# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/17 00:47:35*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153390.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_SRR1153390 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153390.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Dec 17 00:47:33 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1153390.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 57,684,448 |
| Mapped reads | 57,292,204 / 99.32% |
| Unmapped reads | 392,244 / 0.68% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 448,197 / 0.78% |
| Read min/max/mean length | 30 / 100 / 100.32 |
| Duplicated reads (estimated) | 28,664,069 / 49.69% |
| Duplication rate | 31.87% |
| Clipped reads | 7,607,813 / 13.19% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,488,578,854 / 26.77% |
| Number/percentage of C's | 1,285,695,565 / 23.12% |
| Number/percentage of T's | 1,517,475,626 / 27.29% |
| Number/percentage of G's | 1,267,319,419 / 22.79% |
| Number/percentage of N's | 2,209,062 / 0.04% |
| GC Percentage | 45.91% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 1.7968 |
| | |

| | |
|---|---|
| Standard Deviation | 16.2492 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 50.21 |

## 2.5. Mismatches and indels

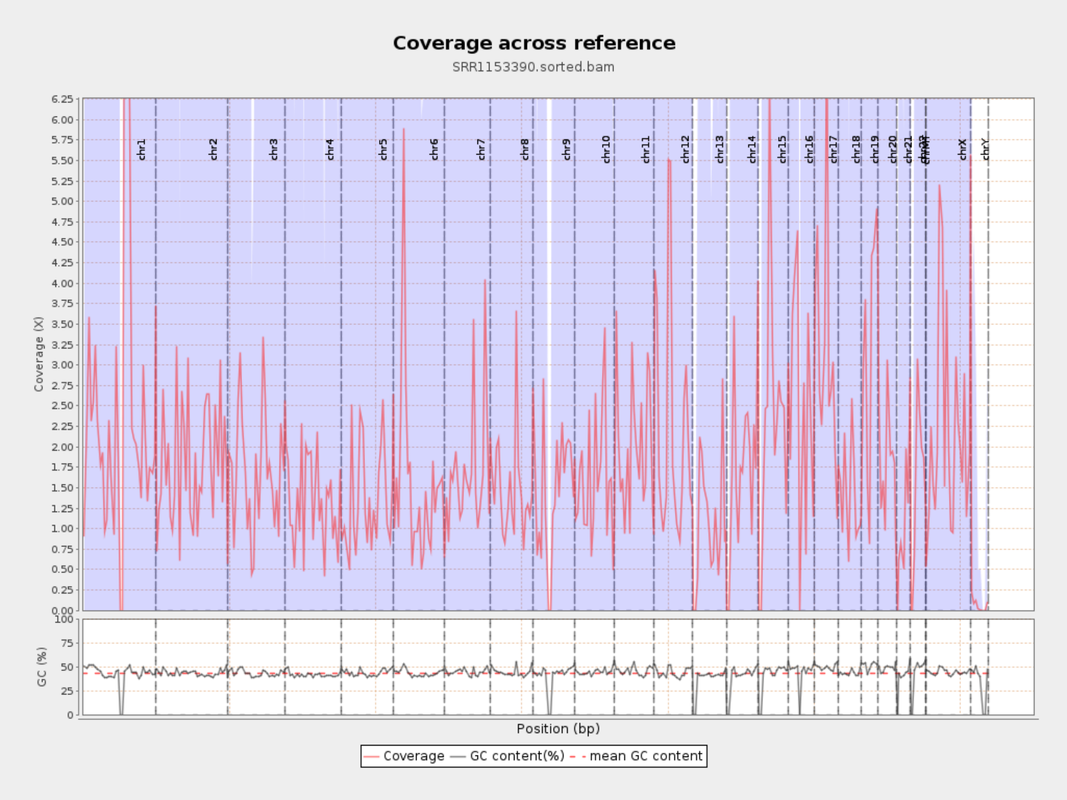
| | |
|---|---|
| General error rate | 0.28% |
| Mismatches | 14,653,129 |
| Insertions | 590,924 |
| Mapped reads with at least one insertion | 1.02% |
| Deletions | 479,962 |
| Mapped reads with at least one deletion | 0.83% |
| Homopolymer indels | 49.79% |

## 2.6. Chromosome stats

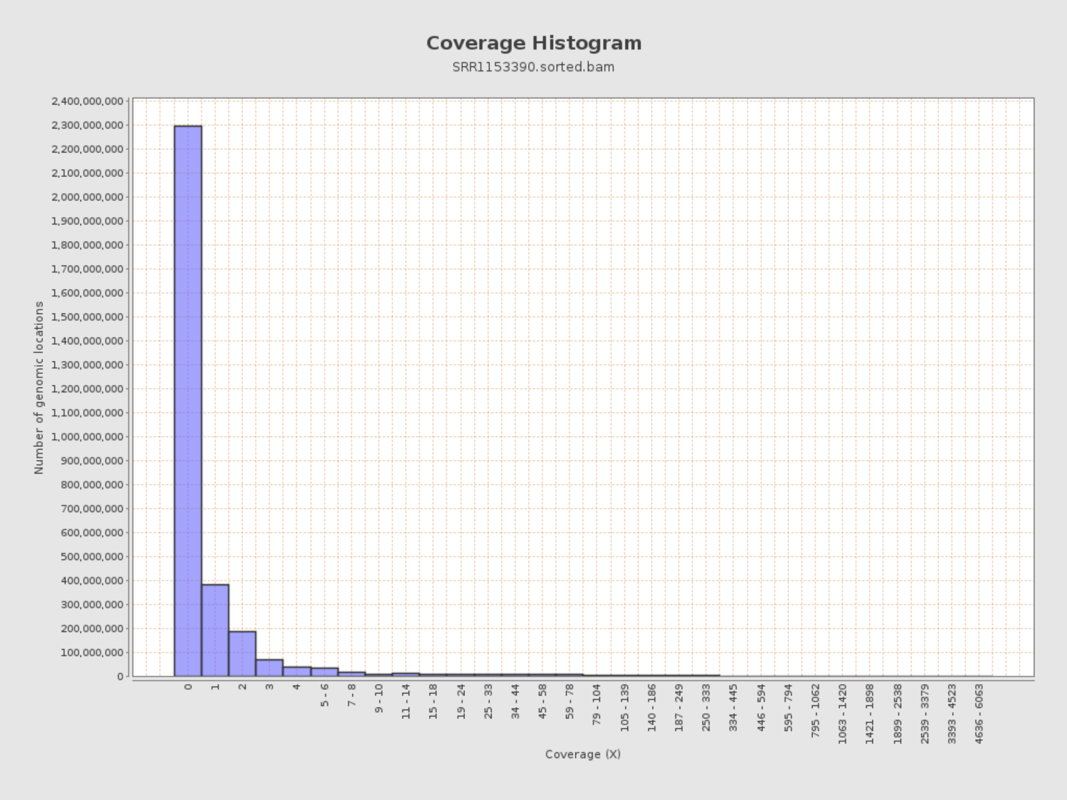
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 608387314 | 2.4409 | 21.5926 |
| chr2 | 243199373 | 440795390 | 1.8125 | 15.0234 |
| chr3 | 198022430 | 332251283 | 1.6778 | 13.6969 |
| chr4 | 191154276 | 257289632 | 1.346 | 11.5413 |
| chr5 | 180915260 | 246867199 | 1.3645 | 12.7421 |
| chr6 | 171115067 | 263878830 | 1.5421 | 13.2695 |
| chr7 | 159138663 | 267812789 | 1.6829 | 15.762 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 215909563 | 1.4752 | 15.5443 |
| chr9 | 141213431 | 201704921 | 1.4284 | 14.3218 |
| chr10 | 135534747 | 222982268 | 1.6452 | 14.1737 |
| chr11 | 135006516 | 272395640 | 2.0176 | 16.3127 |
| chr12 | 133851895 | 309342354 | 2.3111 | 18.5526 |
| chr13 | 115169878 | 124043000 | 1.077 | 11.7176 |
| chr14 | 107349540 | 180150372 | 1.6782 | 15.2299 |
| chr15 | 102531392 | 231293427 | 2.2558 | 19.8321 |
| chr16 | 90354753 | 218134070 | 2.4142 | 19.7745 |
| chr17 | 81195210 | 270268459 | 3.3286 | 23.8782 |
| chr18 | 78077248 | 111831241 | 1.4323 | 13.3169 |
| chr19 | 59128983 | 189277195 | 3.2011 | 21.5195 |
| chr20 | 63025520 | 114230383 | 1.8124 | 14.3299 |
| chr21 | 48129895 | 54411790 | 1.1305 | 14.2983 |
| chr22 | 51304566 | 80269156 | 1.5646 | 15.0979 |
| chrMT | 16571 | 8809 | 0.5316 | 1.5035 |
| chrX | 155270560 | 344916764 | 2.2214 | 21.446 |
| chrY | 59373566 | 3847379 | 0.0648 | 2.4231 |

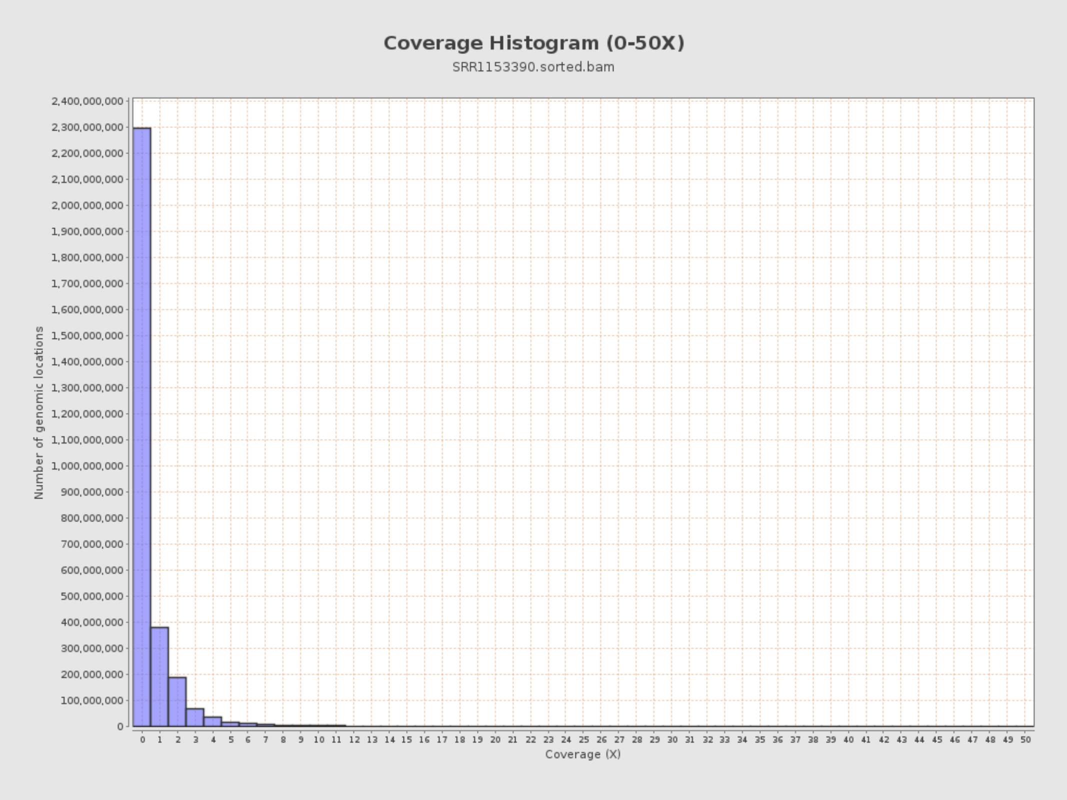
# 3. Results : Coverage across reference



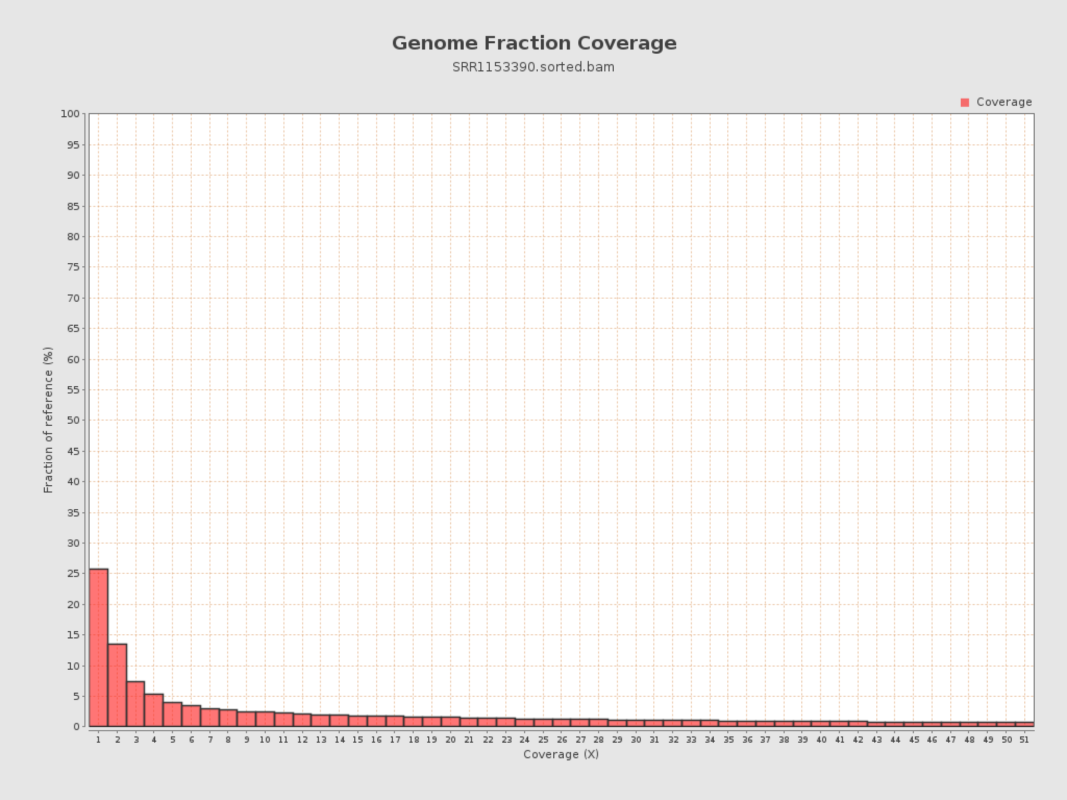
# 4. Results : Coverage Histogram



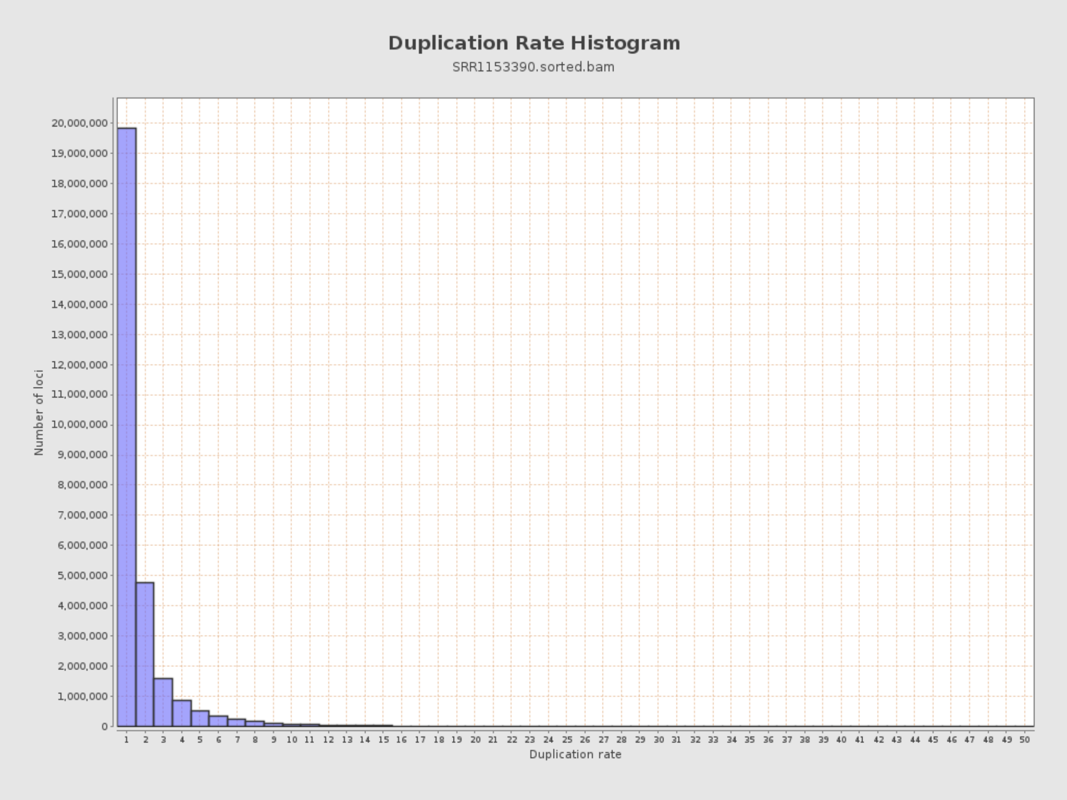
# 5. Results : Coverage Histogram (0-50X)



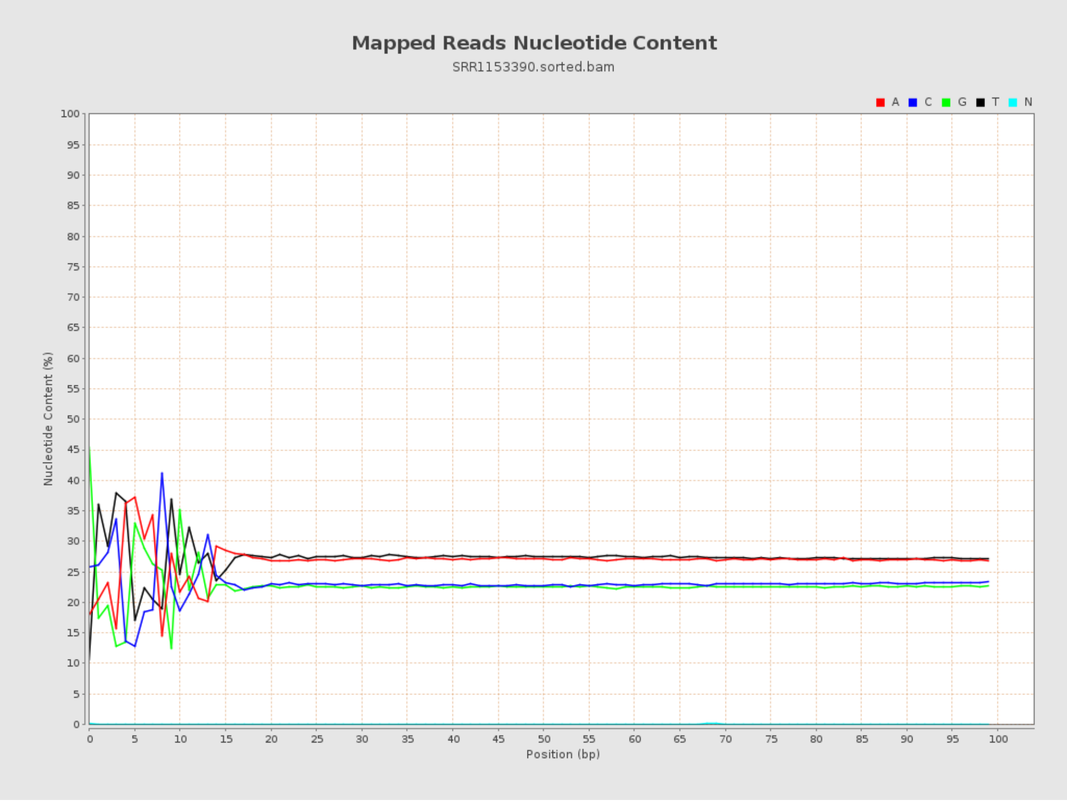
# 6. Results : Genome Fraction Coverage



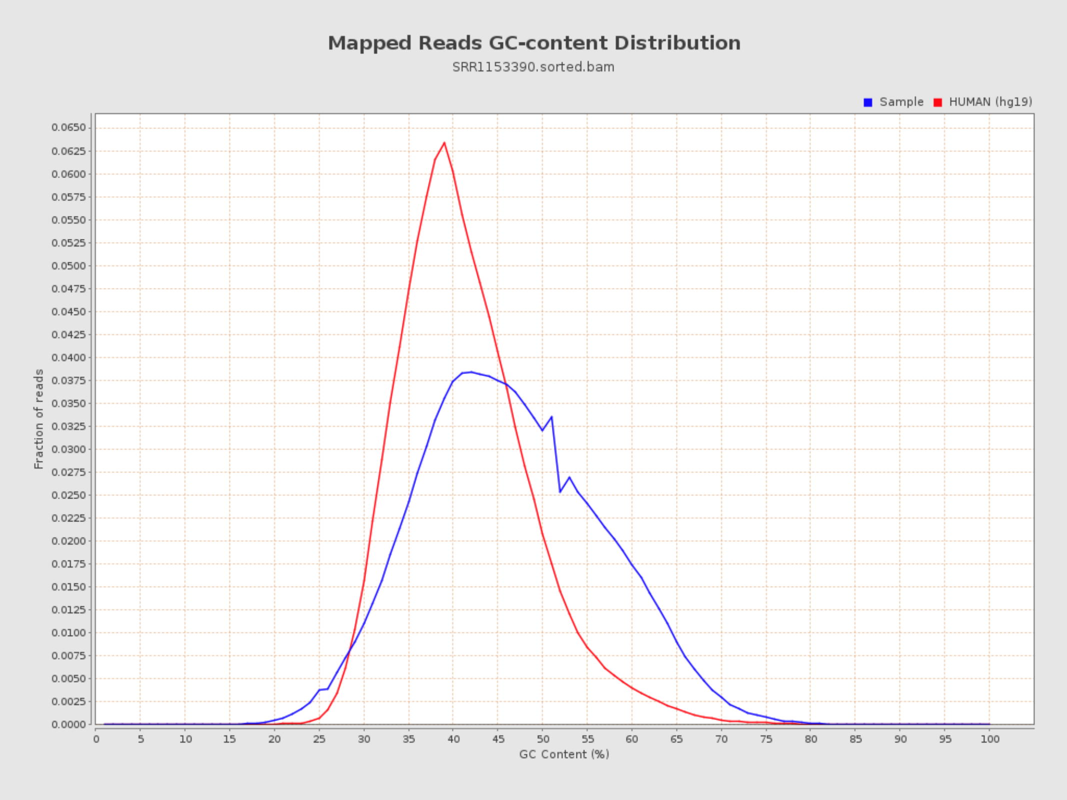
# 7. Results : Duplication Rate Histogram



# 8. Results : Mapped Reads Nucleotide Content

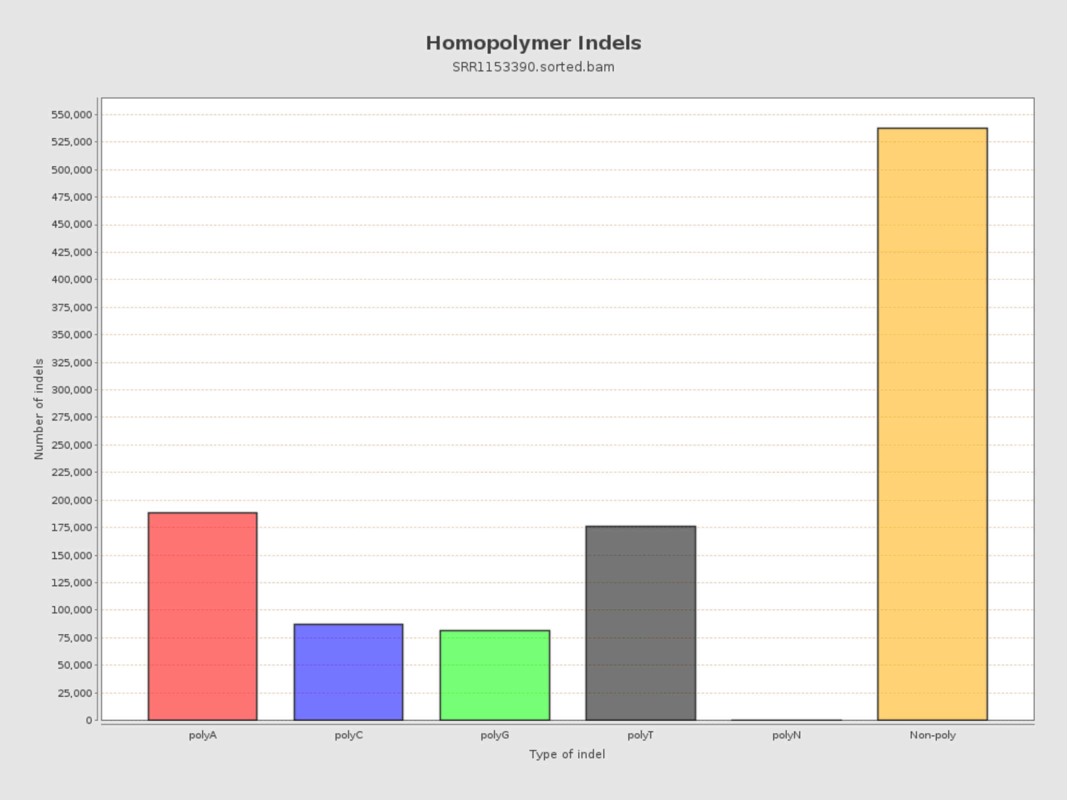


# 9. Results : Mapped Reads GC-content Distribution

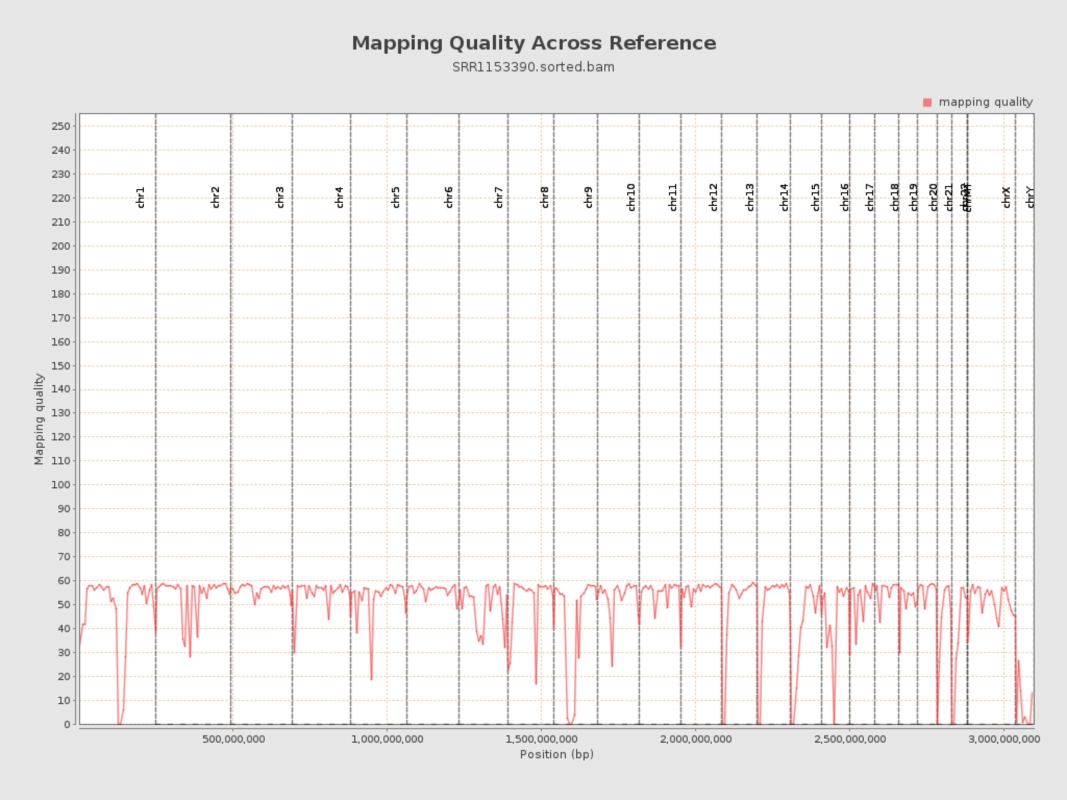


# 10. Results : Mapped Reads Clipping Profile

# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram