# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/16 10:24:59*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153365.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_SRR1153365 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153365.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Dec 16 10:24:59 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1153365.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 46,735,180 |
| Mapped reads | 46,432,066 / 99.35% |
| Unmapped reads | 303,114 / 0.65% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 256,510 / 0.55% |
| Read min/max/mean length | 30 / 100 / 100.23 |
| Duplicated reads (estimated) | 31,140,868 / 66.63% |
| Duplication rate | 57.48% |
| Clipped reads | 5,996,487 / 12.83% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,204,642,041 / 26.65% |
| Number/percentage of C's | 1,047,110,873 / 23.17% |
| Number/percentage of T's | 1,239,249,302 / 27.42% |
| Number/percentage of G's | 1,027,316,256 / 22.73% |
| Number/percentage of N's | 1,317,681 / 0.03% |
| GC Percentage | 45.9% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 1.4602 |
| | |

| | |
|---|---|
| Standard Deviation | 16.9997 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 50.51 |

## 2.5. Mismatches and indels

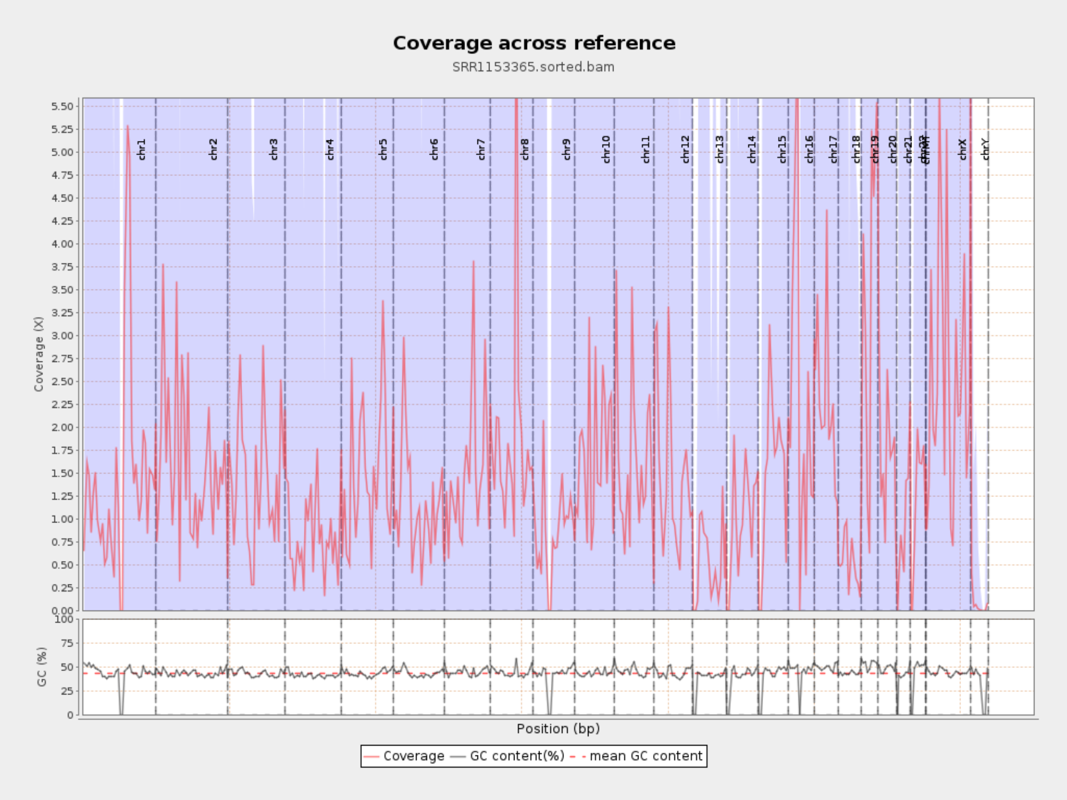
| | |
|---|---|
| General error rate | 0.26% |
| Mismatches | 11,195,672 |
| Insertions | 319,798 |
| Mapped reads with at least one insertion | 0.68% |
| Deletions | 280,804 |
| Mapped reads with at least one deletion | 0.6% |
| Homopolymer indels | 49.89% |

## 2.6. Chromosome stats

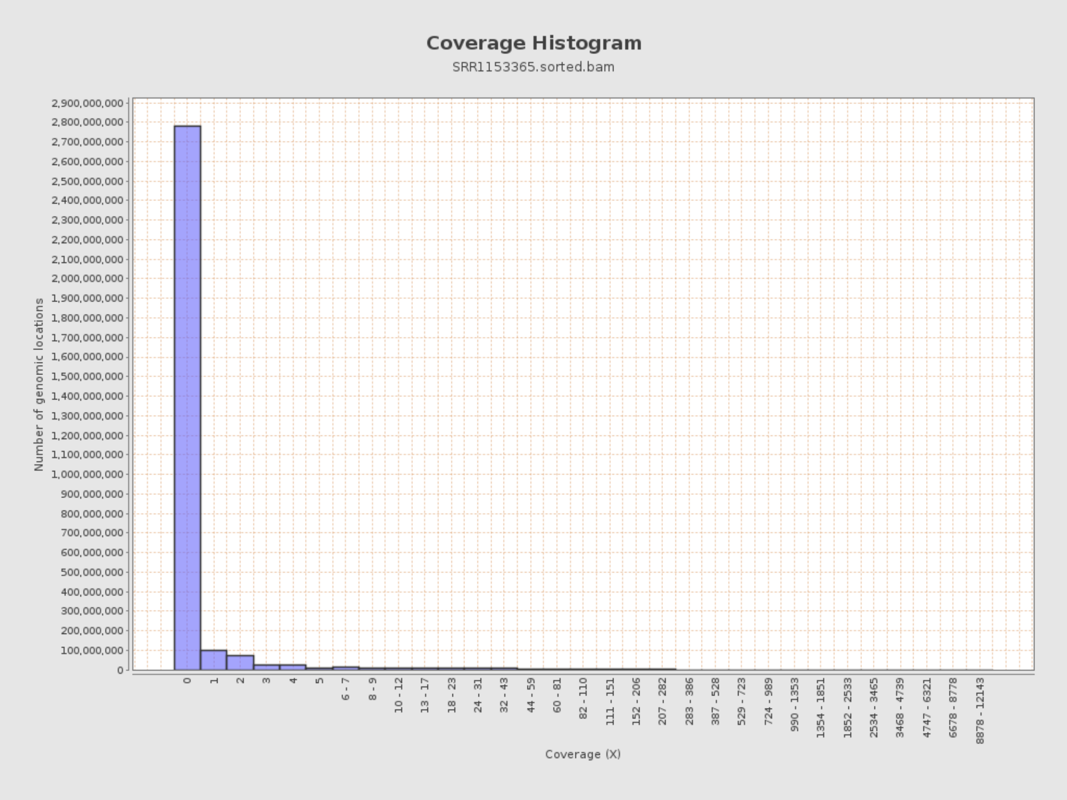
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 359765860 | 1.4434 | 14.3302 |
| chr2 | 243199373 | 390578273 | 1.606 | 16.4966 |
| chr3 | 198022430 | 278456419 | 1.4062 | 14.5216 |
| chr4 | 191154276 | 154016222 | 0.8057 | 10.0218 |
| chr5 | 180915260 | 271790024 | 1.5023 | 17.0013 |
| chr6 | 171115067 | 194251829 | 1.1352 | 12.8251 |
| chr7 | 159138663 | 238563583 | 1.4991 | 16.7116 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 279015685 | 1.9063 | 32.39 |
| chr9 | 141213431 | 119033086 | 0.8429 | 10.1386 |
| chr10 | 135534747 | 234869707 | 1.7329 | 17.8007 |
| chr11 | 135006516 | 221168419 | 1.6382 | 15.3191 |
| chr12 | 133851895 | 208664414 | 1.5589 | 14.9786 |
| chr13 | 115169878 | 58607896 | 0.5089 | 8.0692 |
| chr14 | 107349540 | 105616875 | 0.9839 | 10.5082 |
| chr15 | 102531392 | 149708365 | 1.4601 | 13.4883 |
| chr16 | 90354753 | 201574649 | 2.2309 | 22.5101 |
| chr17 | 81195210 | 189985955 | 2.3399 | 18.6454 |
| chr18 | 78077248 | 41439802 | 0.5308 | 7.5365 |
| chr19 | 59128983 | 201696485 | 3.4111 | 28.0203 |
| chr20 | 63025520 | 108243784 | 1.7175 | 16.8642 |
| chr21 | 48129895 | 45368573 | 0.9426 | 11.1229 |
| chr22 | 51304566 | 61217256 | 1.1932 | 12.7913 |
| chrMT | 16571 | 26517 | 1.6002 | 5.6108 |
| chrX | 155270560 | 402950851 | 2.5952 | 28.0437 |
| chrY | 59373566 | 3585899 | 0.0604 | 2.4031 |

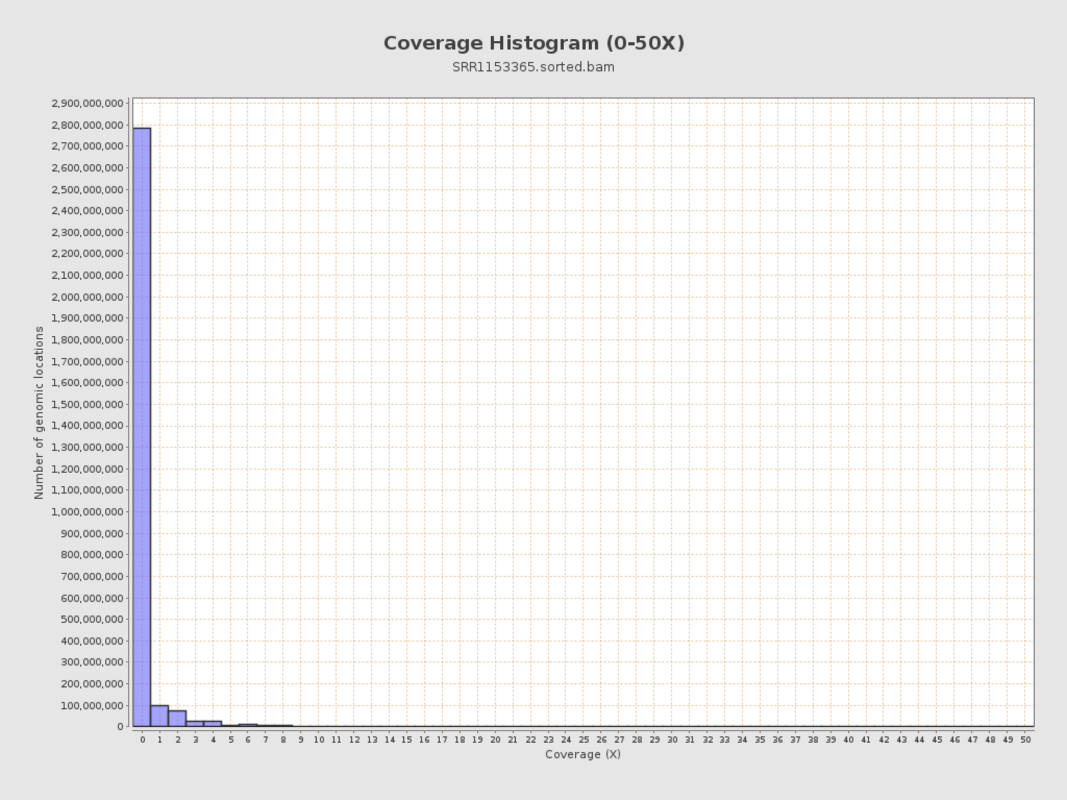
# 3. Results : Coverage across reference



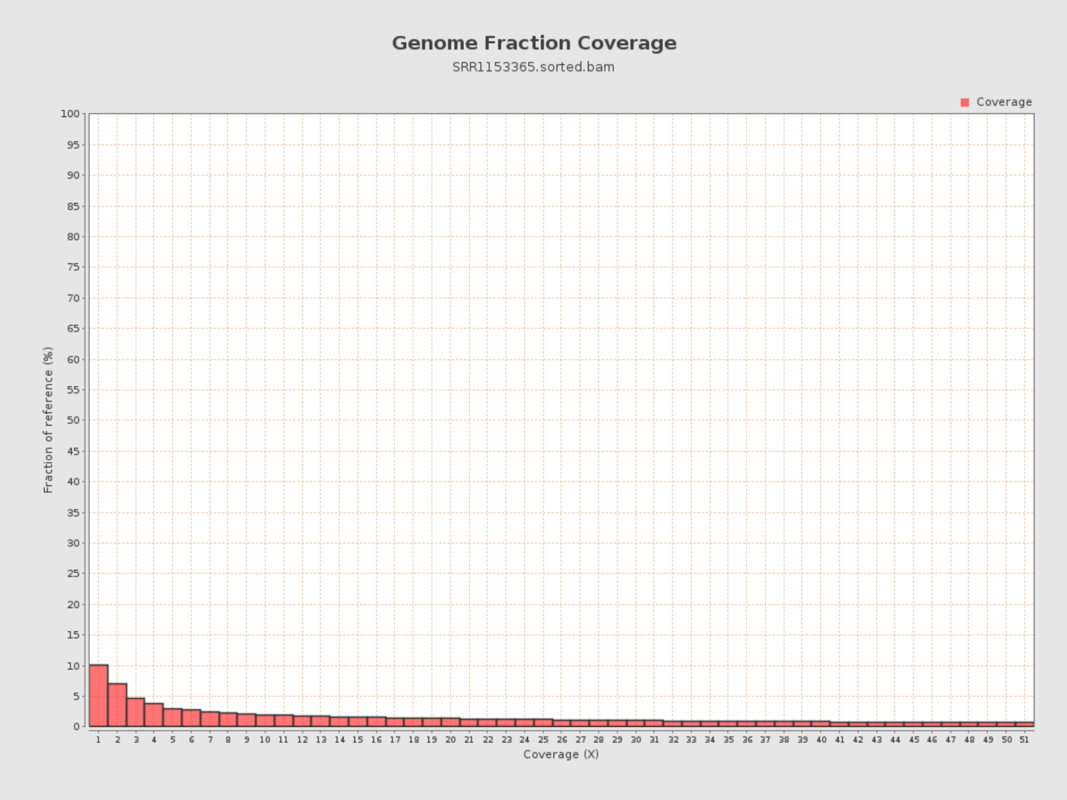
# 4. Results : Coverage Histogram



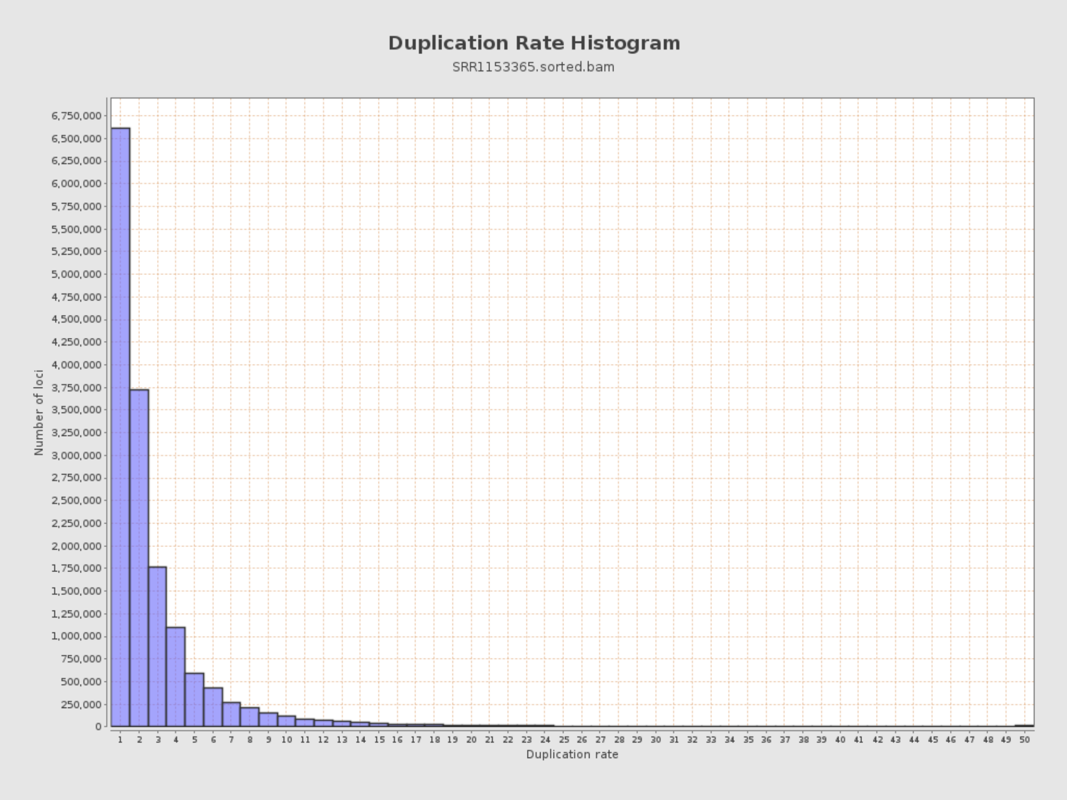
# 5. Results : Coverage Histogram (0-50X)



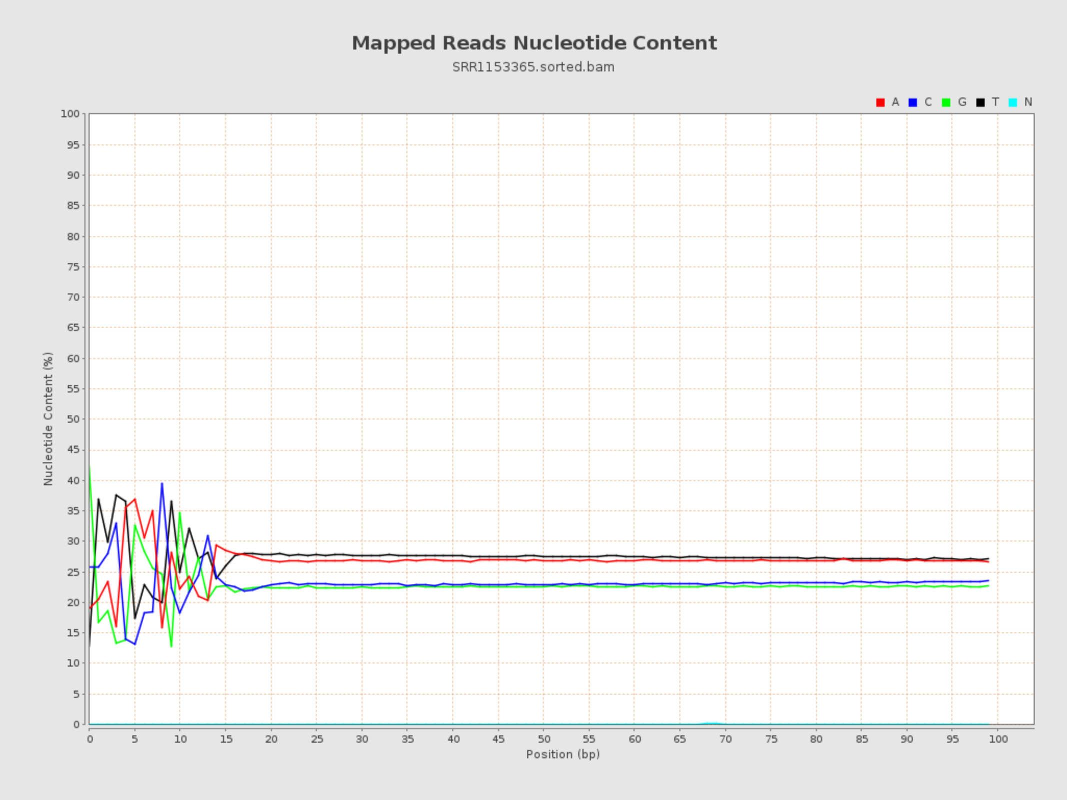
# 6. Results : Genome Fraction Coverage



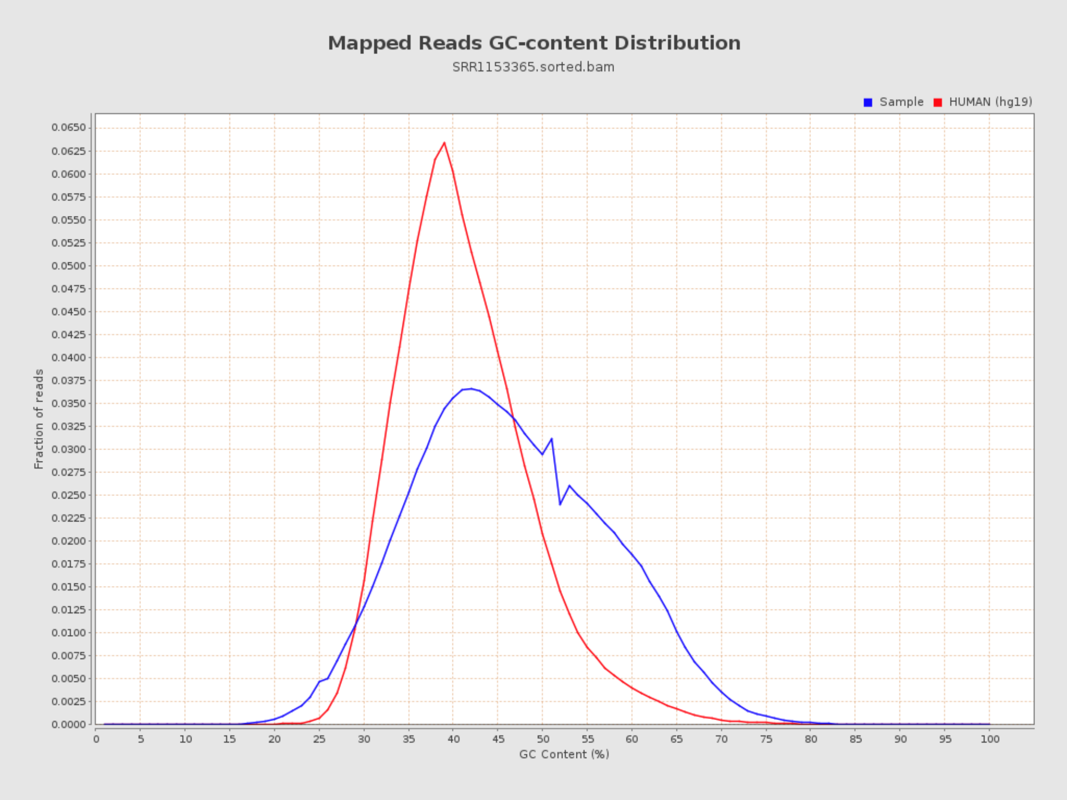
# 7. Results : Duplication Rate Histogram



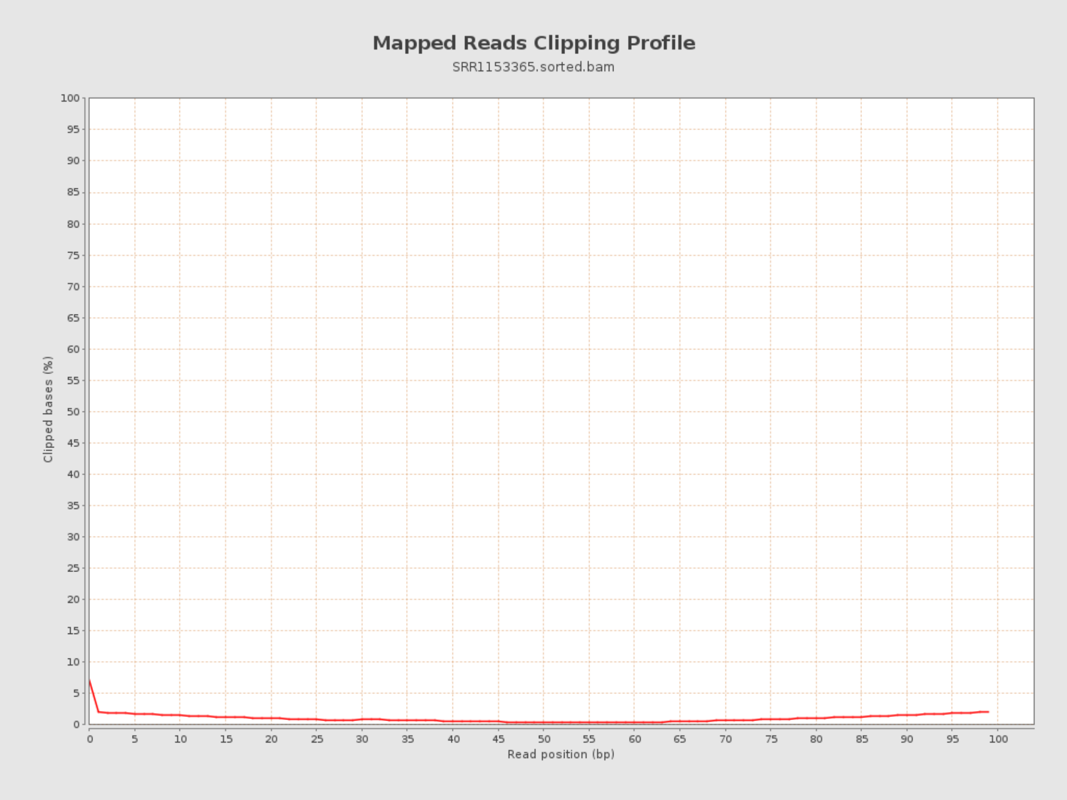
# 8. Results : Mapped Reads Nucleotide Content



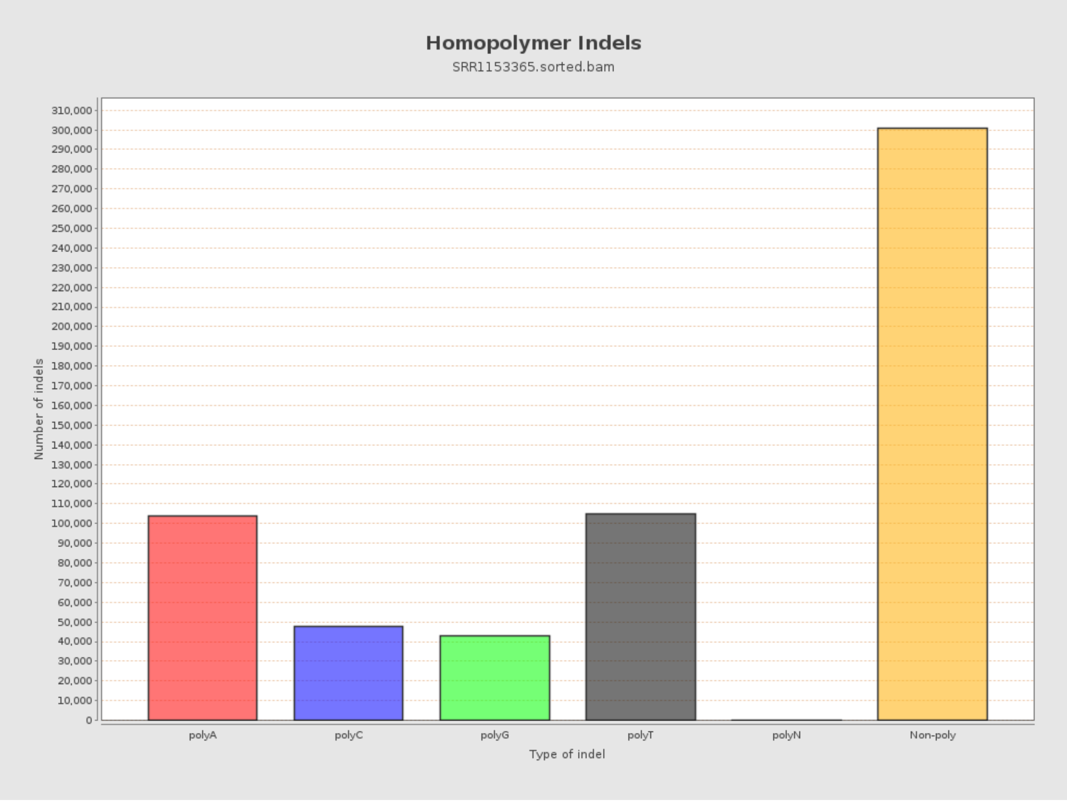
# 9. Results : Mapped Reads GC-content Distribution



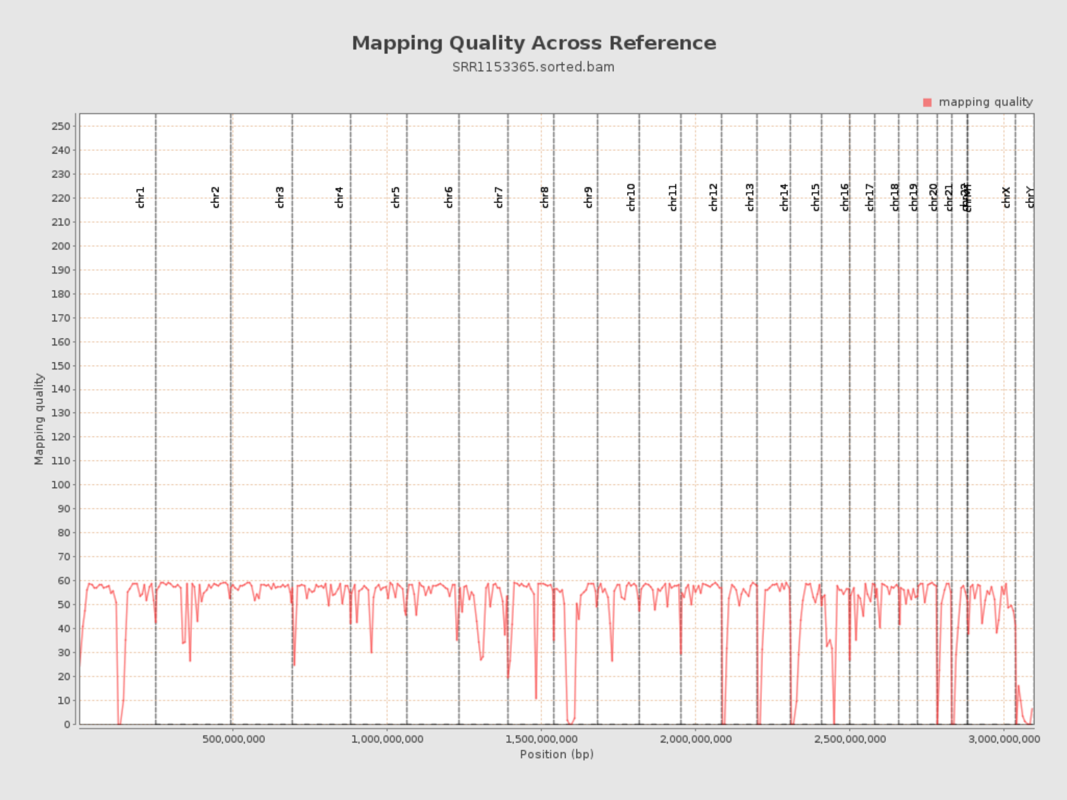
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram