# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/16 19:10:30*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153381.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_SRR1153381 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153381.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Dec 16 19:10:29 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1153381.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 81,611,374 |
| Mapped reads | 81,064,562 / 99.33% |
| Unmapped reads | 546,812 / 0.67% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 424,748 / 0.52% |
| Read min/max/mean length | 30 / 100 / 100.21 |
| Duplicated reads (estimated) | 48,604,964 / 59.56% |
| Duplication rate | 45.81% |
| Clipped reads | 12,206,164 / 14.96% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,951,037,107 / 24.73% |
| Number/percentage of C's | 1,992,757,243 / 25.25% |
| Number/percentage of T's | 1,948,057,829 / 24.69% |
| Number/percentage of G's | 1,997,858,961 / 25.32% |
| Number/percentage of N's | 1,059,697 / 0.01% |
| GC Percentage | 50.57% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 2.5492 |
| | |

| | |
|---|---|
| Standard Deviation | 41.3595 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 48.65 |

## 2.5. Mismatches and indels

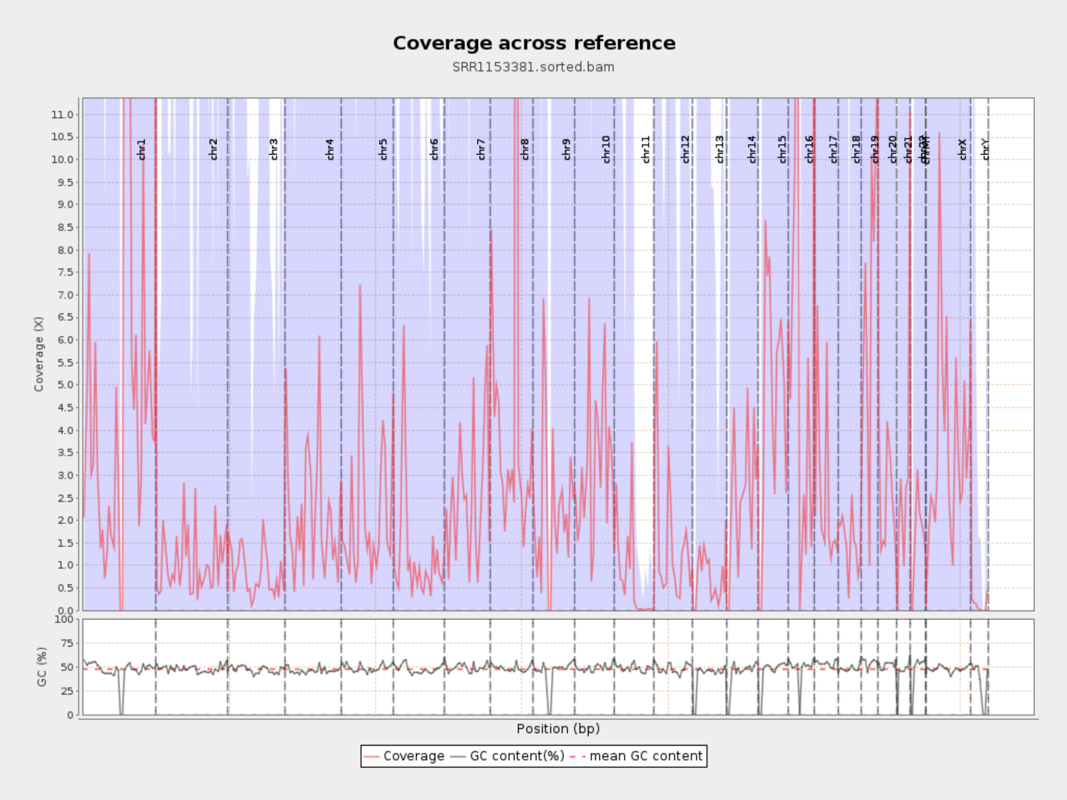
| | |
|---|---|
| General error rate | 0.3% |
| Mismatches | 22,442,946 |
| Insertions | 560,909 |
| Mapped reads with at least one insertion | 0.68% |
| Deletions | 359,862 |
| Mapped reads with at least one deletion | 0.44% |
| Homopolymer indels | 45.55% |

## 2.6. Chromosome stats

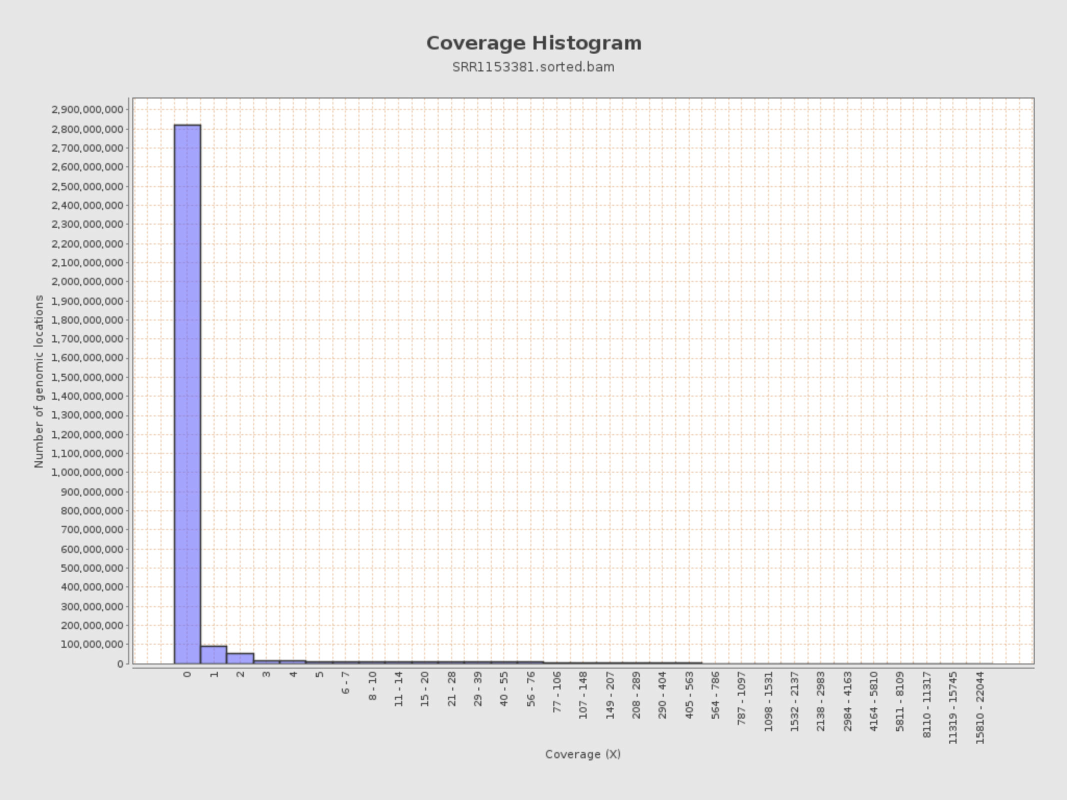
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 1269880140 | 5.0948 | 55.7836 |
| chr2 | 243199373 | 259164839 | 1.0656 | 17.7424 |
| chr3 | 198022430 | 170406368 | 0.8605 | 14.4616 |
| chr4 | 191154276 | 412660222 | 2.1588 | 41.0335 |
| chr5 | 180915260 | 393507119 | 2.1751 | 31.4794 |
| chr6 | 171115067 | 206579138 | 1.2073 | 19.1239 |
| chr7 | 159138663 | 403575225 | 2.536 | 40.7488 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 751213555 | 5.1325 | 111.3314 |
| chr9 | 141213431 | 312135004 | 2.2104 | 27.8654 |
| chr10 | 135534747 | 444231577 | 3.2776 | 34.7349 |
| chr11 | 135006516 | 101590341 | 0.7525 | 13.0512 |
| chr12 | 133851895 | 213131839 | 1.5923 | 25.7405 |
| chr13 | 115169878 | 79013128 | 0.6861 | 13.1277 |
| chr14 | 107349540 | 270269503 | 2.5177 | 27.0888 |
| chr15 | 102531392 | 466582230 | 4.5506 | 39.2058 |
| chr16 | 90354753 | 453633579 | 5.0206 | 47.4837 |
| chr17 | 81195210 | 216255368 | 2.6634 | 37.8812 |
| chr18 | 78077248 | 117800882 | 1.5088 | 21.3241 |
| chr19 | 59128983 | 405079315 | 6.8508 | 57.1918 |
| chr20 | 63025520 | 152727256 | 2.4233 | 24.8776 |
| chr21 | 48129895 | 142880877 | 2.9687 | 65.115 |
| chr22 | 51304566 | 80856259 | 1.576 | 18.8014 |
| chrMT | 16571 | 977 | 0.059 | 0.391 |
| chrX | 155270560 | 560643516 | 3.6108 | 43.765 |
| chrY | 59373566 | 7780224 | 0.131 | 7.3241 |

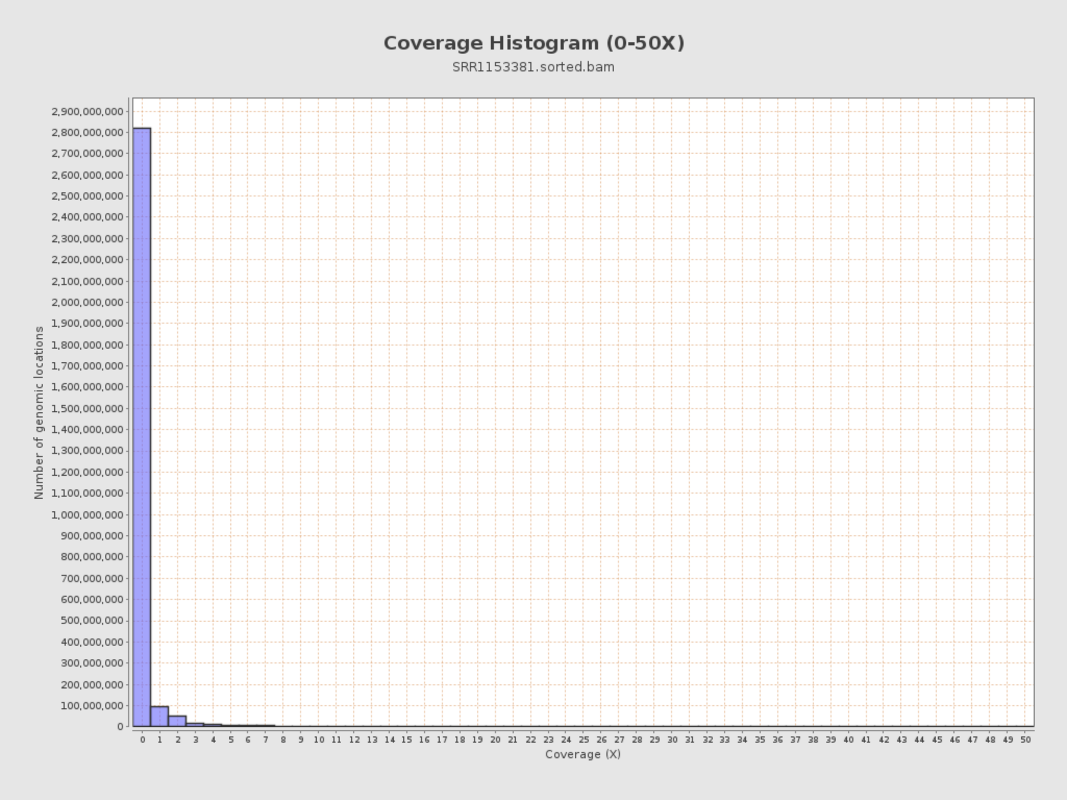
# 3. Results : Coverage across reference



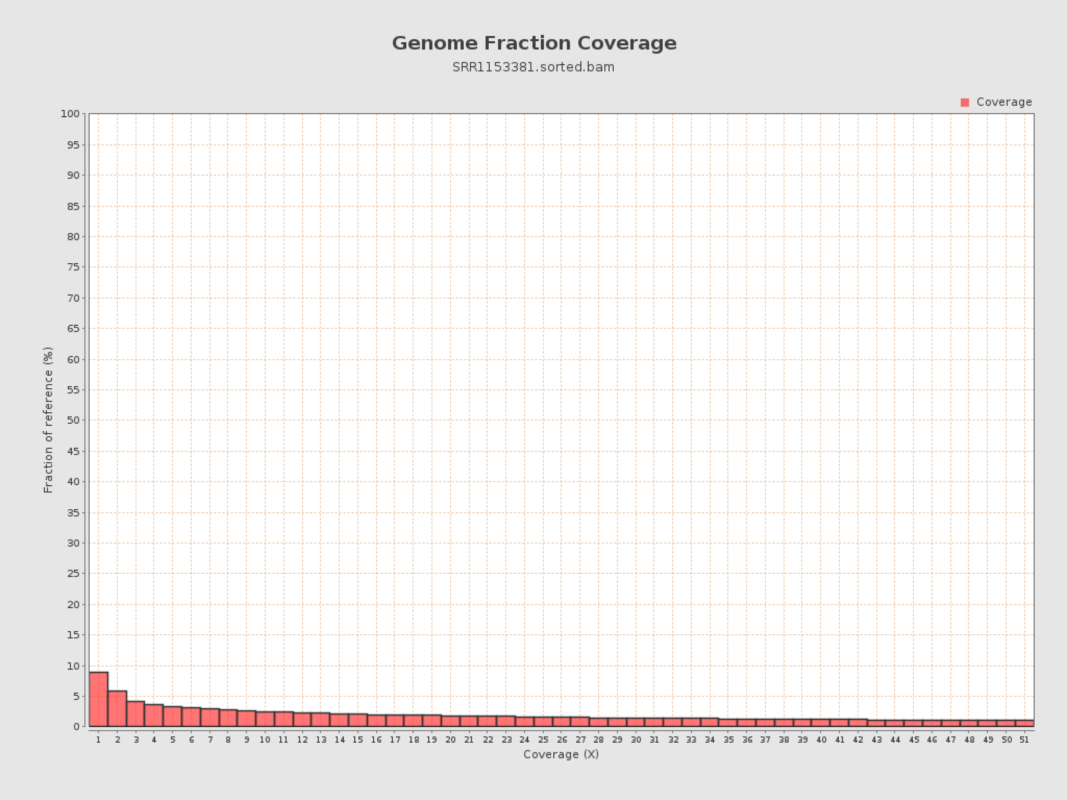
# 4. Results : Coverage Histogram



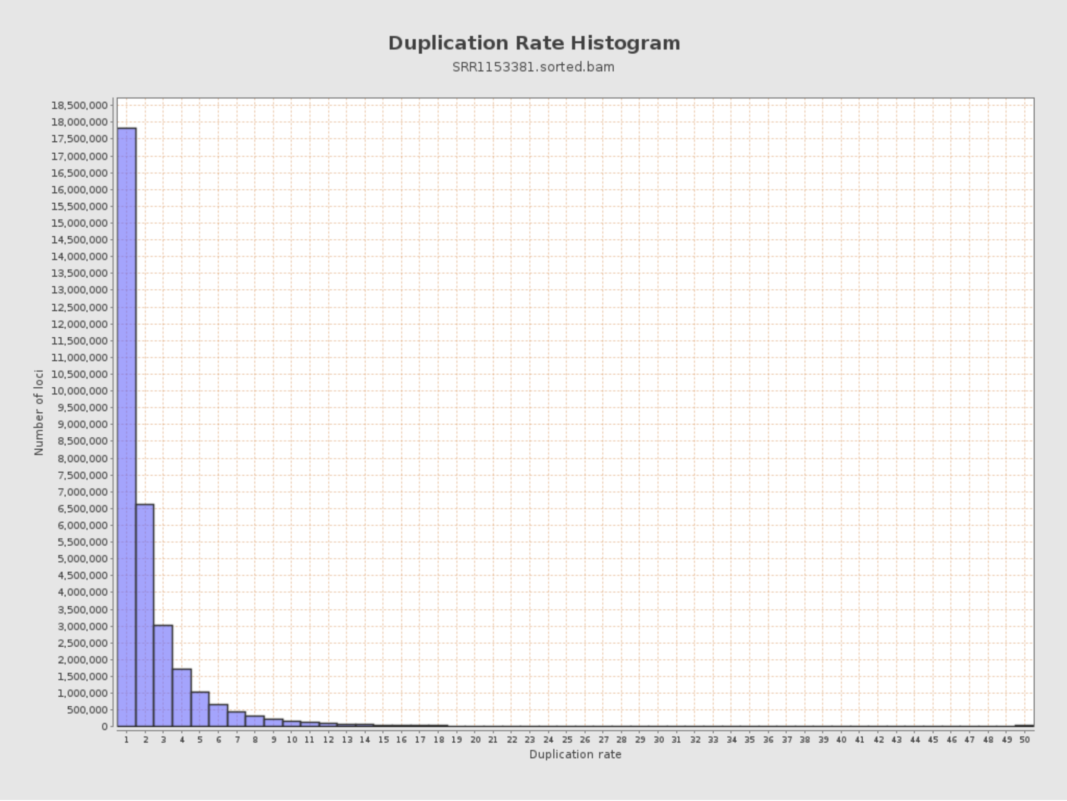
# 5. Results : Coverage Histogram (0-50X)



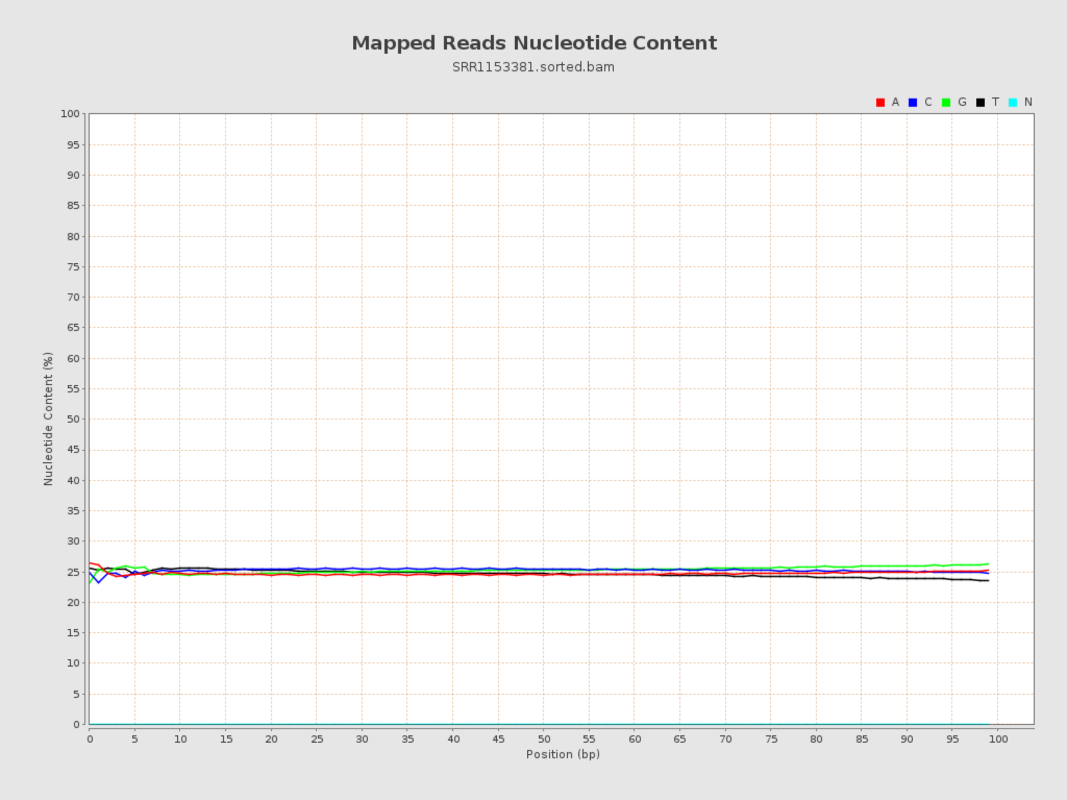
# 6. Results : Genome Fraction Coverage



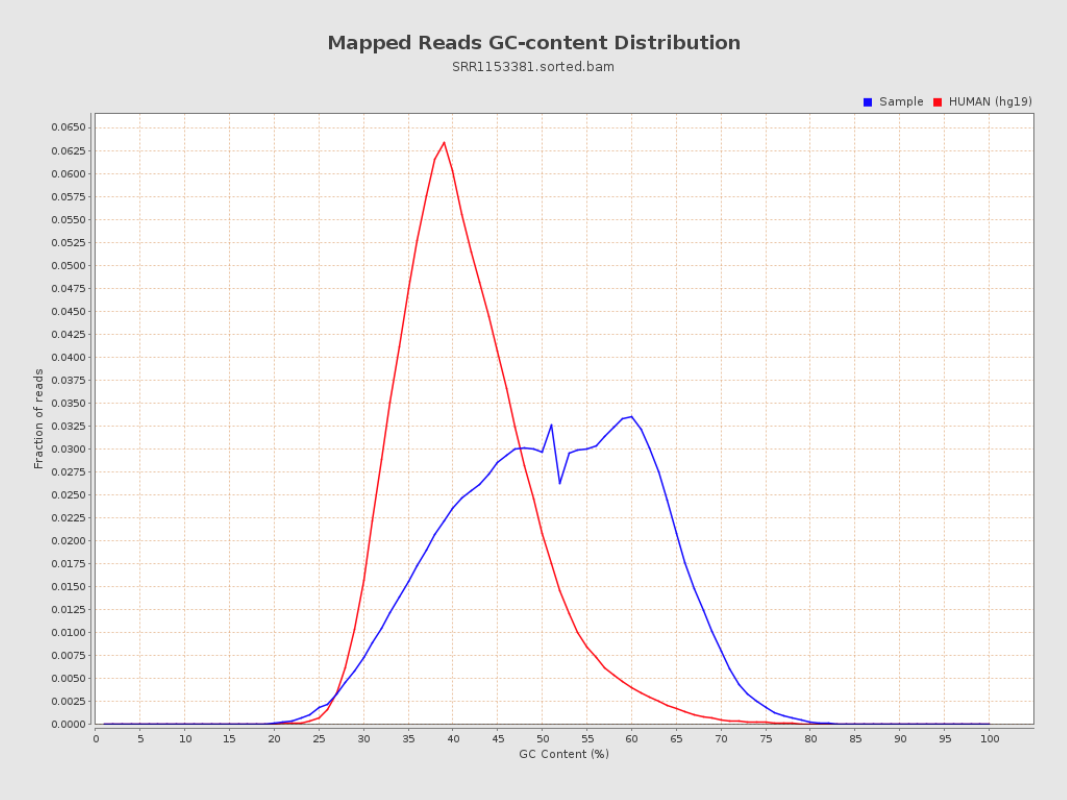
# 7. Results : Duplication Rate Histogram



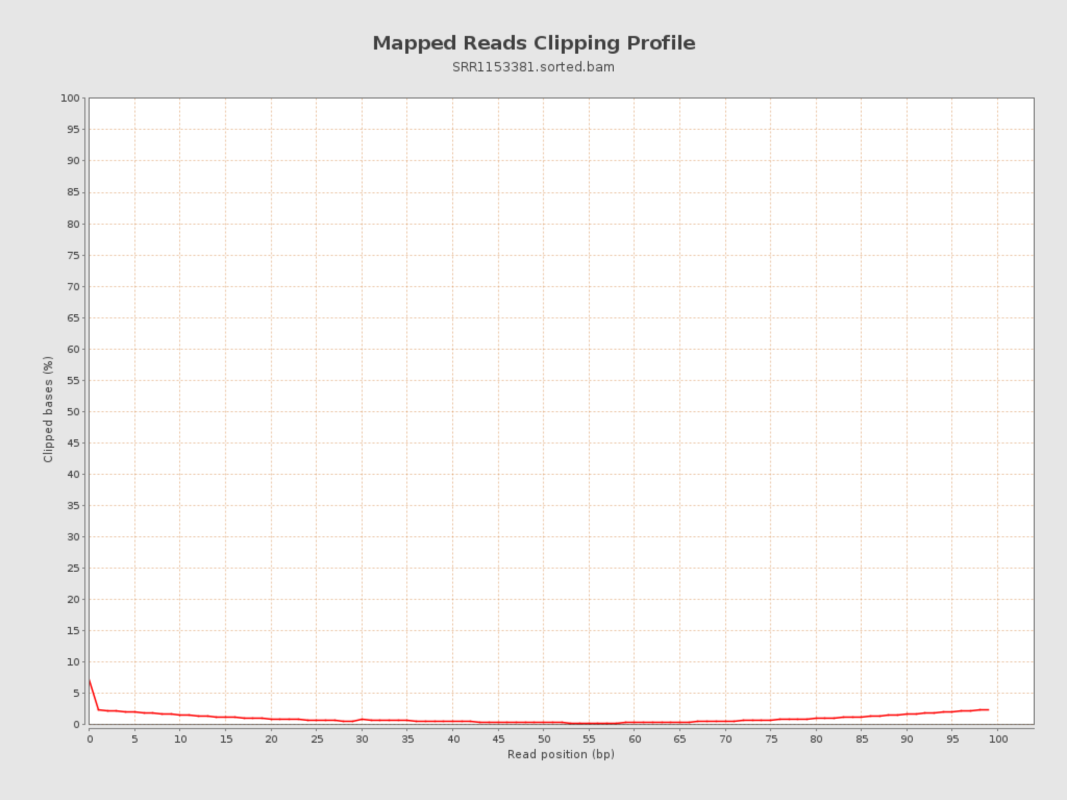
# 8. Results : Mapped Reads Nucleotide Content



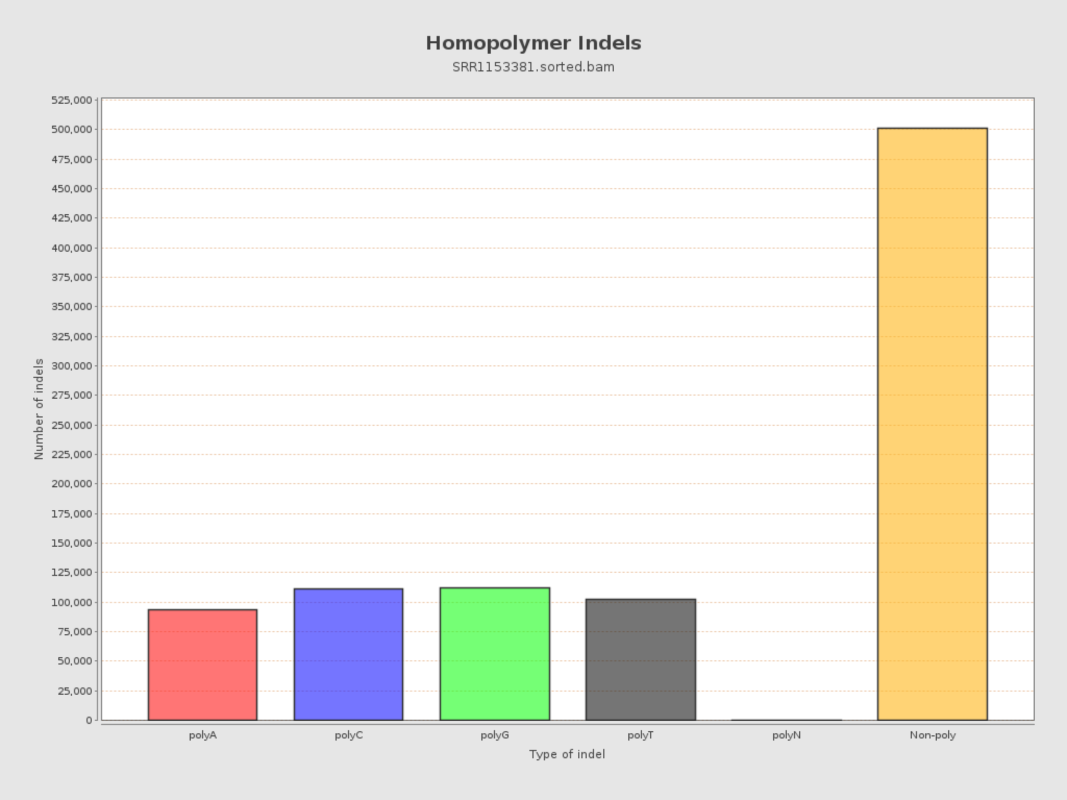
# 9. Results : Mapped Reads GC-content Distribution



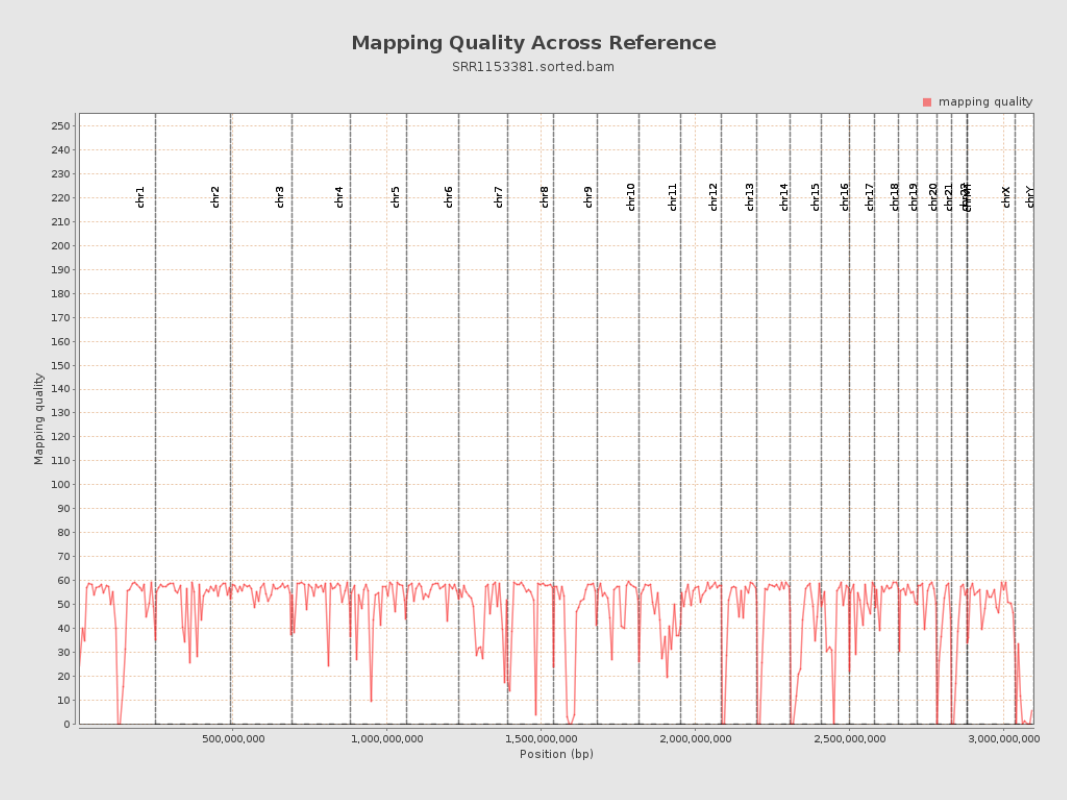
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram