# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 06:22:45*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524929.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_SRR10524929 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524929.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 06:22:41 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524929.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 710,203 |
| Mapped reads | 659,069 / 92.8% |
| Unmapped reads | 51,134 / 7.2% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 2,492 / 0.35% |
| Read min/max/mean length | 30 / 76 / 76.12 |
| Duplicated reads (estimated) | 20,177 / 2.84% |
| Duplication rate | 2.41% |
| Clipped reads | 660,254 / 92.97% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 9,399,262 / 24.53% |
| Number/percentage of C's | 6,875,567 / 17.95% |
| Number/percentage of T's | 11,998,141 / 31.32% |
| Number/percentage of G's | 10,036,432 / 26.2% |
| Number/percentage of N's | 322 / 0% |
| GC Percentage | 44.15% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0124 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1447 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.78 |

## 2.5. Mismatches and indels

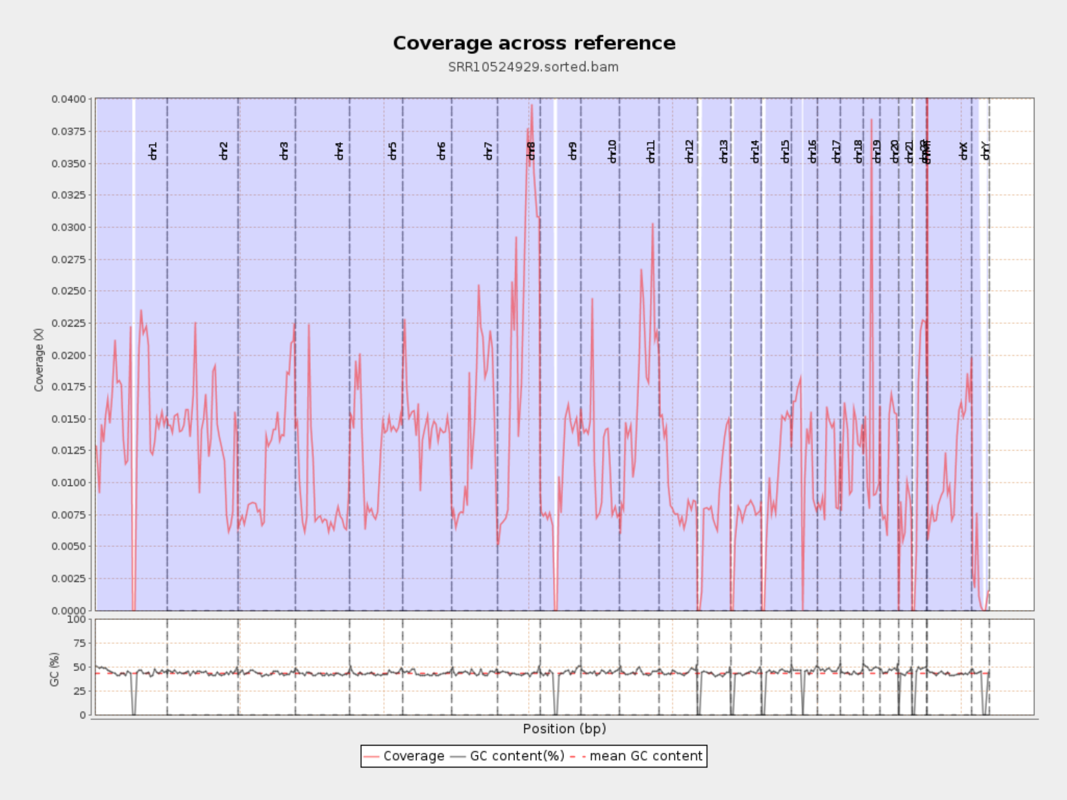
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 190,149 |
| Insertions | 2,474 |
| Mapped reads with at least one insertion | 0.37% |
| Deletions | 7,259 |
| Mapped reads with at least one deletion | 1.09% |
| Homopolymer indels | 43.73% |

## 2.6. Chromosome stats

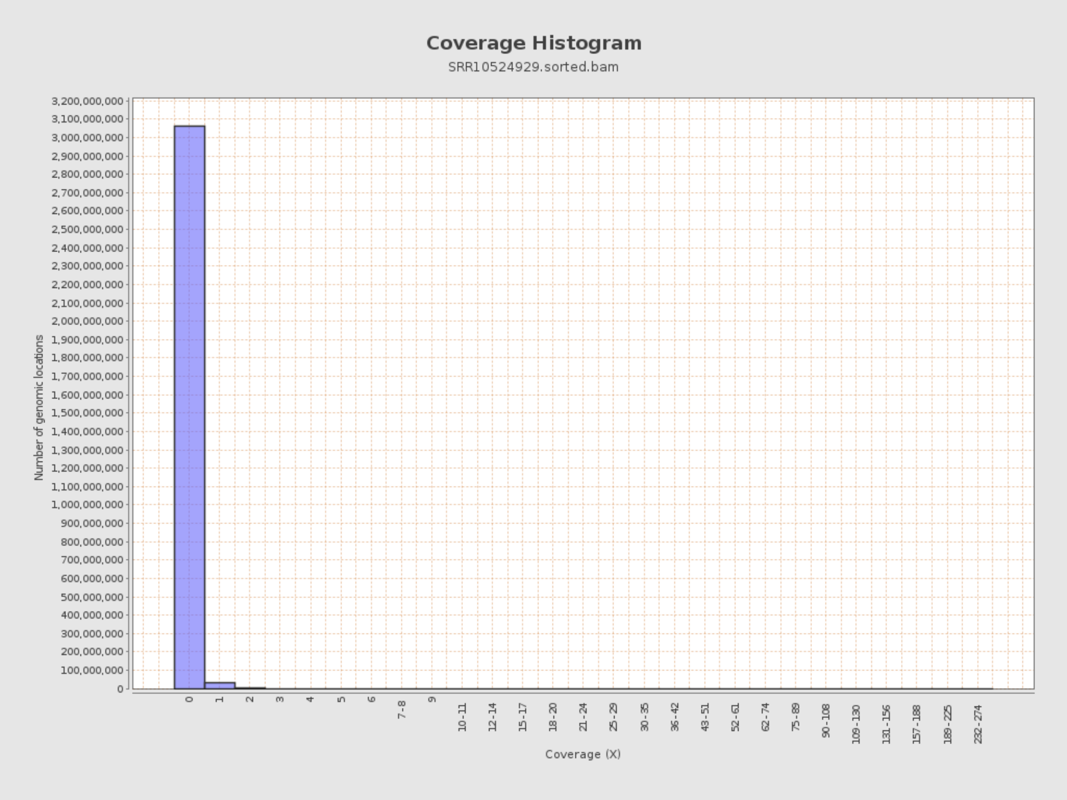
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3743170 | 0.015 | 0.2371 |
| chr2 | 243199373 | 3380664 | 0.0139 | 0.1686 |
| chr3 | 198022430 | 2339479 | 0.0118 | 0.1149 |
| chr4 | 191154276 | 1690596 | 0.0088 | 0.1148 |
| chr5 | 180915260 | 2330653 | 0.0129 | 0.12 |
| chr6 | 171115067 | 2518711 | 0.0147 | 0.1325 |
| chr7 | 159138663 | 2279234 | 0.0143 | 0.1607 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3236922 | 0.0221 | 0.1852 |
| chr9 | 141213431 | 1389797 | 0.0098 | 0.1182 |
| chr10 | 135534747 | 1627834 | 0.012 | 0.1491 |
| chr11 | 135006516 | 2350453 | 0.0174 | 0.1508 |
| chr12 | 133851895 | 1257560 | 0.0094 | 0.1048 |
| chr13 | 115169878 | 942892 | 0.0082 | 0.0961 |
| chr14 | 107349540 | 723754 | 0.0067 | 0.0883 |
| chr15 | 102531392 | 996975 | 0.0097 | 0.1041 |
| chr16 | 90354753 | 1132681 | 0.0125 | 0.1221 |
| chr17 | 81195210 | 889258 | 0.011 | 0.1128 |
| chr18 | 78077248 | 1006183 | 0.0129 | 0.1834 |
| chr19 | 59128983 | 838415 | 0.0142 | 0.1747 |
| chr20 | 63025520 | 734358 | 0.0117 | 0.1151 |
| chr21 | 48129895 | 337832 | 0.007 | 0.1026 |
| chr22 | 51304566 | 731074 | 0.0142 | 0.1269 |
| chrMT | 16571 | 3441 | 0.2077 | 0.5186 |
| chrX | 155270560 | 1728088 | 0.0111 | 0.1162 |
| chrY | 59373566 | 111816 | 0.0019 | 0.0803 |

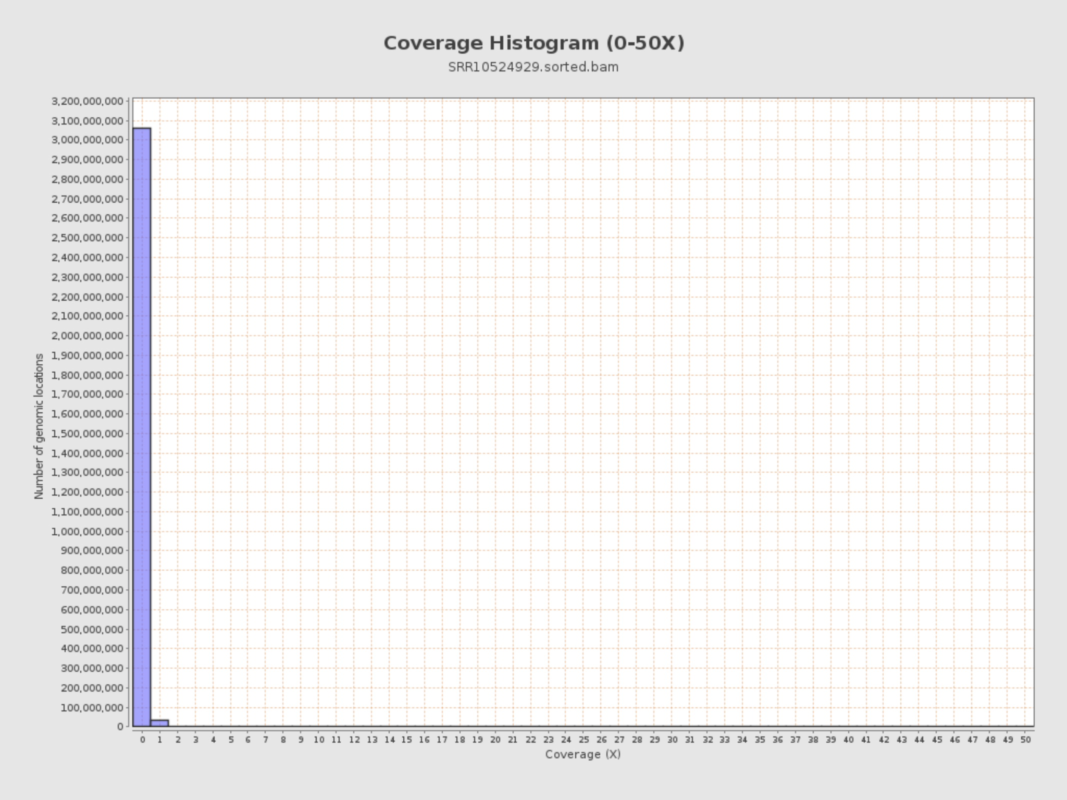
# 3. Results : Coverage across reference



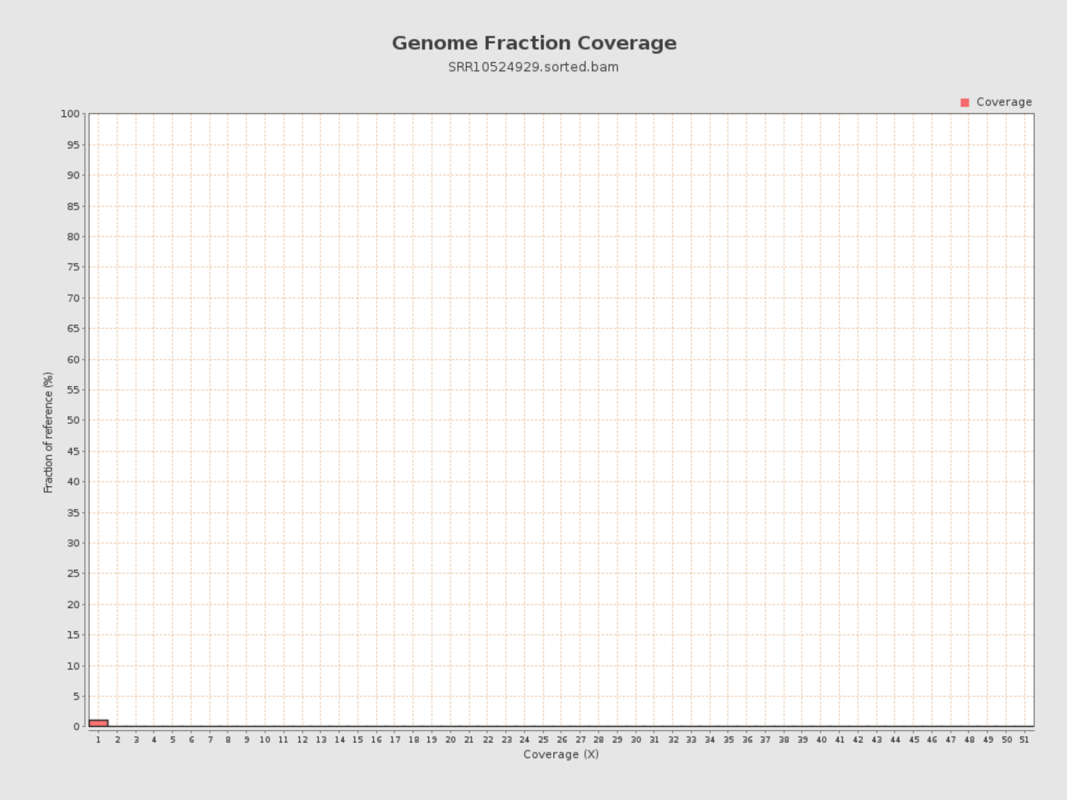
# 4. Results : Coverage Histogram



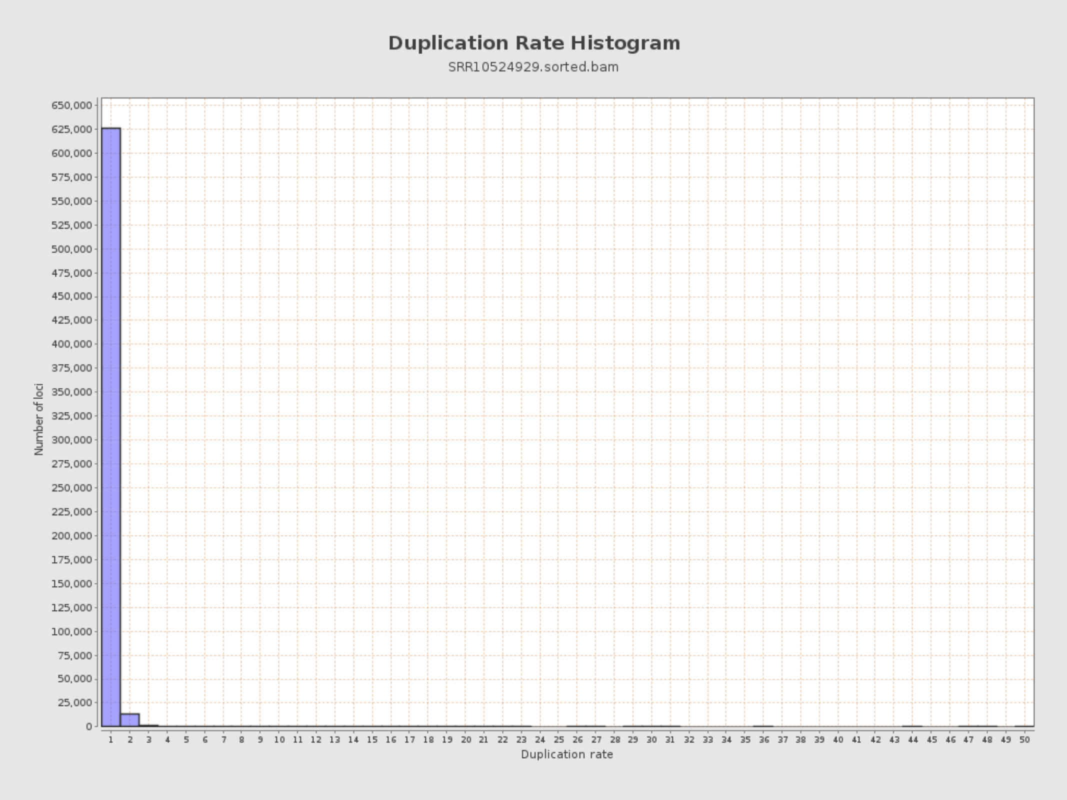
# 5. Results : Coverage Histogram (0-50X)



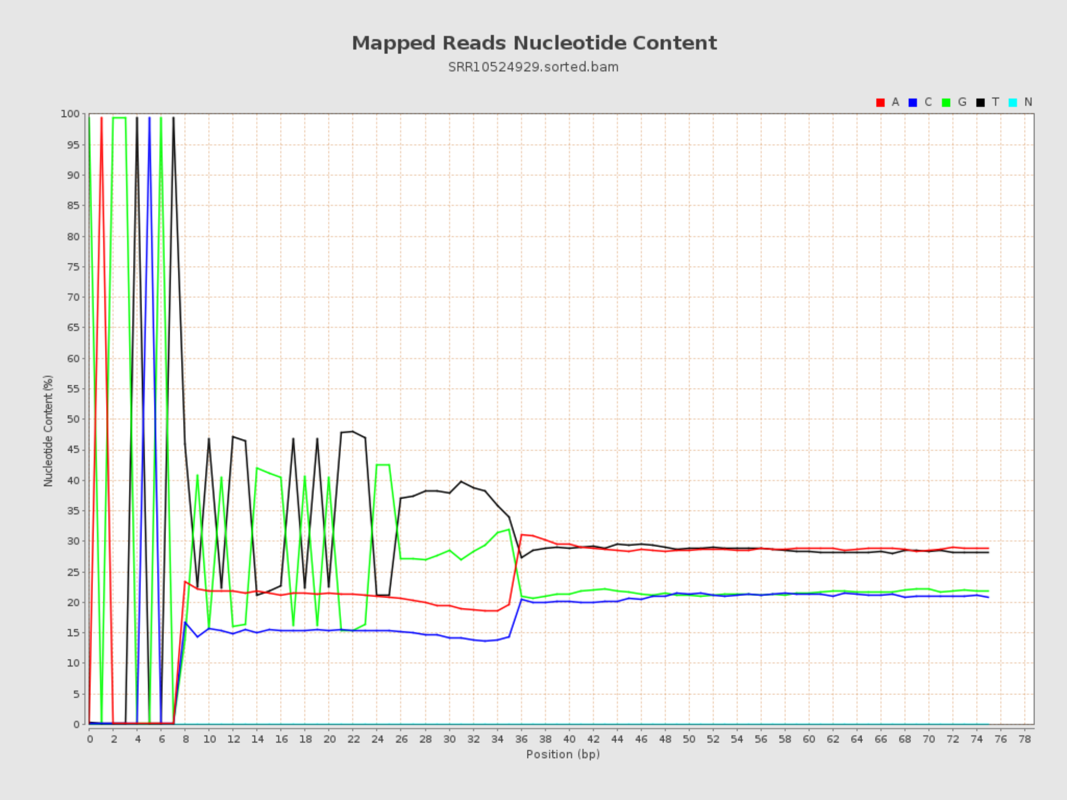
# 6. Results : Genome Fraction Coverage



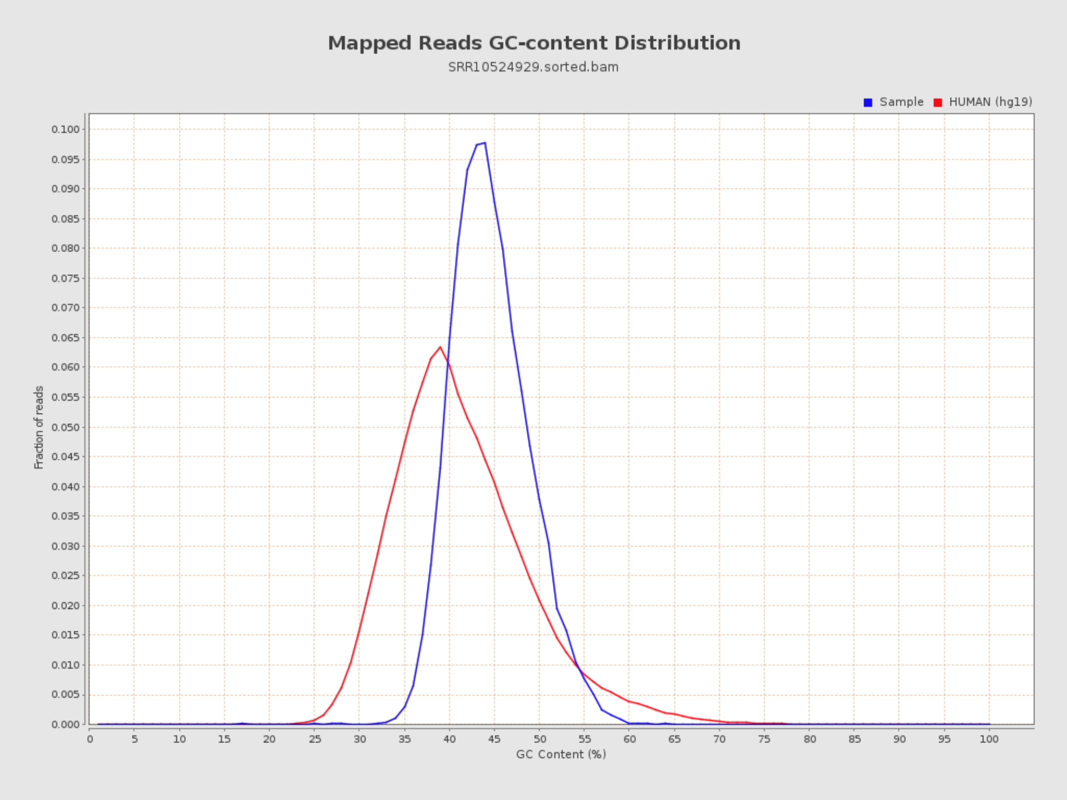
# 7. Results : Duplication Rate Histogram



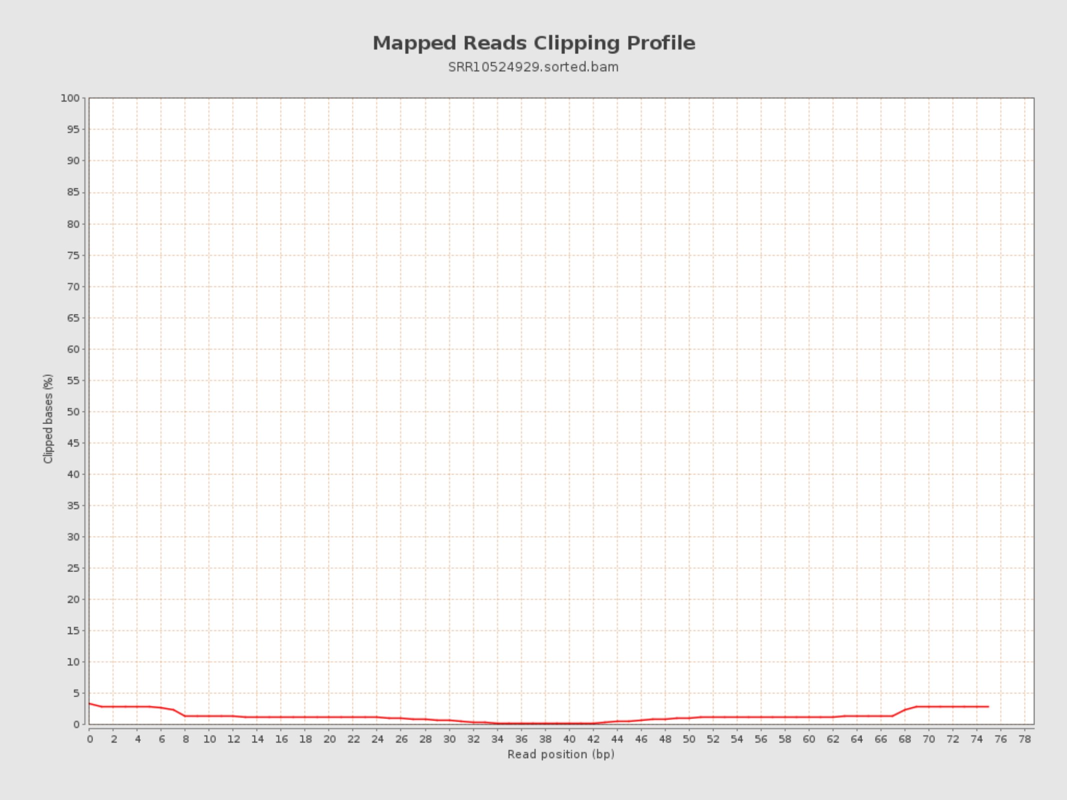
# 8. Results : Mapped Reads Nucleotide Content



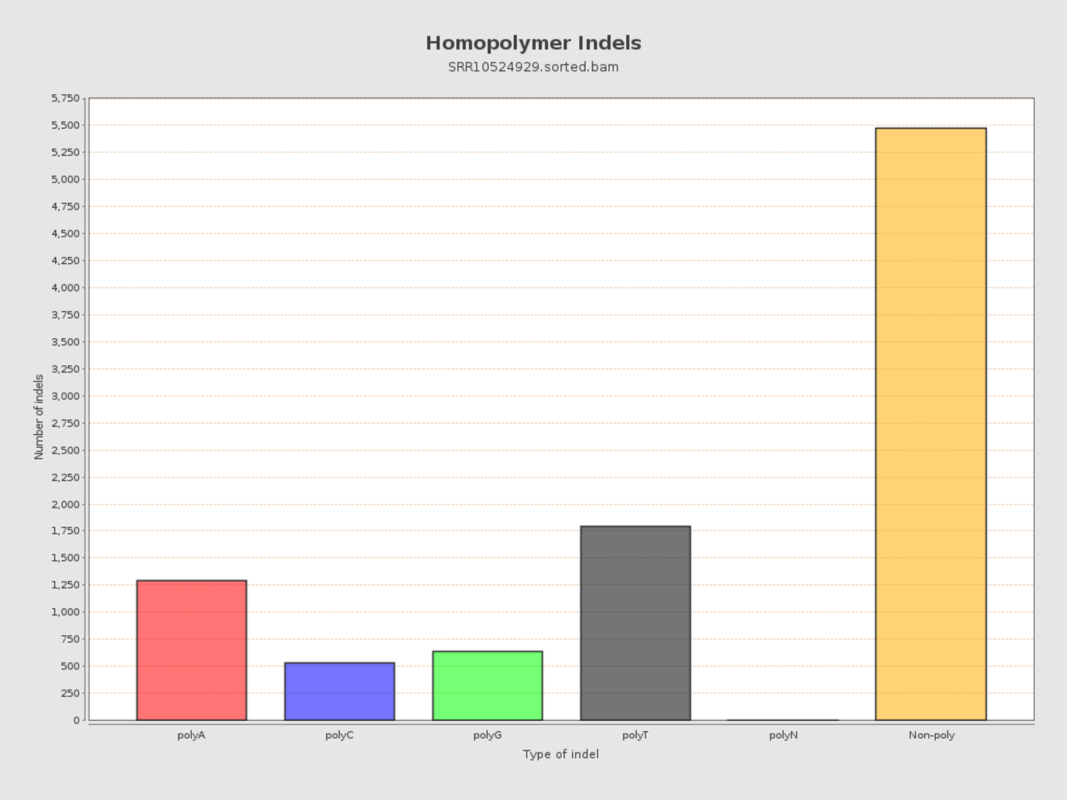
# 9. Results : Mapped Reads GC-content Distribution



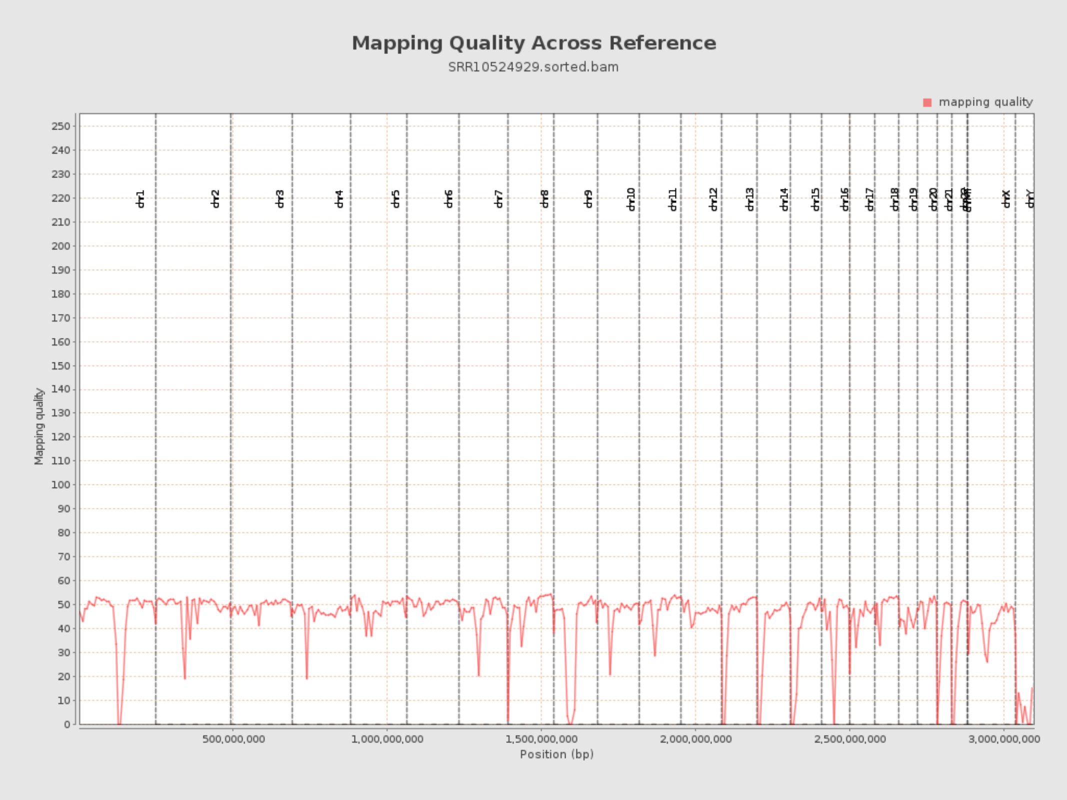
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram