# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 06:28:32*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548991.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_SRR1548991 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548991.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 06:28:31 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1548991.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 8,665,980 |
| Mapped reads | 7,487,346 / 86.4% |
| Unmapped reads | 1,178,634 / 13.6% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Read min/max/mean length | 40 / 40 / 40 |
| Duplicated reads (estimated) | 668,663 / 7.72% |
| Duplication rate | 8.32% |
| Clipped reads | 379,004 / 4.37% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 89,675,592 / 30.17% |
| Number/percentage of C's | 58,288,205 / 19.61% |
| Number/percentage of T's | 90,190,967 / 30.35% |
| Number/percentage of G's | 59,039,910 / 19.87% |
| Number/percentage of N's | 3,016 / 0% |
| GC Percentage | 39.48% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.096 |
| Standard Deviation | 0.7575 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.67 |

## 2.5. Mismatches and indels

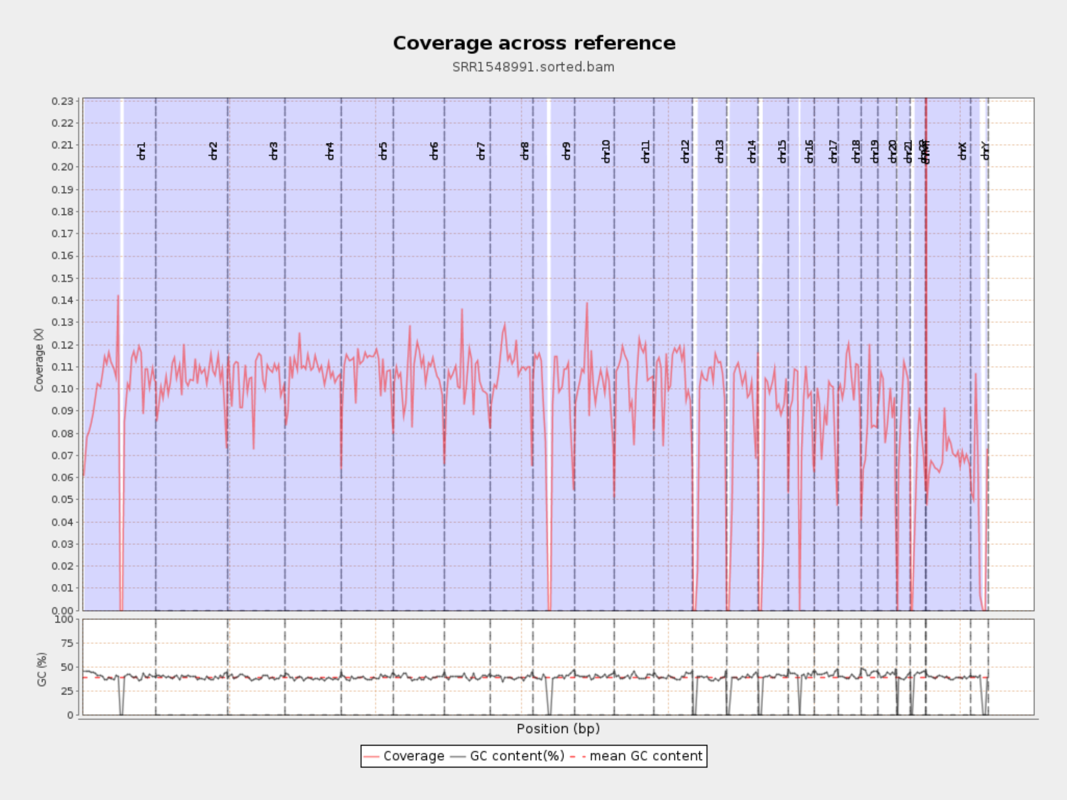
| | |
|---|---|
| General error rate | 0.29% |
| Mismatches | 839,901 |
| Insertions | 9,188 |
| Mapped reads with at least one insertion | 0.12% |
| Deletions | 23,949 |
| Mapped reads with at least one deletion | 0.32% |
| Homopolymer indels | 43.91% |

## 2.6. Chromosome stats

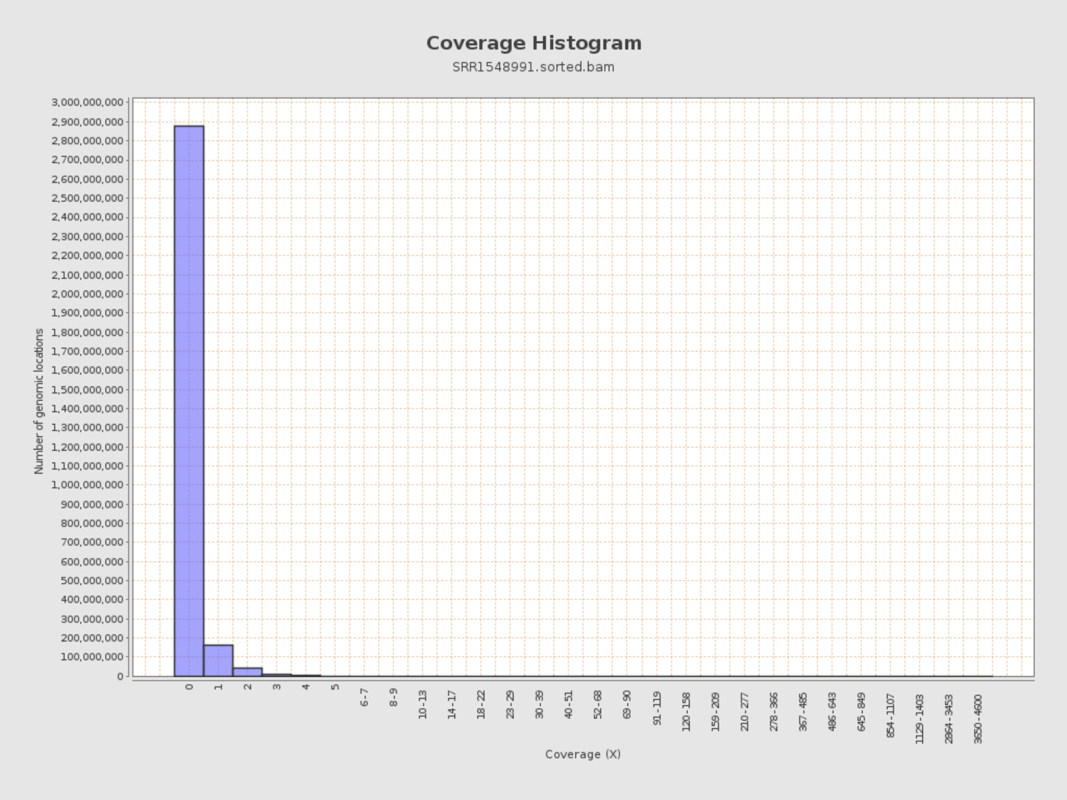
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 24154929 | 0.0969 | 1.1035 |
| chr2 | 243199373 | 25414853 | 0.1045 | 0.5327 |
| chr3 | 198022430 | 20743594 | 0.1048 | 0.4167 |
| chr4 | 191154276 | 20672056 | 0.1081 | 0.4523 |
| chr5 | 180915260 | 19658699 | 0.1087 | 0.4284 |
| chr6 | 171115067 | 18275988 | 0.1068 | 0.4775 |
| chr7 | 159138663 | 16423408 | 0.1032 | 0.7342 |
| chr8 | 146364022 | 15958352 | 0.109 | 2.2917 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr9 | 141213431 | 12696590 | 0.0899 | 0.4984 |
| chr10 | 135534747 | 13936026 | 0.1028 | 0.5637 |
| chr11 | 135006516 | 14362134 | 0.1064 | 0.5326 |
| chr12 | 133851895 | 14129563 | 0.1056 | 0.4321 |
| chr13 | 115169878 | 10174747 | 0.0883 | 0.3811 |
| chr14 | 107349540 | 8946672 | 0.0833 | 0.442 |
| chr15 | 102531392 | 8154193 | 0.0795 | 0.3593 |
| chr16 | 90354753 | 7583236 | 0.0839 | 0.4018 |
| chr17 | 81195210 | 7066103 | 0.087 | 0.4145 |
| chr18 | 78077248 | 8184536 | 0.1048 | 0.9948 |
| chr19 | 59128983 | 4836394 | 0.0818 | 0.8572 |
| chr20 | 63025520 | 5742451 | 0.0911 | 0.4033 |
| chr21 | 48129895 | 4008776 | 0.0833 | 0.4267 |
| chr22 | 51304566 | 2794195 | 0.0545 | 0.3243 |
| chrMT | 16571 | 10309 | 0.6221 | 1.1519 |
| chrX | 155270560 | 10648234 | 0.0686 | 0.4075 |
| chrY | 59373566 | 2652224 | 0.0447 | 0.4288 |

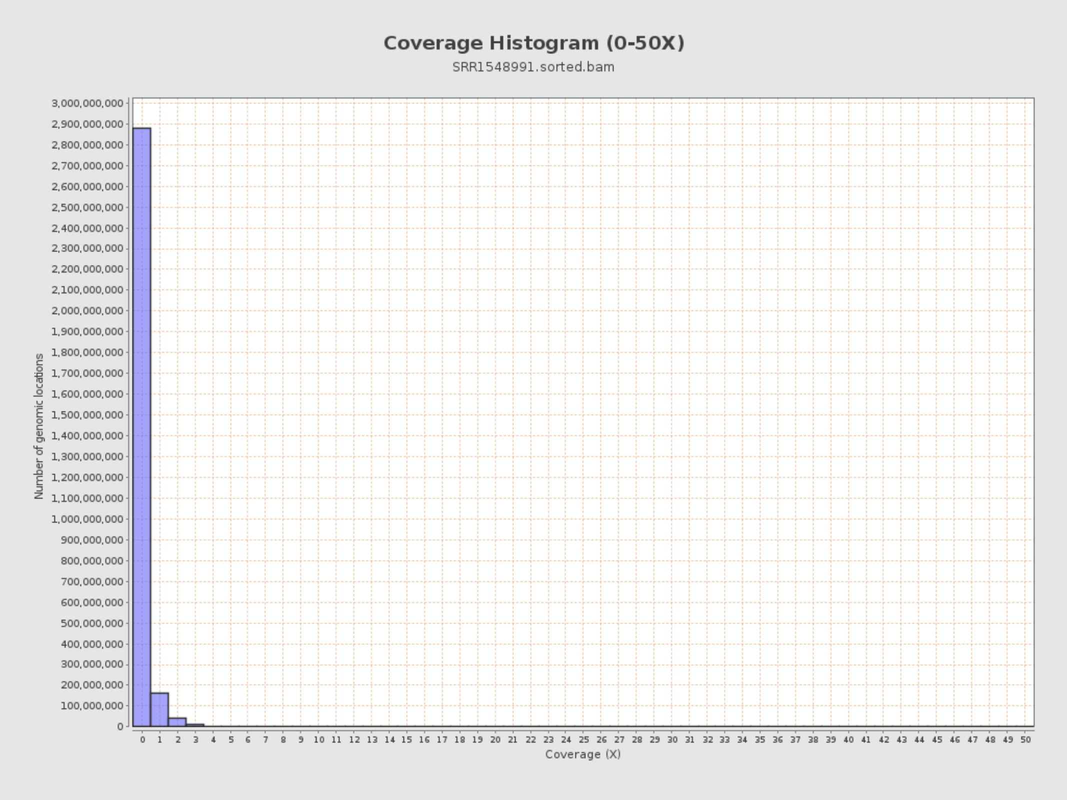
# 3. Results : Coverage across reference



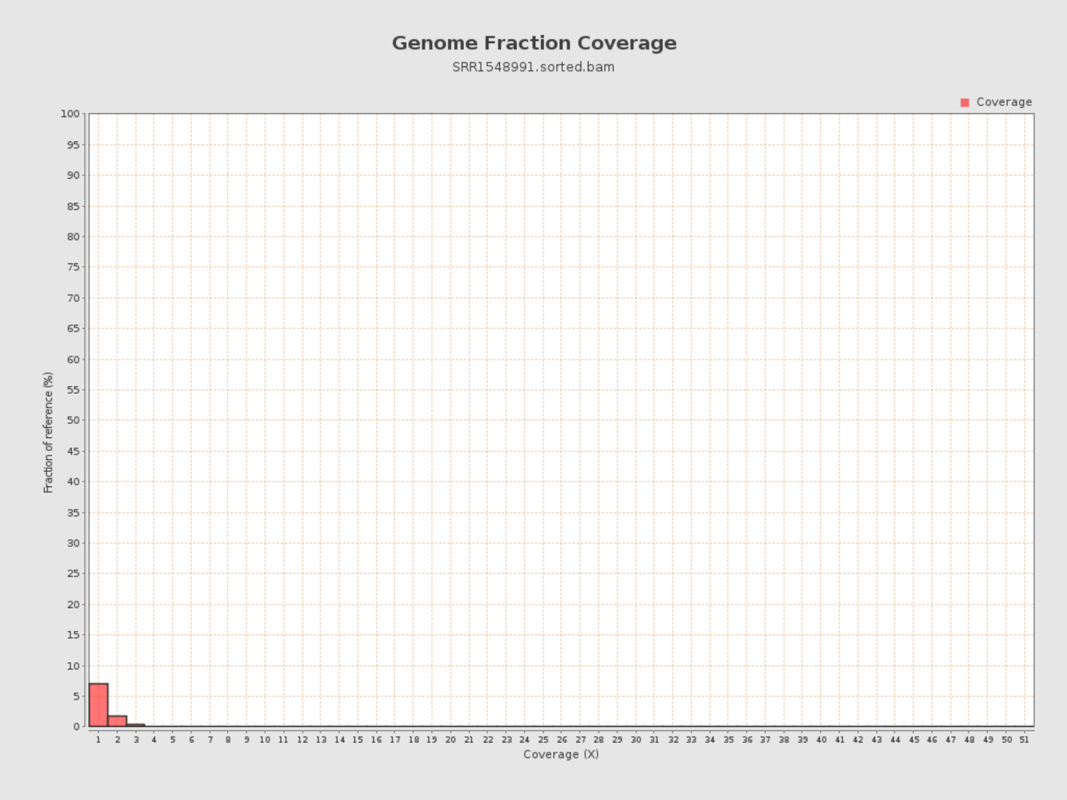
# 4. Results : Coverage Histogram



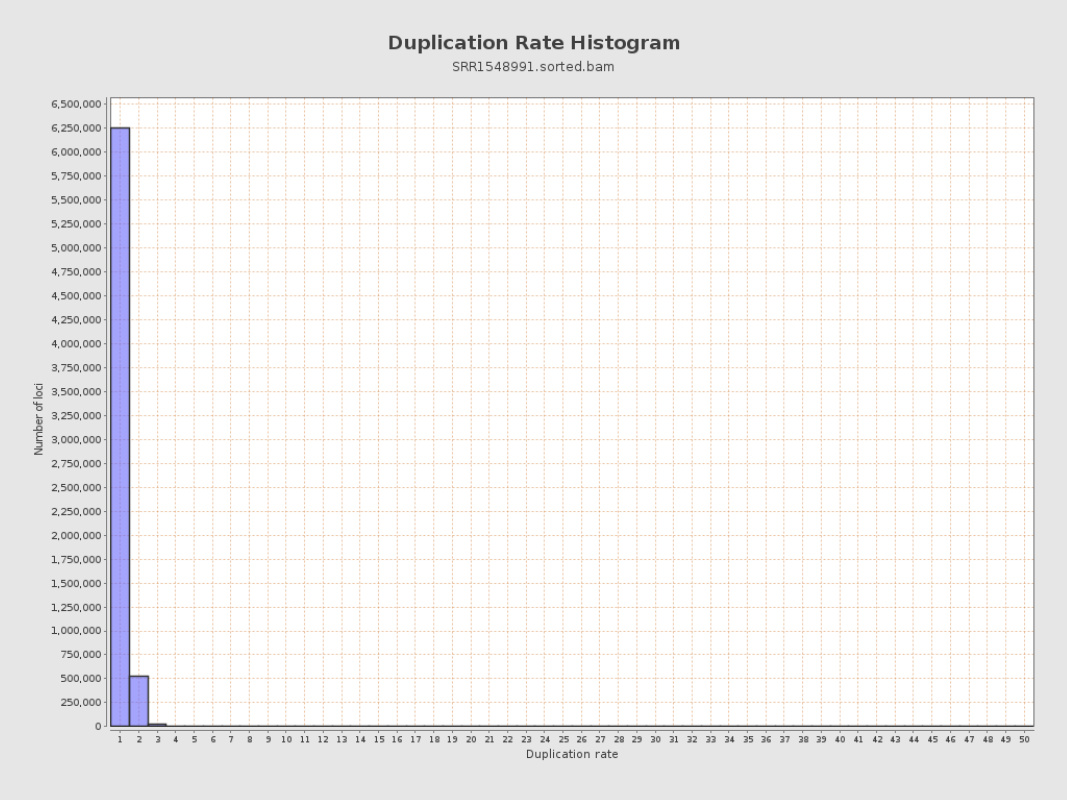
# 5. Results : Coverage Histogram (0-50X)



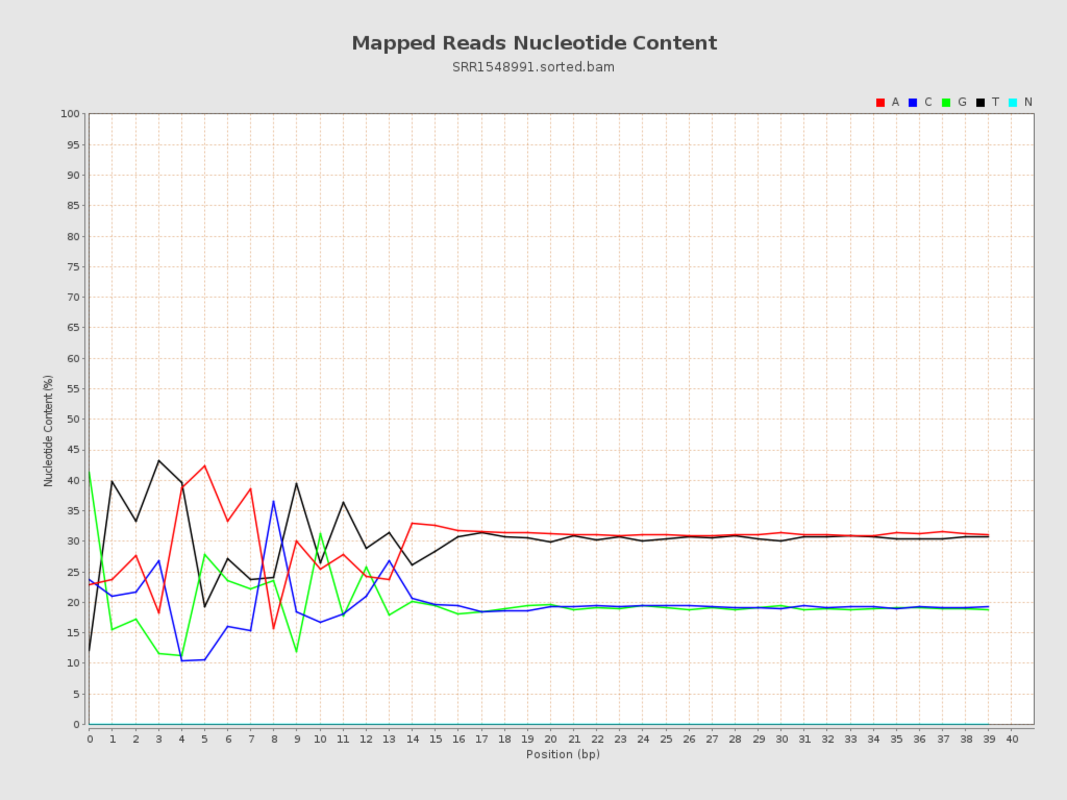
# 6. Results : Genome Fraction Coverage



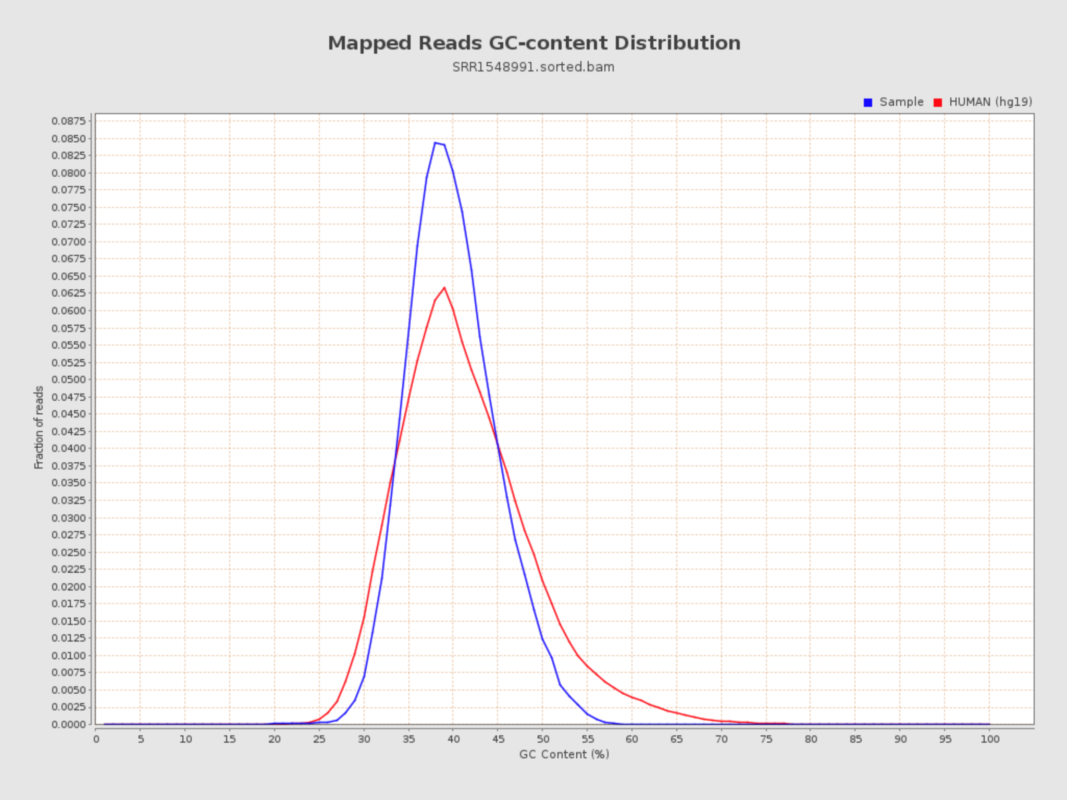
# 7. Results : Duplication Rate Histogram



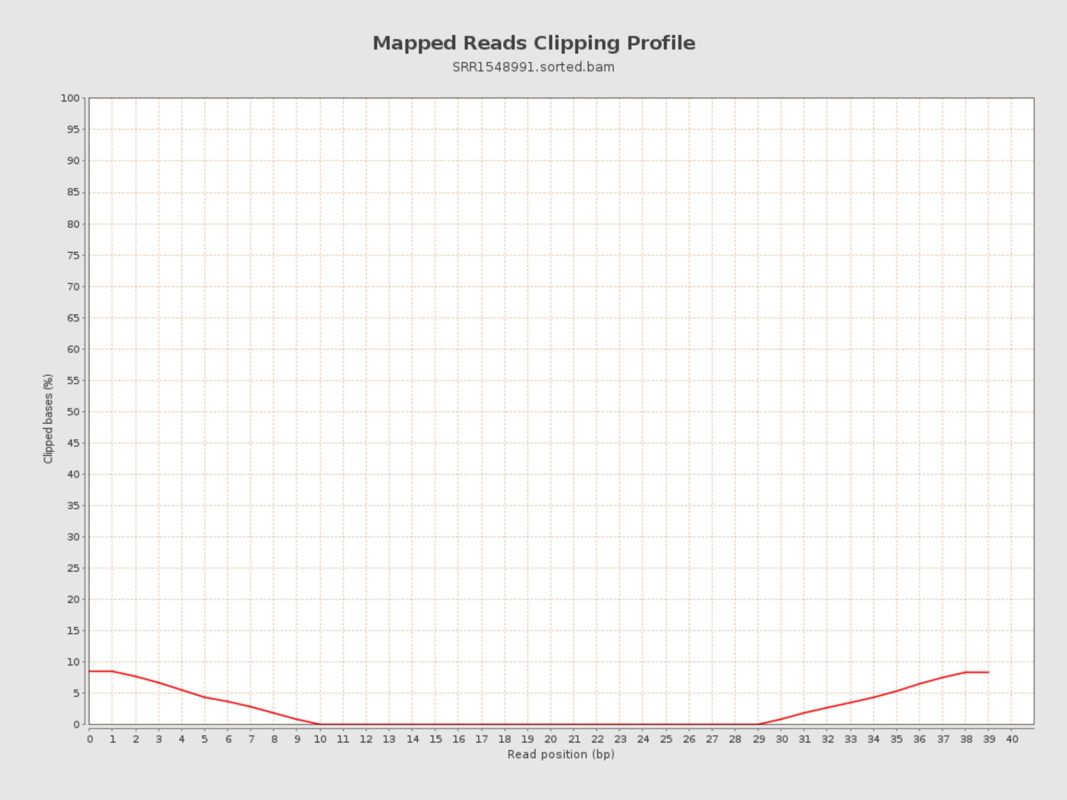
# 8. Results : Mapped Reads Nucleotide Content



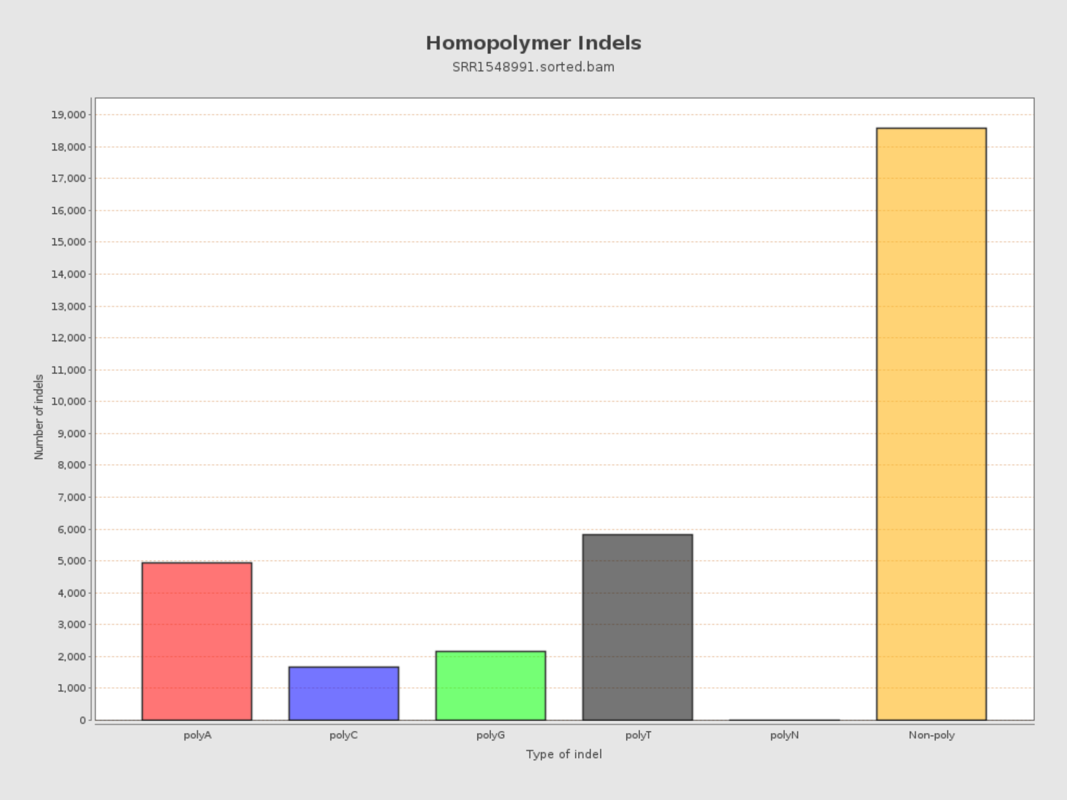
# 9. Results : Mapped Reads GC-content Distribution



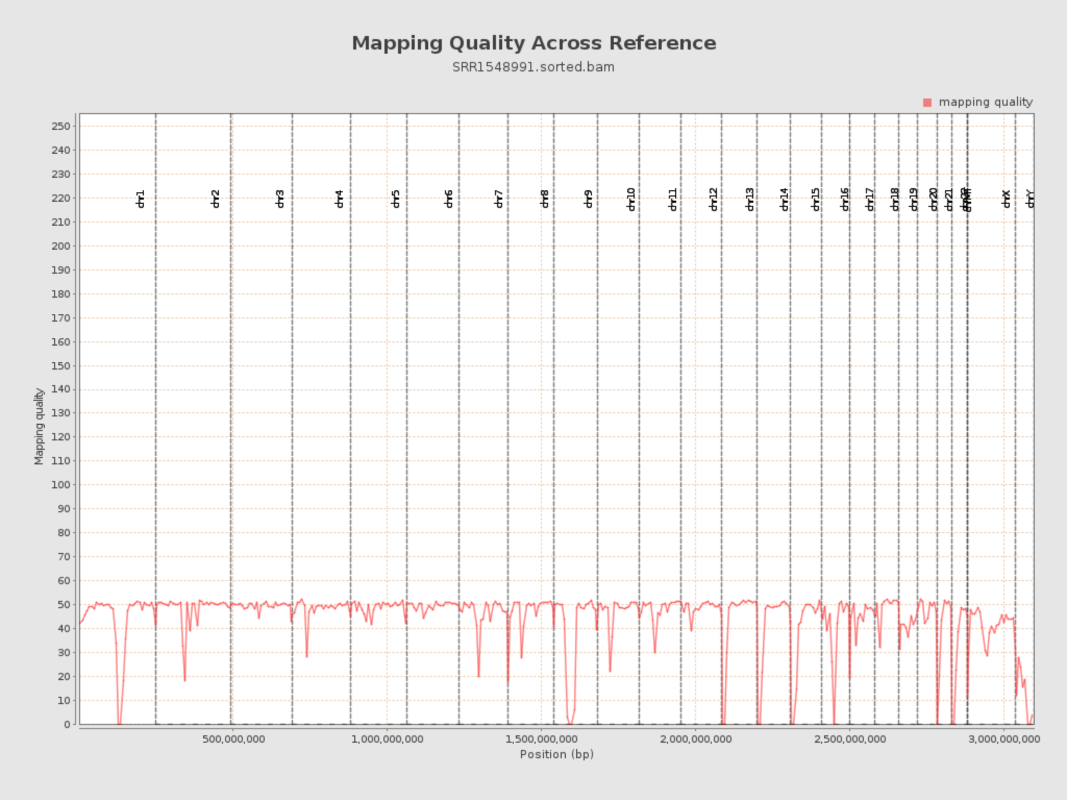
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram