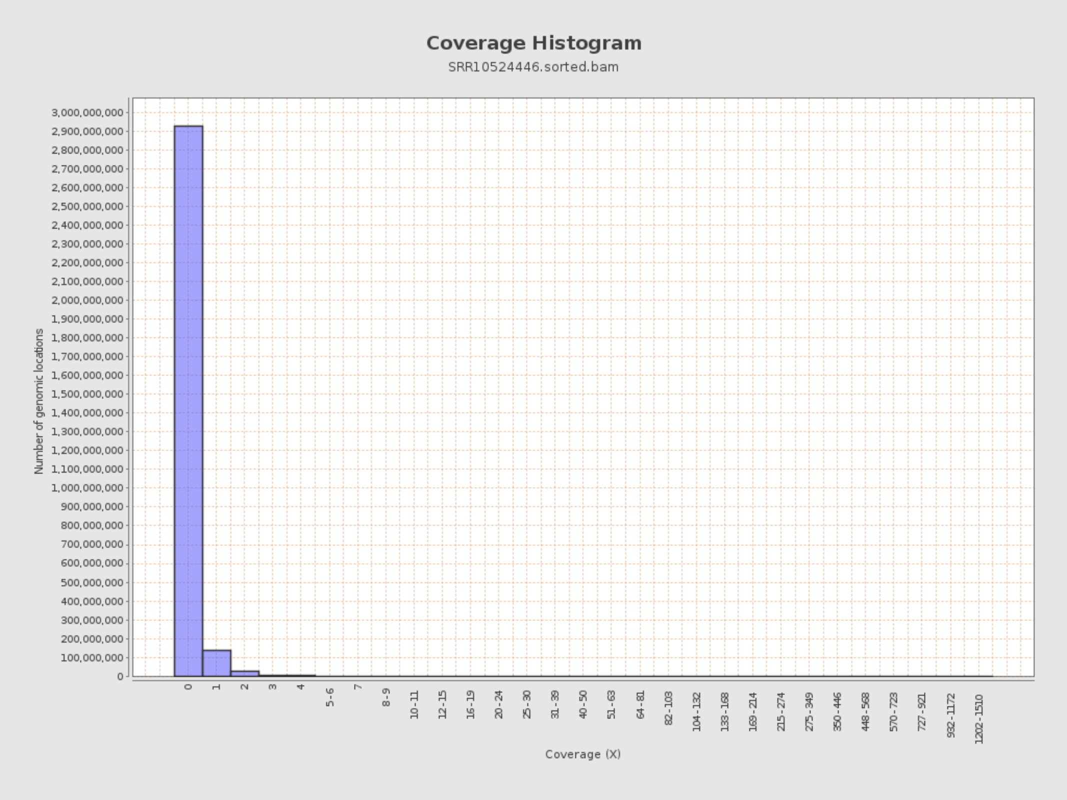
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 20902879 | 0.0839 | 1.1707 |
| chr2 | 243199373 | 16693624 | 0.0686 | 0.627 |
| chr3 | 198022430 | 11842879 | 0.0598 | 0.304 |
| chr4 | 191154276 | 12202480 | 0.0638 | 0.3778 |
| chr5 | 180915260 | 11544019 | 0.0638 | 0.3167 |
| chr6 | 171115067 | 9230326 | 0.0539 | 0.4195 |
| chr7 | 159138663 | 10749587 | 0.0675 | 0.8239 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 19821501 | 0.1354 | 0.601 |
| chr9 | 141213431 | 8967200 | 0.0635 | 0.4815 |
| chr10 | 135534747 | 11185117 | 0.0825 | 0.559 |
| chr11 | 135006516 | 7333333 | 0.0543 | 0.5526 |
| chr12 | 133851895 | 9917863 | 0.0741 | 0.341 |
| chr13 | 115169878 | 4779477 | 0.0415 | 0.2561 |
| chr14 | 107349540 | 5027172 | 0.0468 | 0.2833 |
| chr15 | 102531392 | 5664284 | 0.0552 | 0.3086 |
| chr16 | 90354753 | 6537245 | 0.0724 | 0.3738 |
| chr17 | 81195210 | 7278707 | 0.0896 | 0.4106 |
| chr18 | 78077248 | 5110052 | 0.0654 | 0.9453 |
| chr19 | 59128983 | 4212634 | 0.0712 | 0.7904 |
| chr20 | 63025520 | 6870942 | 0.109 | 0.4193 |
| chr21 | 48129895 | 2908540 | 0.0604 | 0.3456 |
| chr22 | 51304566 | 1660045 | 0.0324 | 0.2214 |
| chrMT | 16571 | 72780 | 4.392 | 3.4682 |
| chrX | 155270560 | 12601983 | 0.0812 | 0.4261 |
| chrY | 59373566 | 657709 | 0.0111 | 0.2811 |

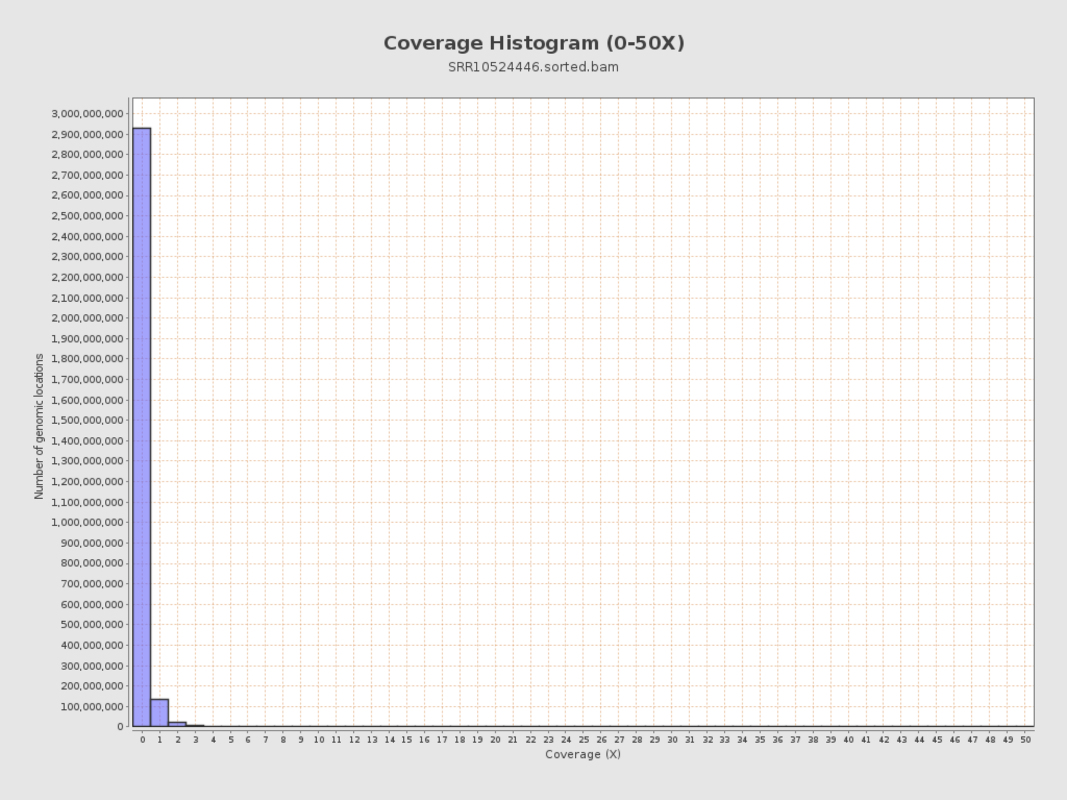
# 3. Results : Coverage across reference



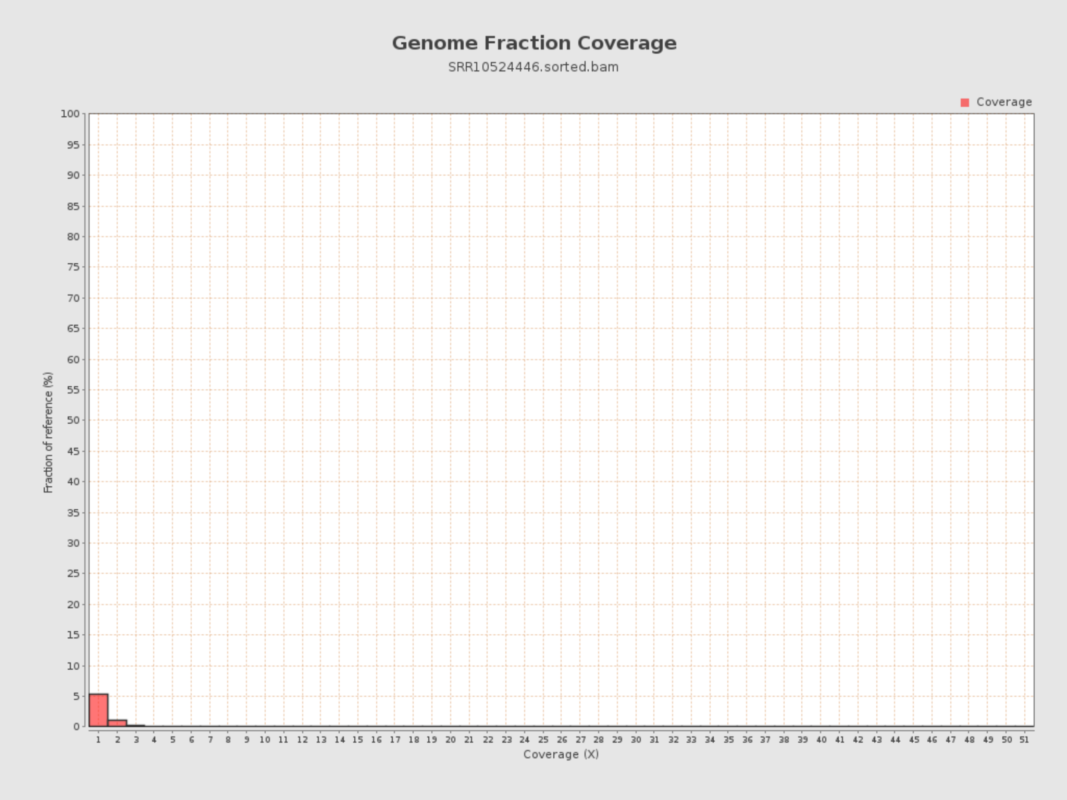
# 4. Results : Coverage Histogram



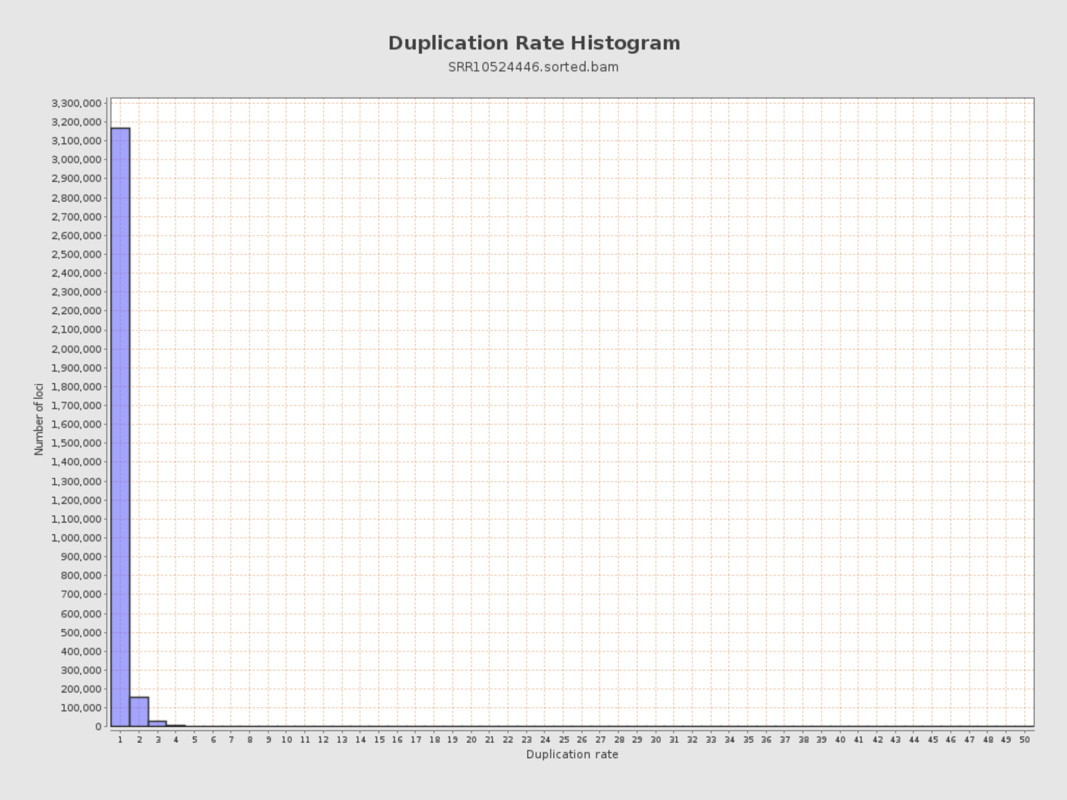
# 5. Results : Coverage Histogram (0-50X)



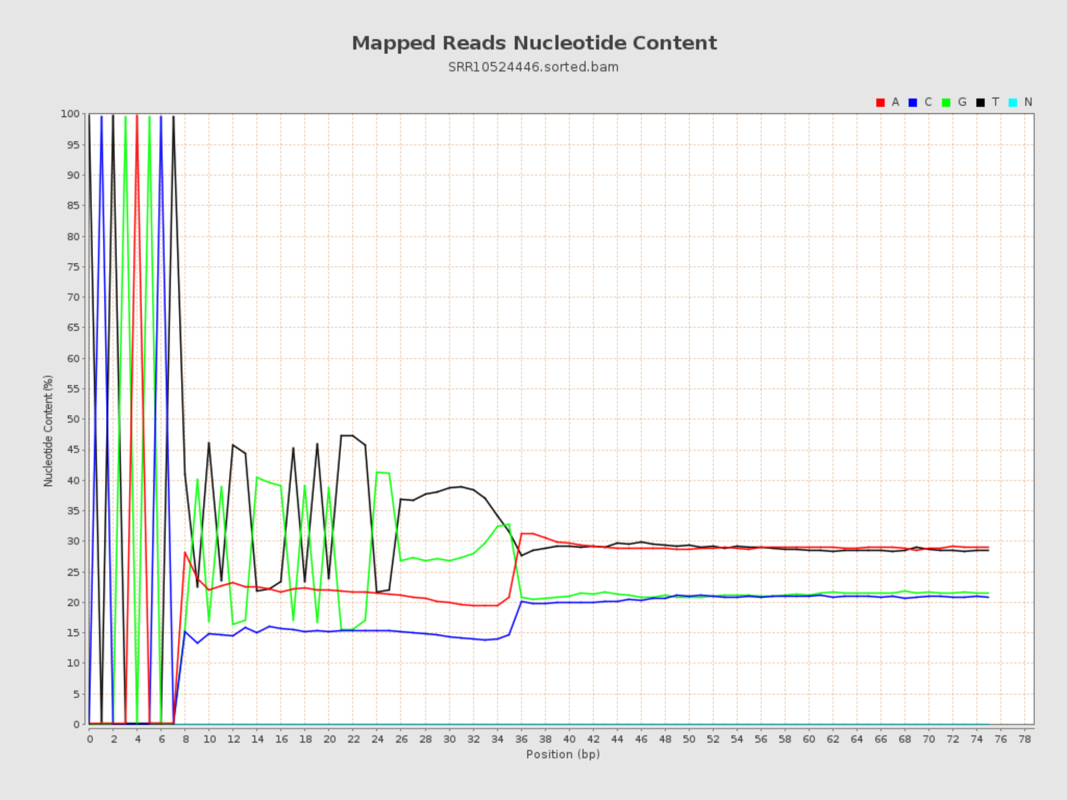
# 6. Results : Genome Fraction Coverage



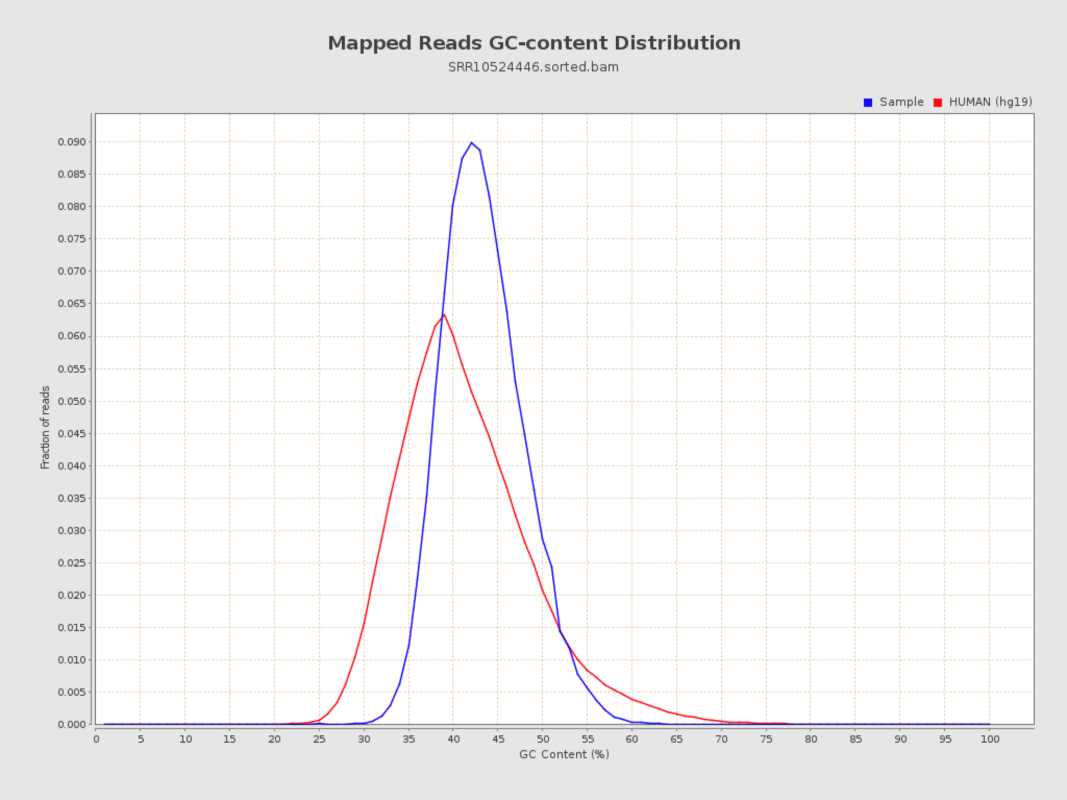
# 7. Results : Duplication Rate Histogram



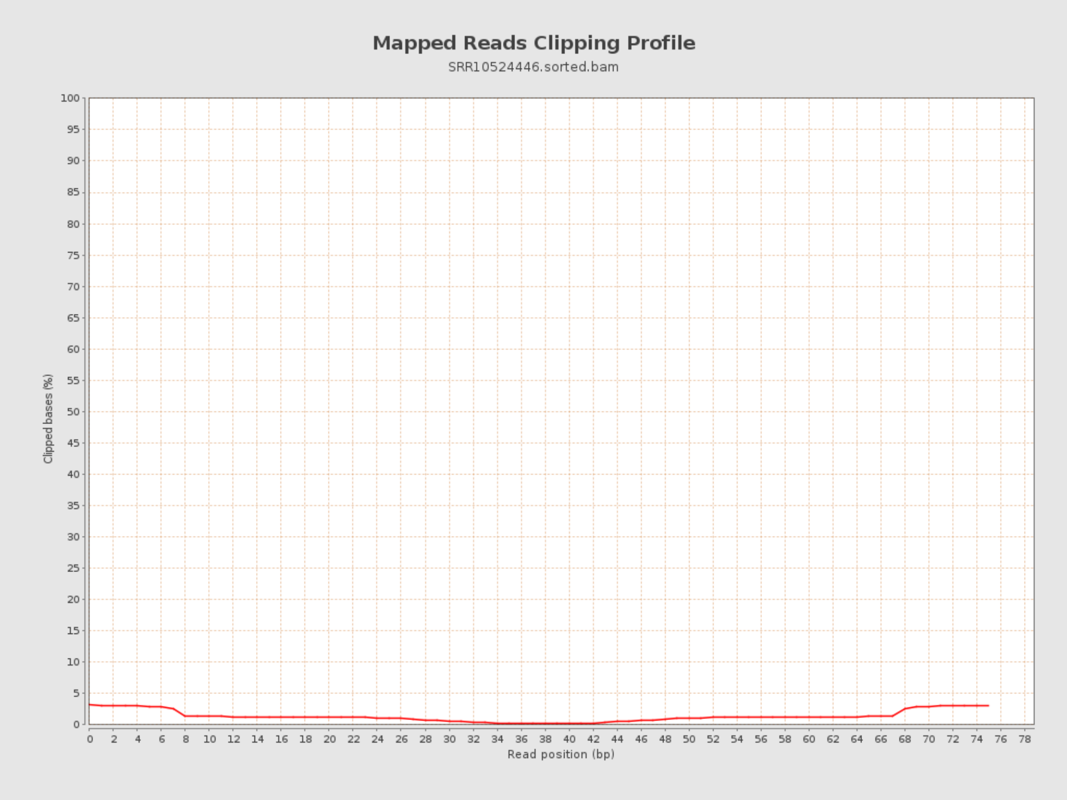
# 8. Results : Mapped Reads Nucleotide Content



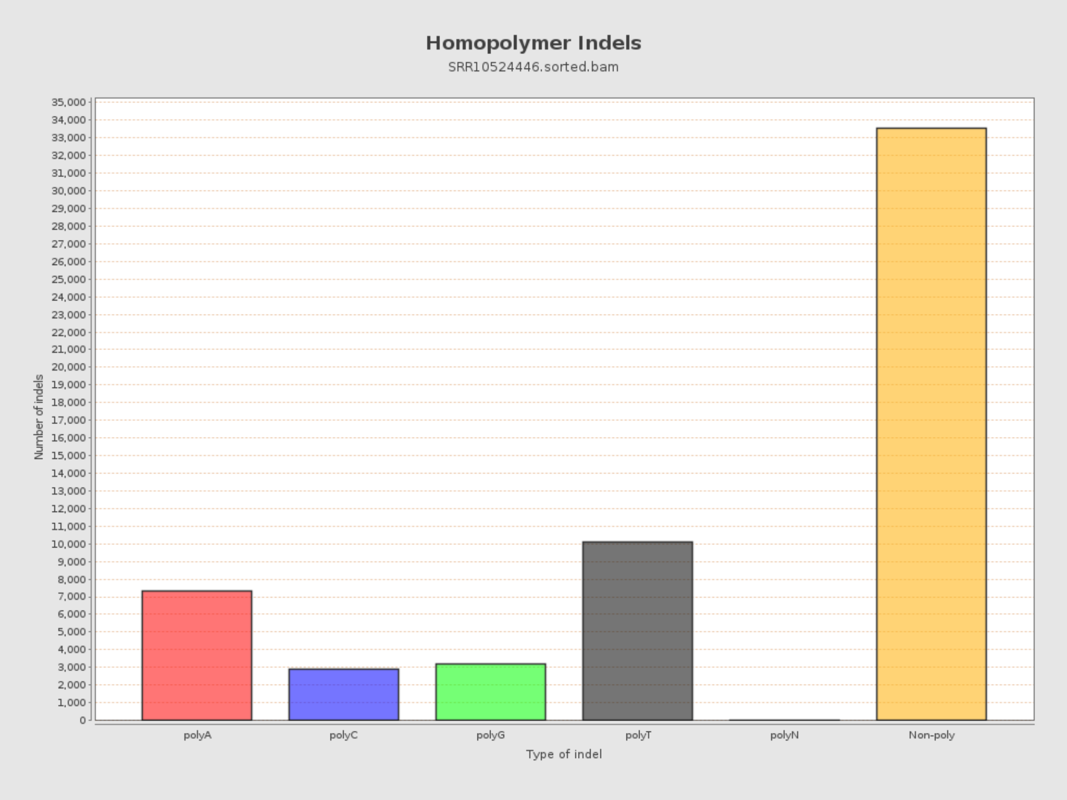
# 9. Results : Mapped Reads GC-content Distribution



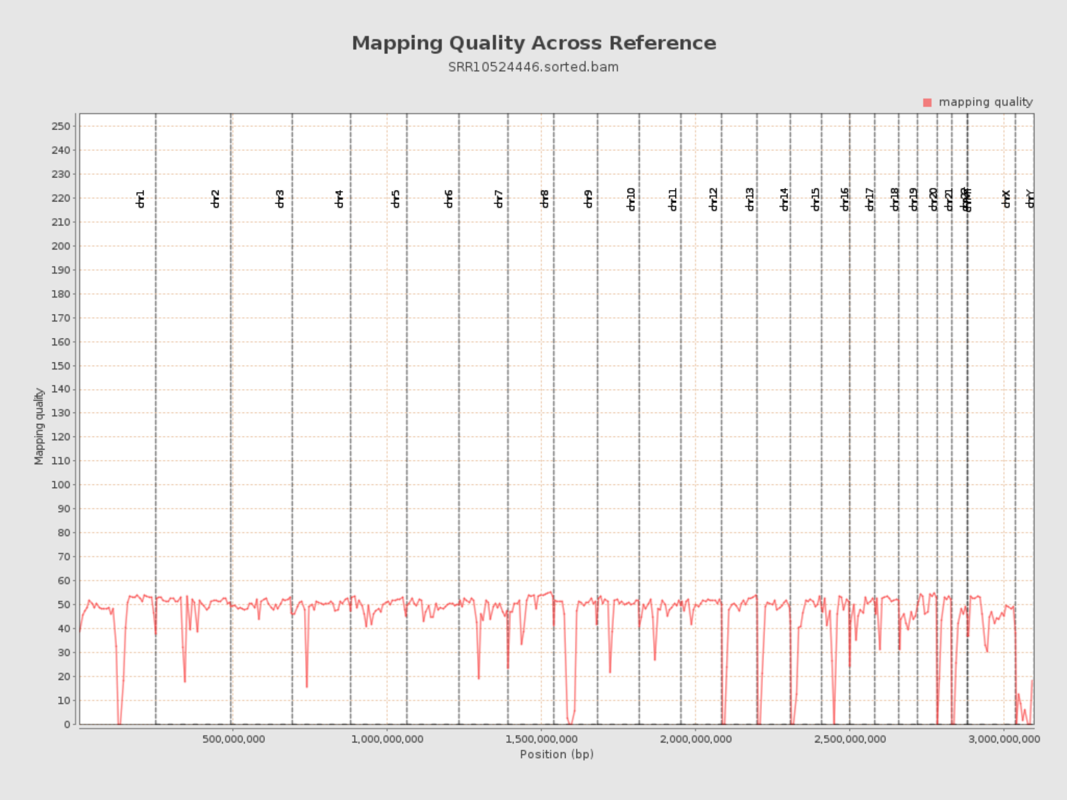
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram