# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 08:30:42*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549139.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_SRR1549139 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549139.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 08:30:38 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1549139.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 13,247,905 |
| Mapped reads | 11,524,497 / 86.99% |
| Unmapped reads | 1,723,408 / 13.01% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Read min/max/mean length | 40 / 40 / 40 |
| Duplicated reads (estimated) | 652,378 / 4.92% |
| Duplication rate | 4.4% |
| Clipped reads | 594,193 / 4.49% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 133,129,335 / 29.1% |
| Number/percentage of C's | 94,950,368 / 20.76% |
| Number/percentage of T's | 134,361,209 / 29.37% |
| Number/percentage of G's | 94,884,997 / 20.74% |
| Number/percentage of N's | 100,638 / 0.02% |
| GC Percentage | 41.5% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1478 |
| Standard Deviation | 1.0051 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.86 |

## 2.5. Mismatches and indels

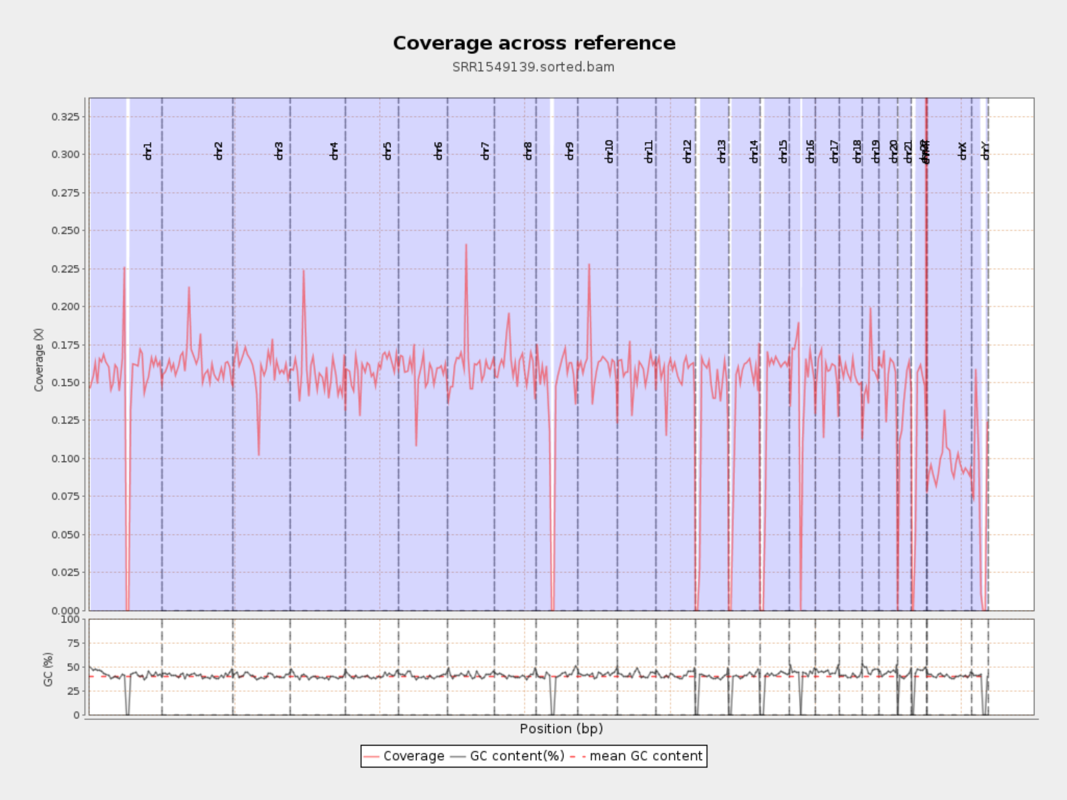
| | |
|---|---|
| General error rate | 0.33% |
| Mismatches | 1,501,930 |
| Insertions | 11,319 |
| Mapped reads with at least one insertion | 0.1% |
| Deletions | 37,995 |
| Mapped reads with at least one deletion | 0.33% |
| Homopolymer indels | 44.99% |

## 2.6. Chromosome stats

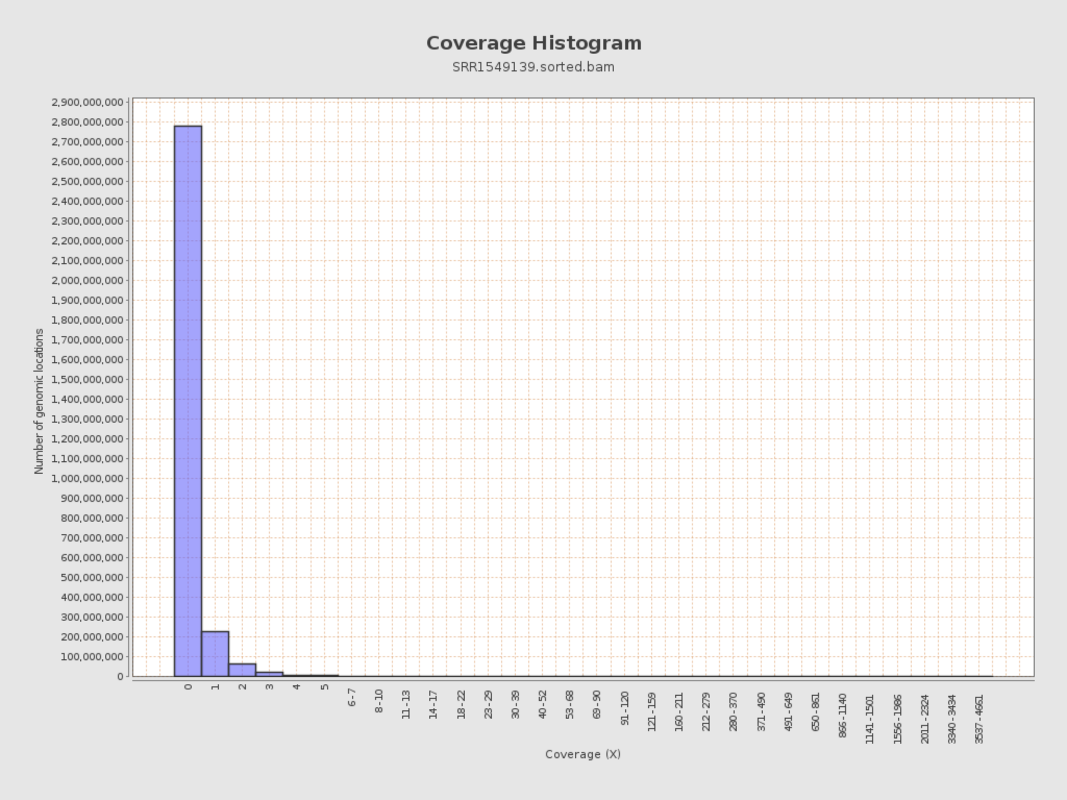
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 37488517 | 0.1504 | 1.7382 |
| chr2 | 243199373 | 39489162 | 0.1624 | 0.8538 |
| chr3 | 198022430 | 31553504 | 0.1593 | 0.5379 |
| chr4 | 191154276 | 29888112 | 0.1564 | 0.6777 |
| chr5 | 180915260 | 28699843 | 0.1586 | 0.5526 |
| chr6 | 171115067 | 26900454 | 0.1572 | 0.5917 |
| chr7 | 159138663 | 25818908 | 0.1622 | 1.2473 |
| chr8 | 146364022 | 23723031 | 0.1621 | 2.3549 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr9 | 141213431 | 19521557 | 0.1382 | 0.7222 |
| chr10 | 135534747 | 22149846 | 0.1634 | 0.9627 |
| chr11 | 135006516 | 21305696 | 0.1578 | 0.734 |
| chr12 | 133851895 | 20997188 | 0.1569 | 0.5568 |
| chr13 | 115169878 | 14747528 | 0.1281 | 0.4797 |
| chr14 | 107349540 | 14053652 | 0.1309 | 0.6273 |
| chr15 | 102531392 | 13670351 | 0.1333 | 0.4877 |
| chr16 | 90354753 | 13301843 | 0.1472 | 0.5897 |
| chr17 | 81195210 | 12483804 | 0.1538 | 0.5869 |
| chr18 | 78077248 | 12196783 | 0.1562 | 1.4189 |
| chr19 | 59128983 | 9130926 | 0.1544 | 1.4158 |
| chr20 | 63025520 | 9789725 | 0.1553 | 0.5974 |
| chr21 | 48129895 | 6058889 | 0.1259 | 0.6503 |
| chr22 | 51304566 | 5414113 | 0.1055 | 0.4729 |
| chrMT | 16571 | 201562 | 12.1635 | 14.3993 |
| chrX | 155270560 | 14891229 | 0.0959 | 0.5228 |
| chrY | 59373566 | 3998982 | 0.0674 | 0.7315 |

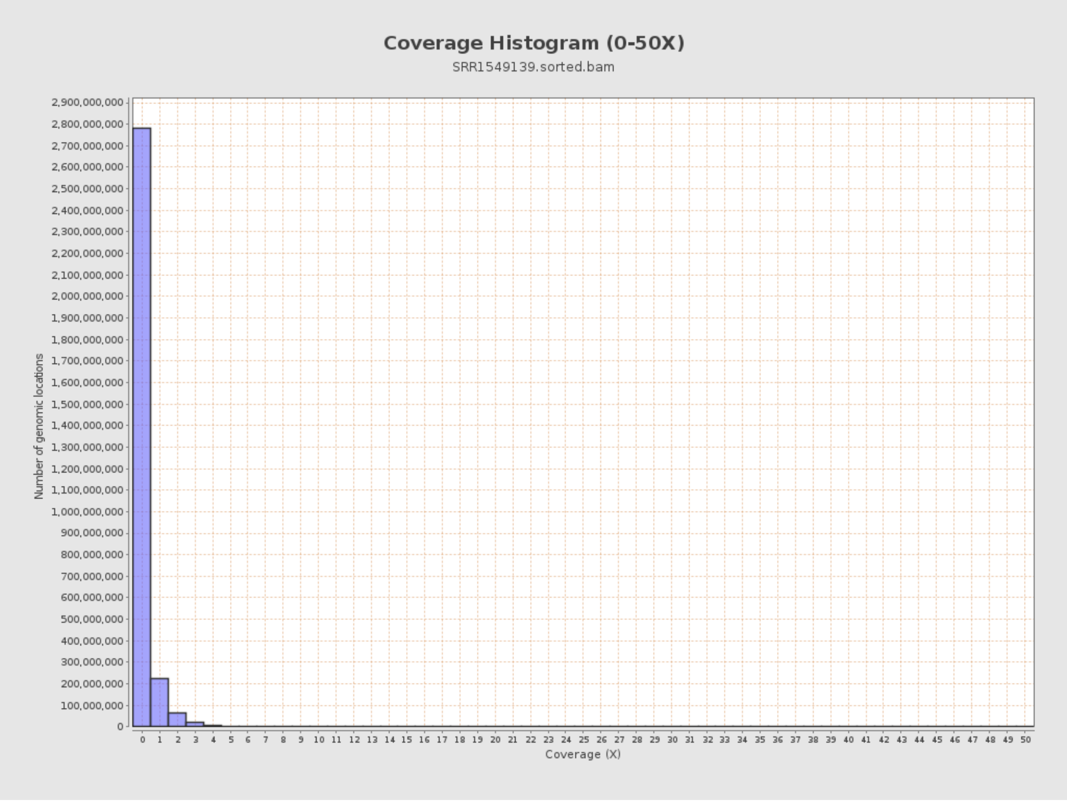
# 3. Results : Coverage across reference



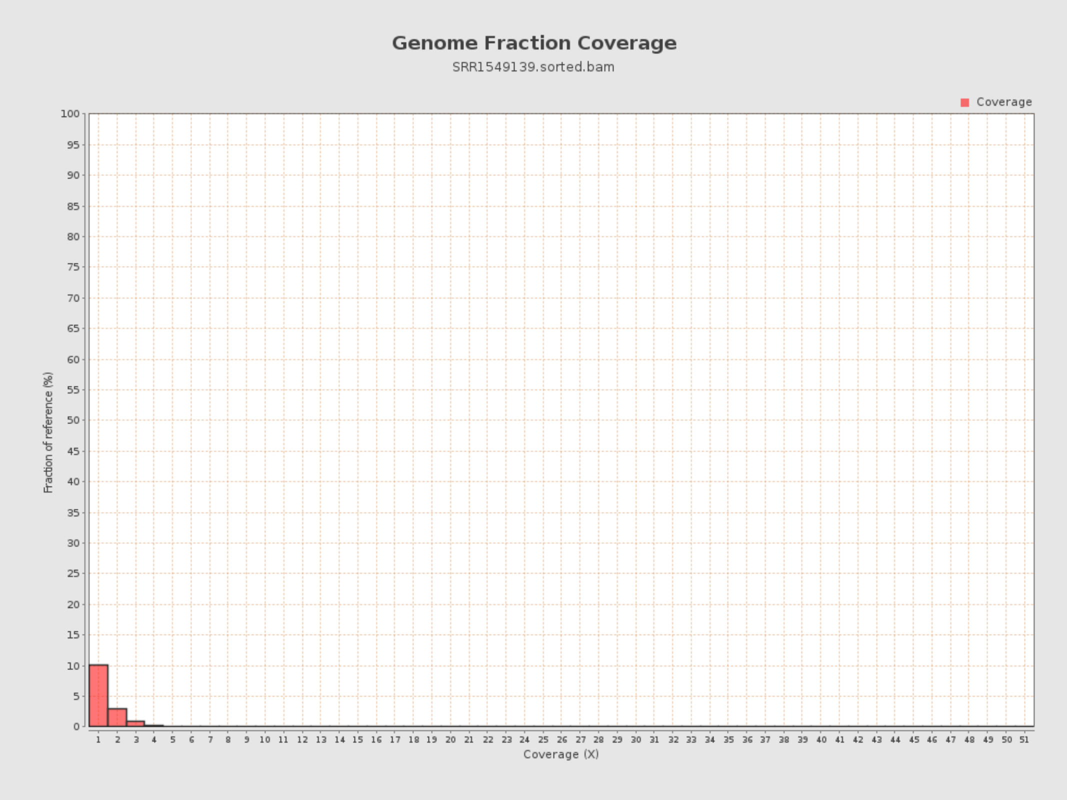
# 4. Results : Coverage Histogram



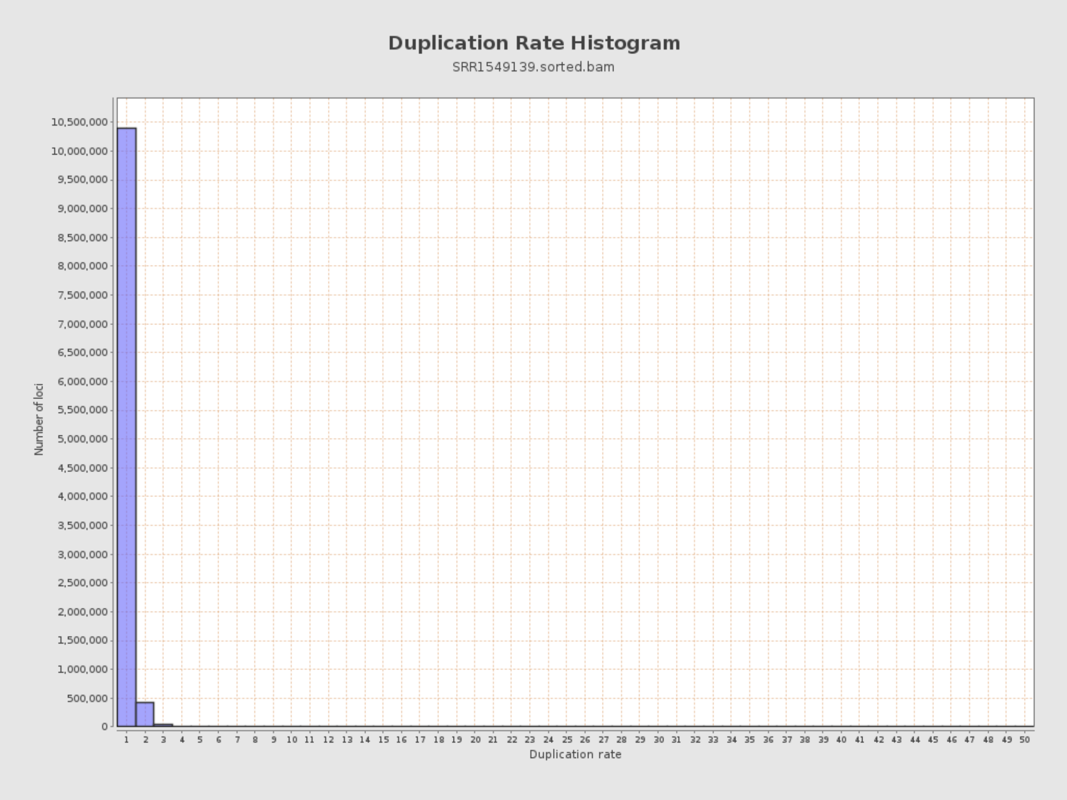
# 5. Results : Coverage Histogram (0-50X)



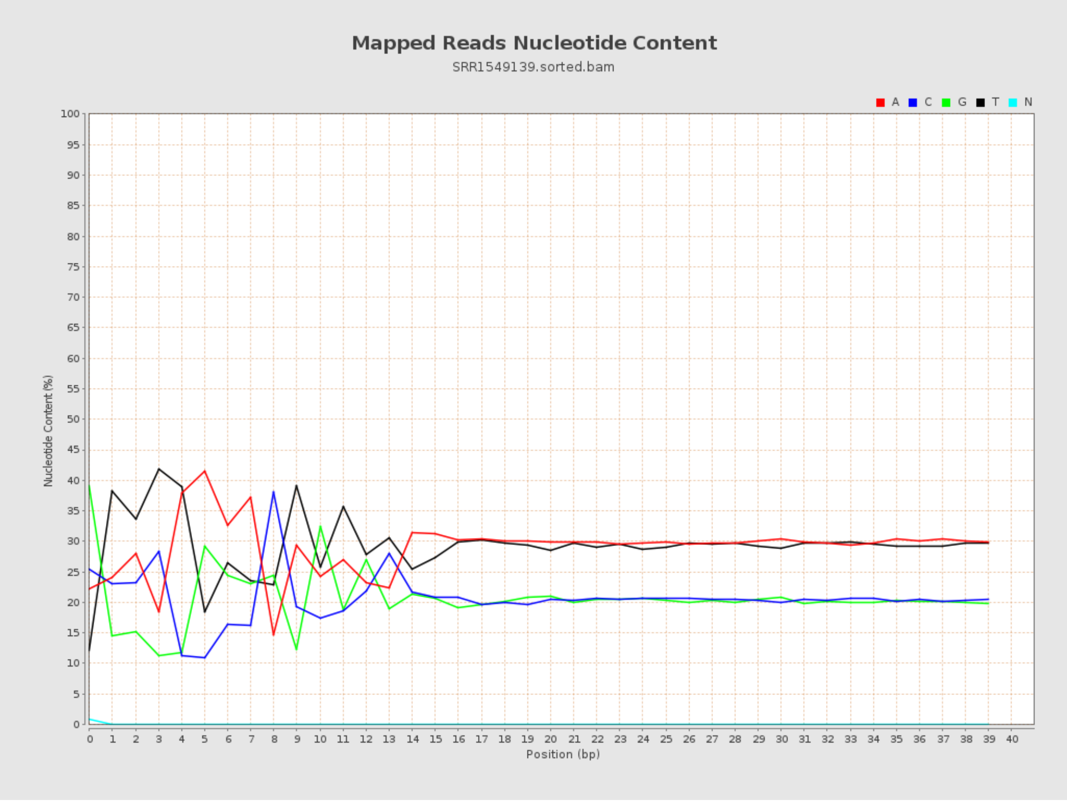
# 6. Results : Genome Fraction Coverage



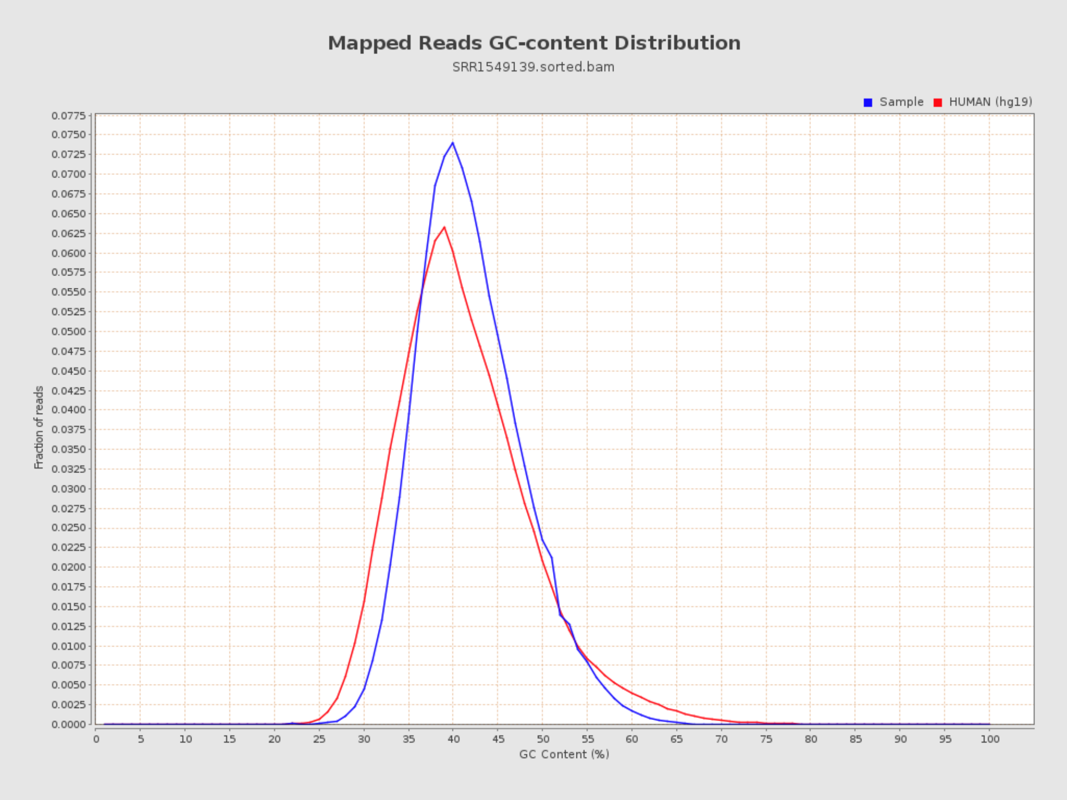
# 7. Results : Duplication Rate Histogram



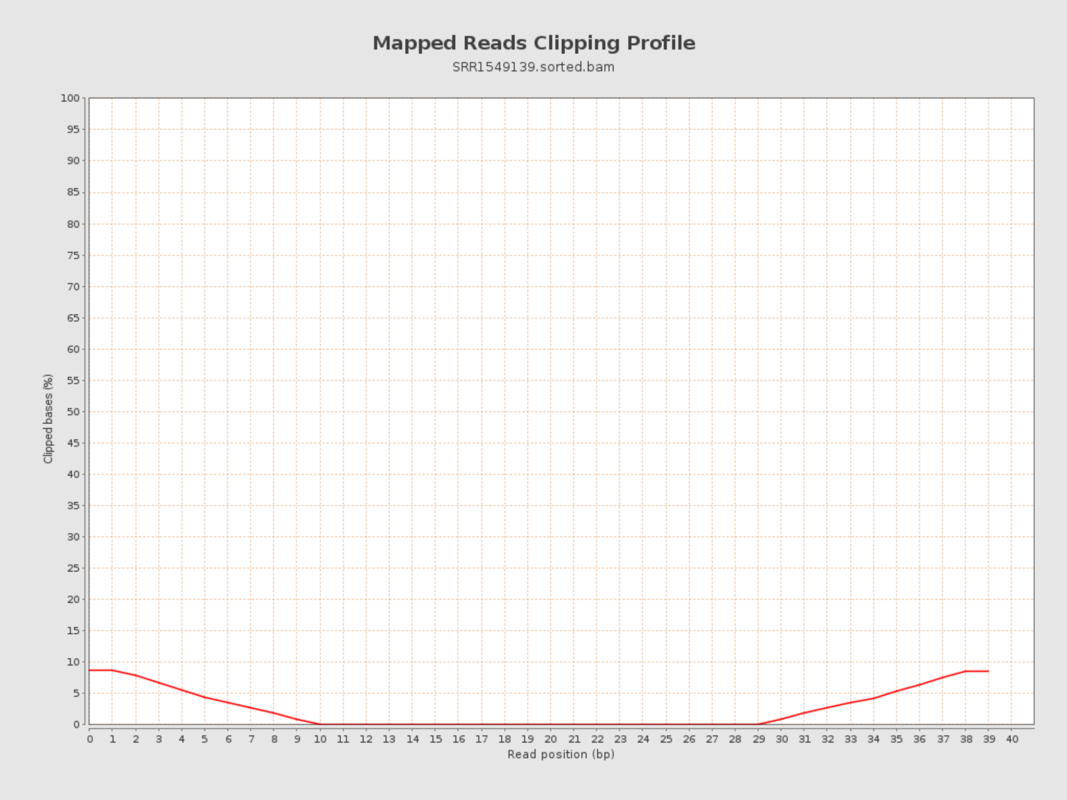
# 8. Results : Mapped Reads Nucleotide Content



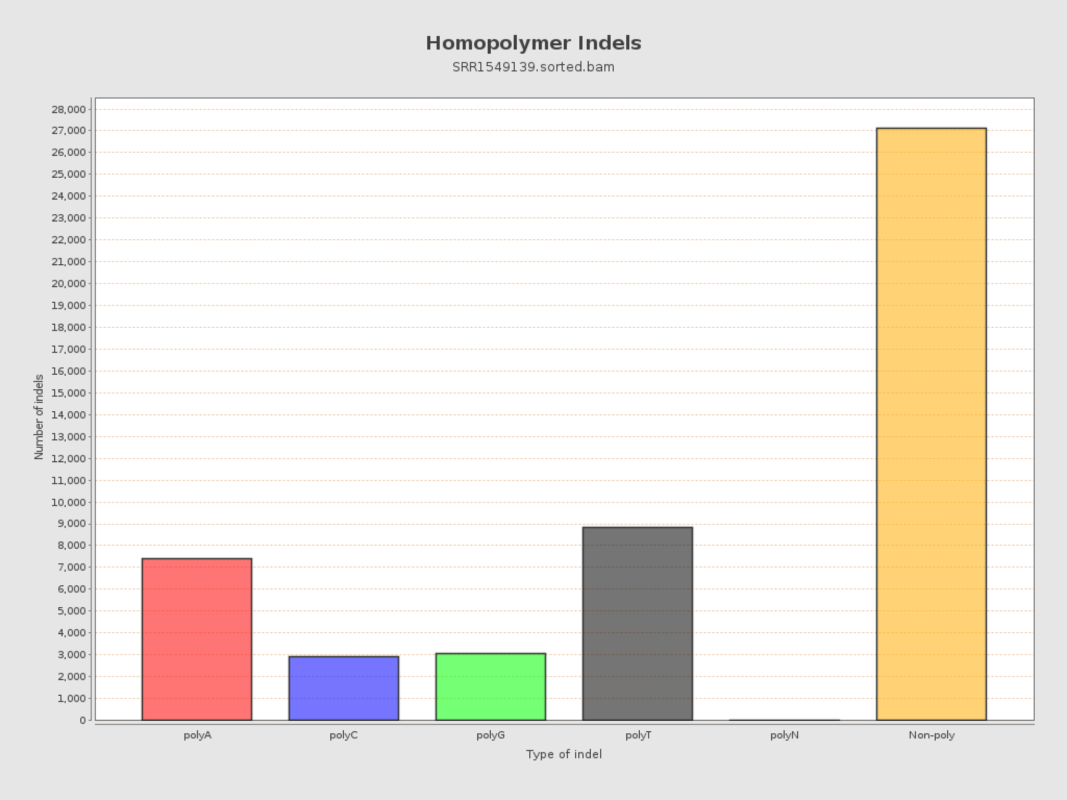
# 9. Results : Mapped Reads GC-content Distribution



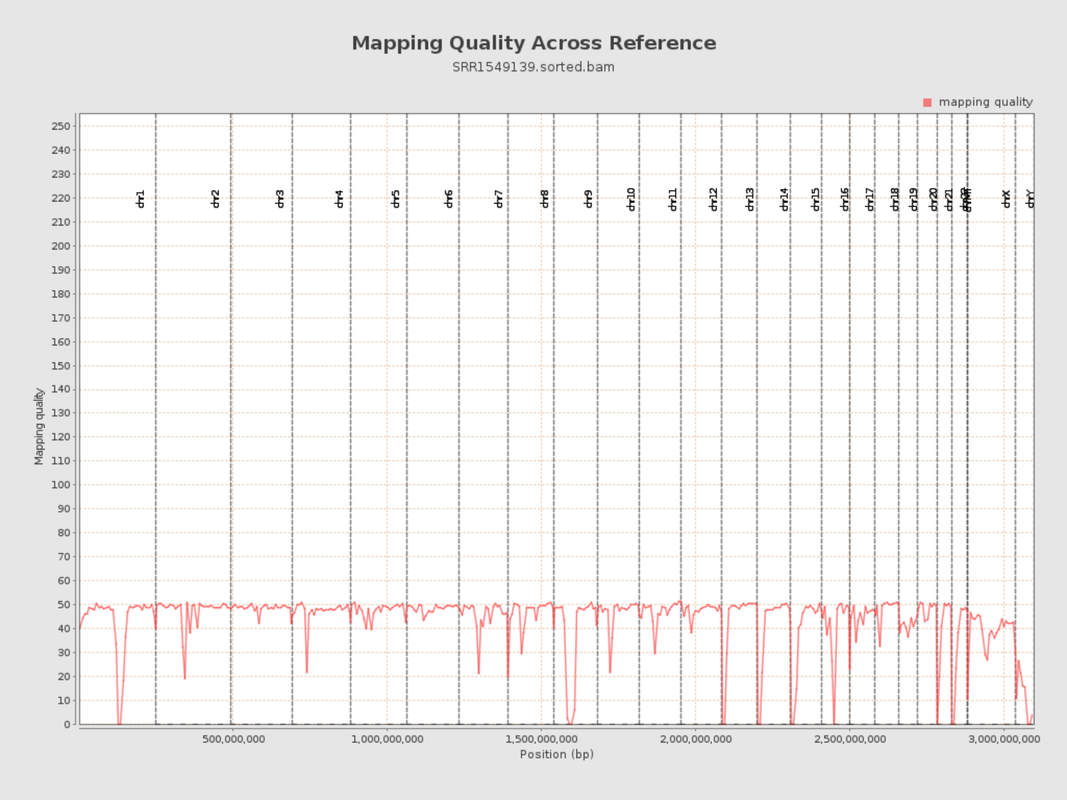
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram