# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 10:56:17*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549151.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_SRR1549151 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549151.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 10:56:17 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1549151.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 14,621,038 |
| Mapped reads | 12,749,863 / 87.2% |
| Unmapped reads | 1,871,175 / 12.8% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Read min/max/mean length | 40 / 40 / 40 |
| Duplicated reads (estimated) | 707,715 / 4.84% |
| Duplication rate | 4.38% |
| Clipped reads | 638,483 / 4.37% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 147,983,662 / 29.24% |
| Number/percentage of C's | 104,347,206 / 20.62% |
| Number/percentage of T's | 149,512,796 / 29.54% |
| Number/percentage of G's | 104,185,965 / 20.58% |
| Number/percentage of N's | 102,302 / 0.02% |
| GC Percentage | 41.2% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1635 |
| Standard Deviation | 1.0091 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.85 |

## 2.5. Mismatches and indels

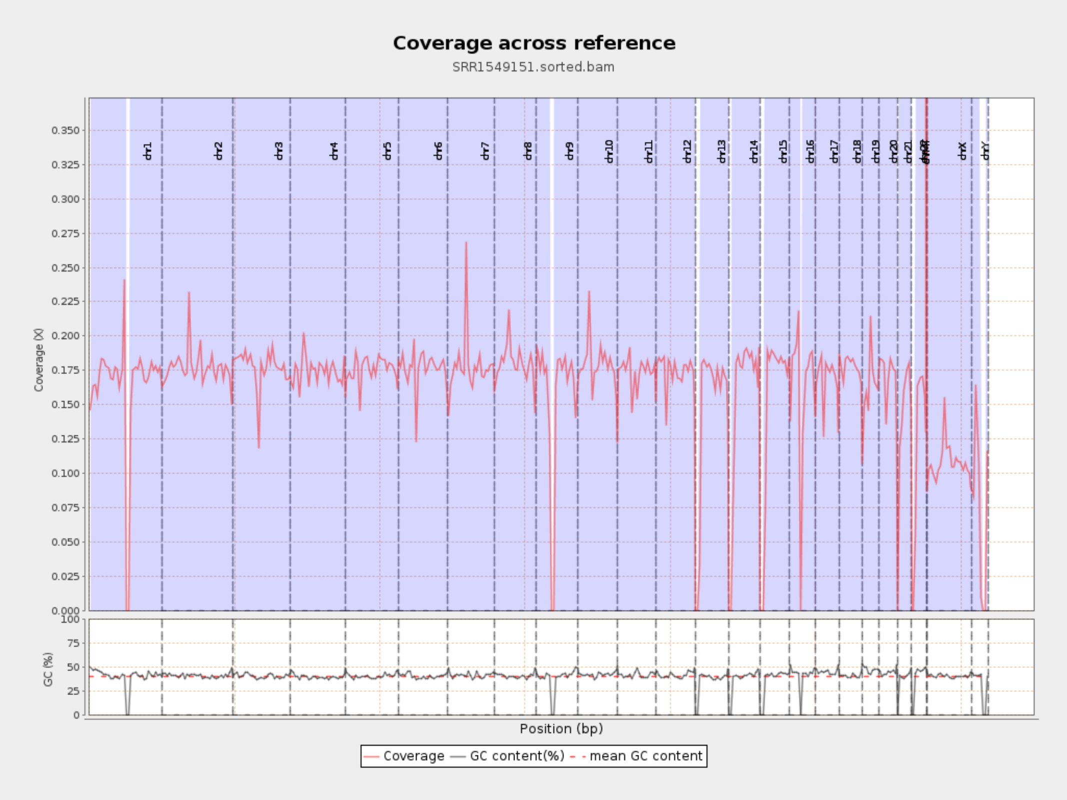
| | |
|---|---|
| General error rate | 0.32% |
| Mismatches | 1,585,992 |
| Insertions | 12,412 |
| Mapped reads with at least one insertion | 0.1% |
| Deletions | 41,277 |
| Mapped reads with at least one deletion | 0.32% |
| Homopolymer indels | 45.23% |

## 2.6. Chromosome stats

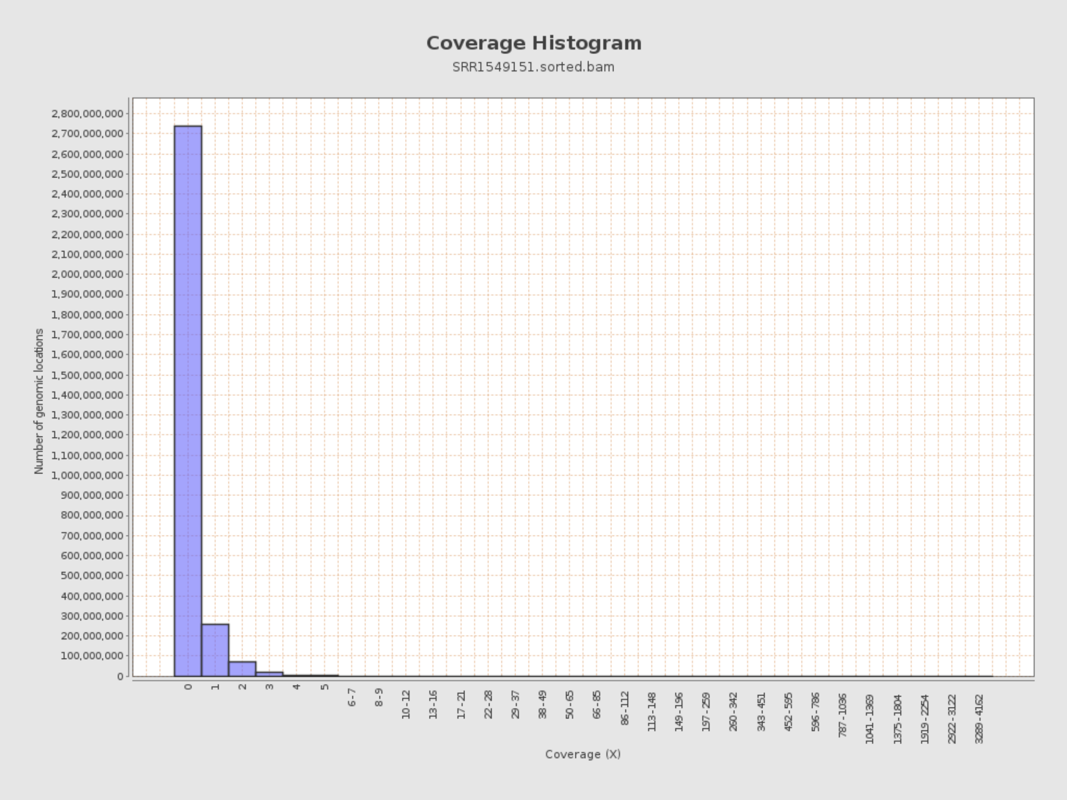
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 40672206 | 0.1632 | 1.7587 |
| chr2 | 243199373 | 43161633 | 0.1775 | 0.8385 |
| chr3 | 198022430 | 35102280 | 0.1773 | 0.5561 |
| chr4 | 191154276 | 33288951 | 0.1741 | 0.6053 |
| chr5 | 180915260 | 31850670 | 0.1761 | 0.567 |
| chr6 | 171115067 | 30280693 | 0.177 | 0.6423 |
| chr7 | 159138663 | 28429318 | 0.1786 | 1.4321 |
| chr8 | 146364022 | 26334711 | 0.1799 | 2.1389 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr9 | 141213431 | 21674943 | 0.1535 | 0.7817 |
| chr10 | 135534747 | 24428919 | 0.1802 | 0.8801 |
| chr11 | 135006516 | 23423847 | 0.1735 | 0.768 |
| chr12 | 133851895 | 23324538 | 0.1743 | 0.5894 |
| chr13 | 115169878 | 16628234 | 0.1444 | 0.4921 |
| chr14 | 107349540 | 16203188 | 0.1509 | 0.7055 |
| chr15 | 102531392 | 15280667 | 0.149 | 0.5029 |
| chr16 | 90354753 | 14660323 | 0.1623 | 0.6069 |
| chr17 | 81195210 | 13614086 | 0.1677 | 0.6015 |
| chr18 | 78077248 | 13896018 | 0.178 | 1.6349 |
| chr19 | 59128983 | 9746556 | 0.1648 | 1.4746 |
| chr20 | 63025520 | 10734809 | 0.1703 | 0.5997 |
| chr21 | 48129895 | 6688774 | 0.139 | 0.6041 |
| chr22 | 51304566 | 5796373 | 0.113 | 0.4791 |
| chrMT | 16571 | 61108 | 3.6876 | 4.5957 |
| chrX | 155270560 | 16730860 | 0.1078 | 0.5822 |
| chrY | 59373566 | 4171471 | 0.0703 | 0.6247 |

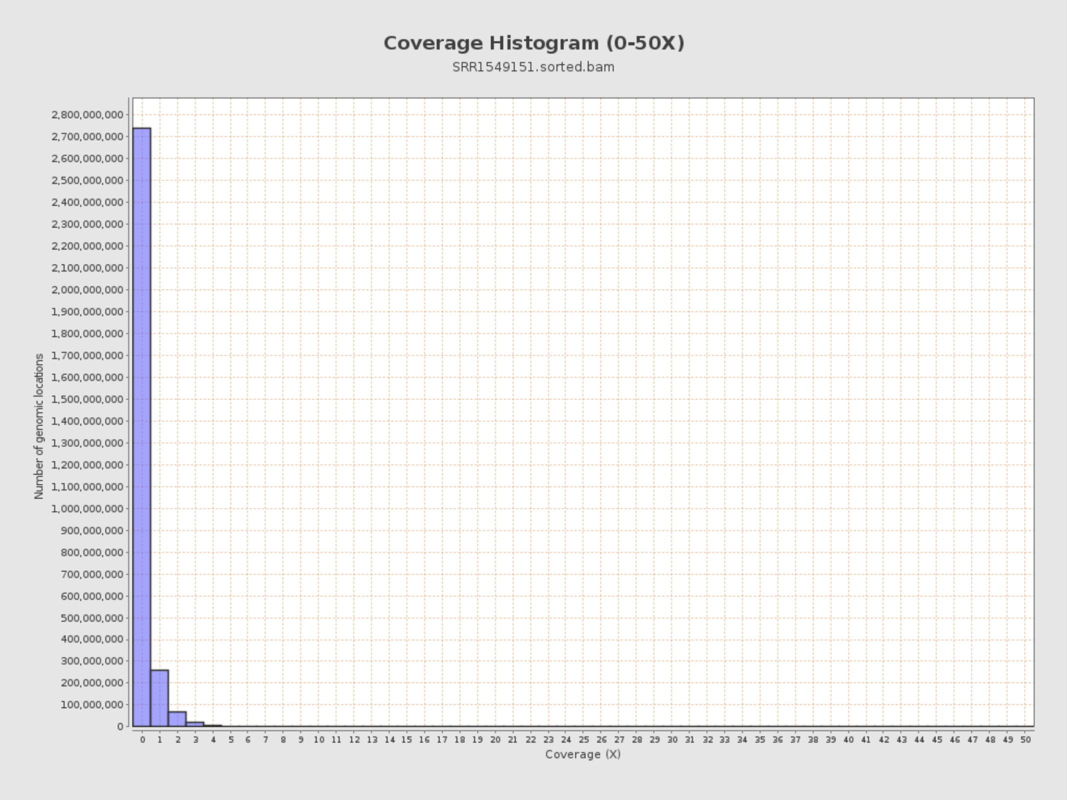
# 3. Results : Coverage across reference



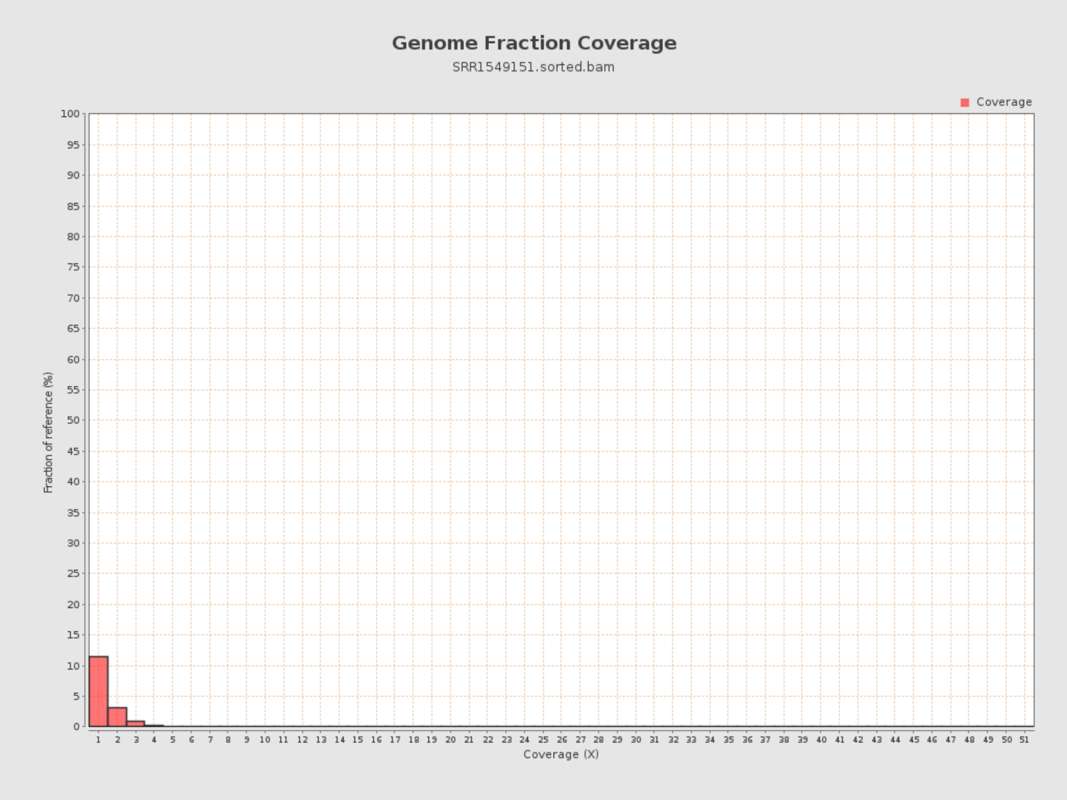
# 4. Results : Coverage Histogram



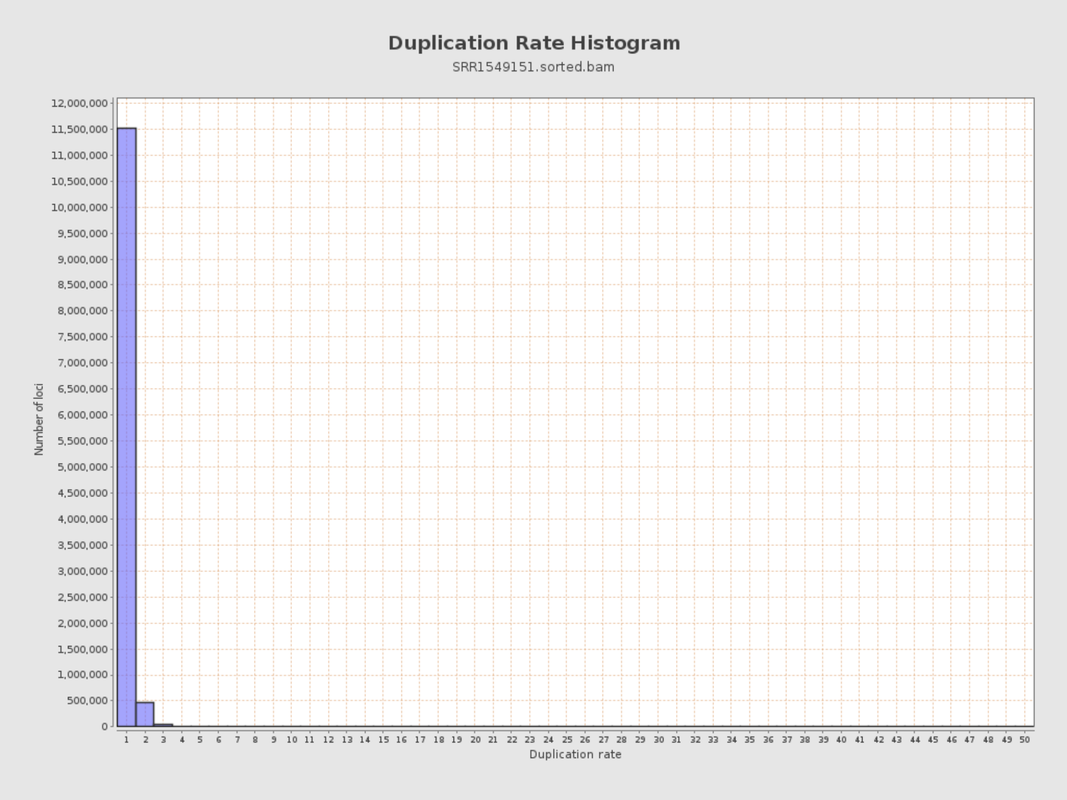
# 5. Results : Coverage Histogram (0-50X)



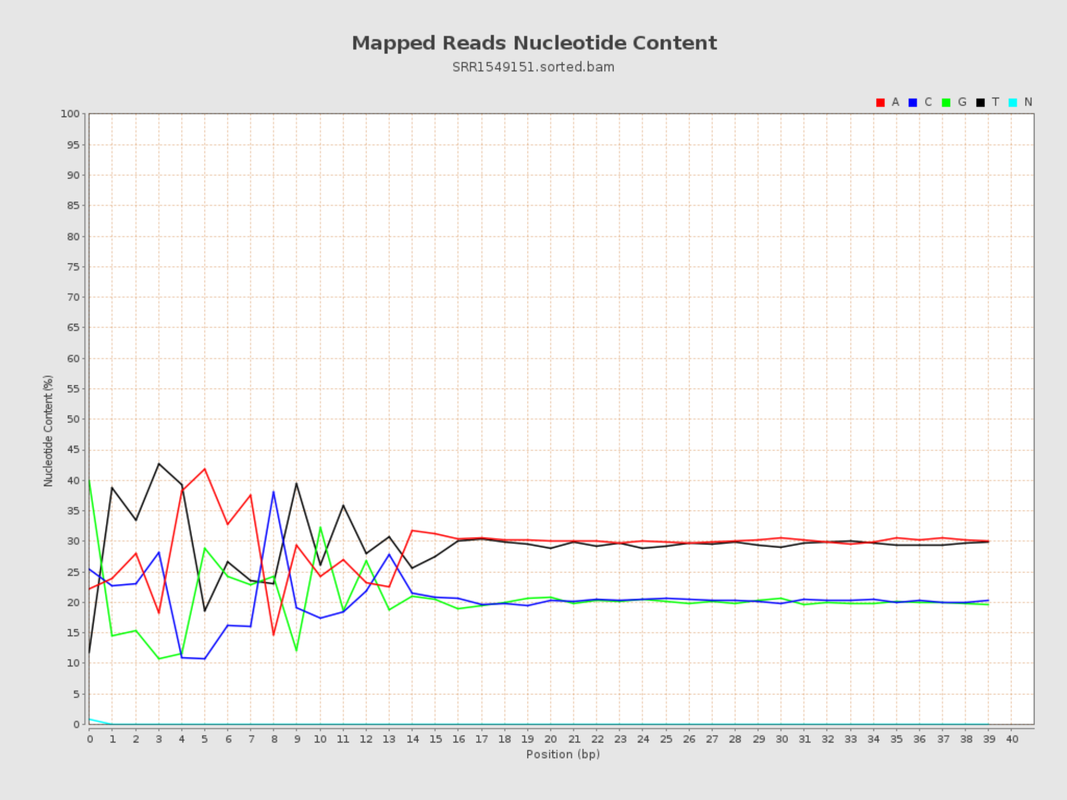
# 6. Results : Genome Fraction Coverage



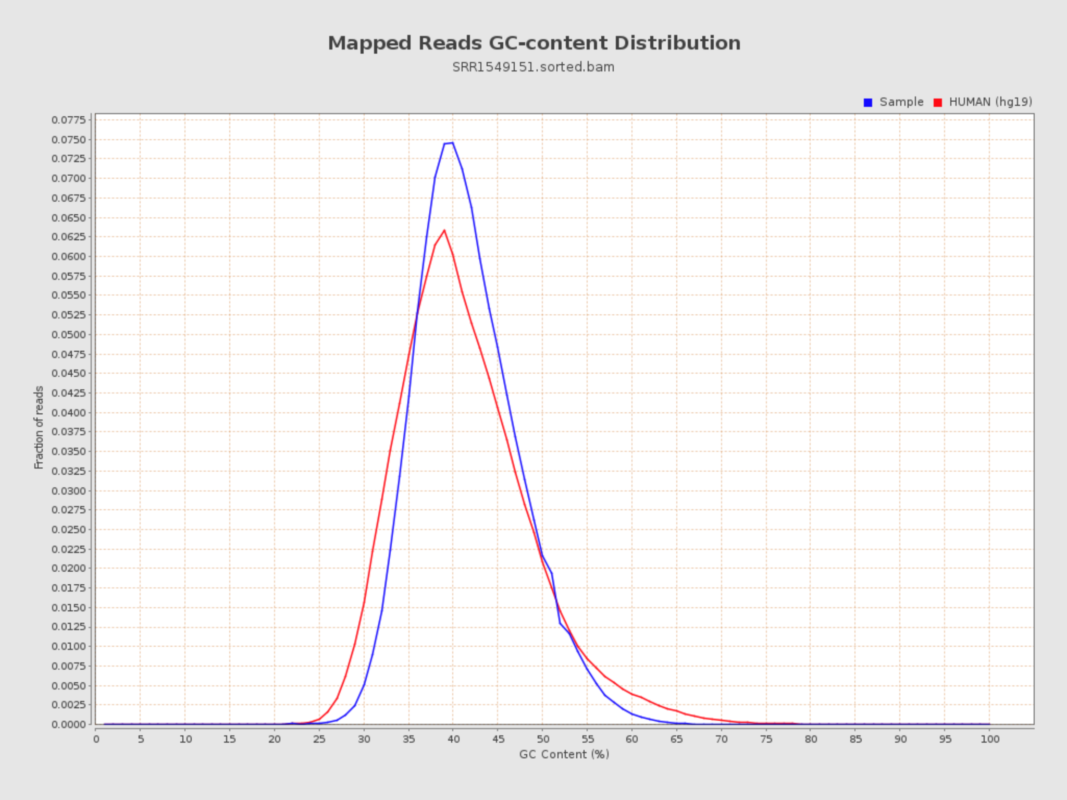
# 7. Results : Duplication Rate Histogram



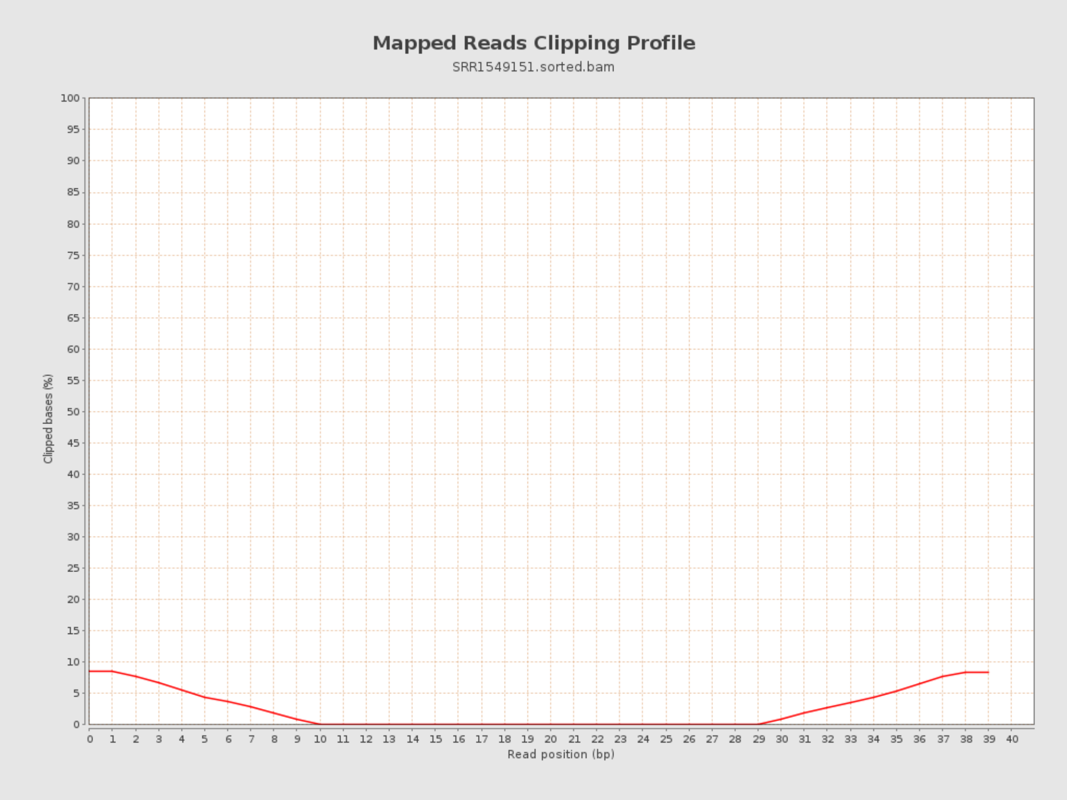
# 8. Results : Mapped Reads Nucleotide Content



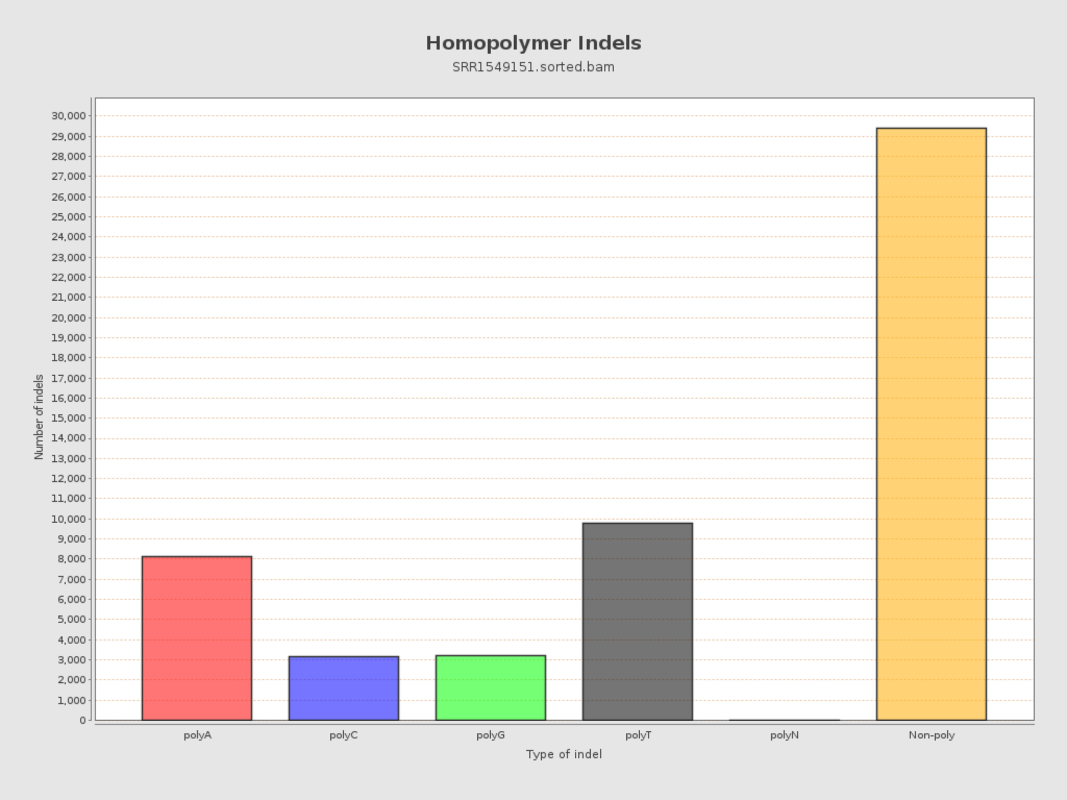
# 9. Results : Mapped Reads GC-content Distribution



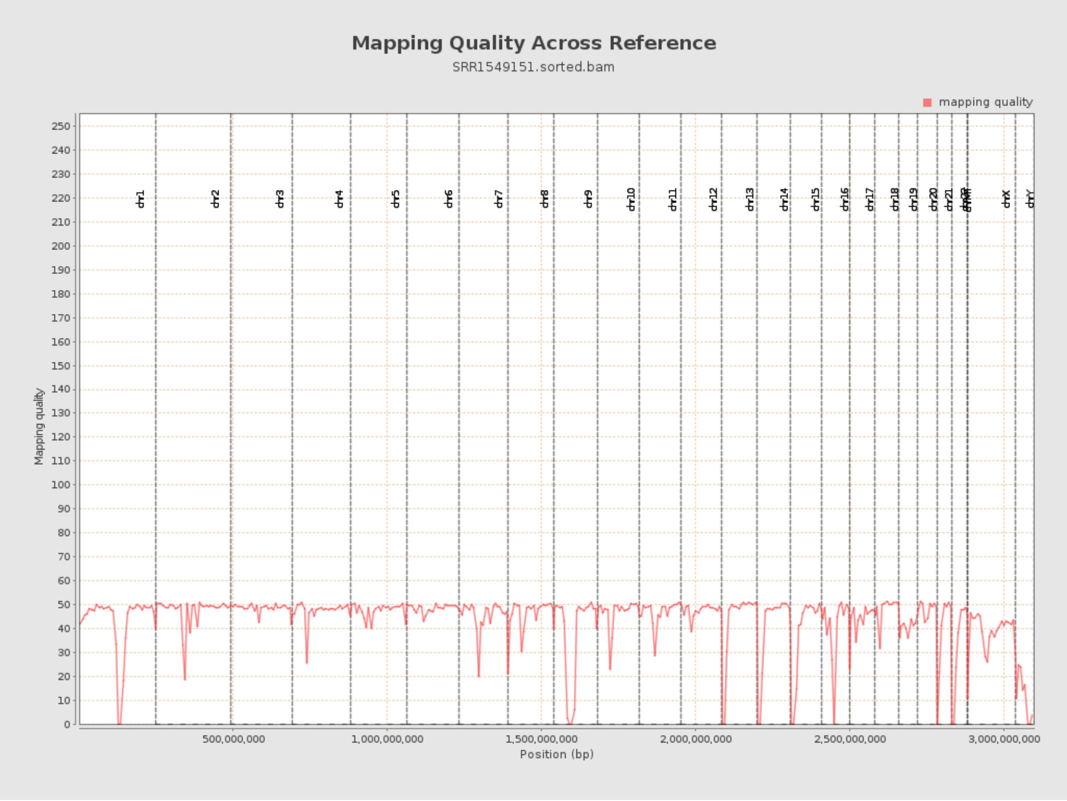
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram