# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/15 16:10:29*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153330.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_SRR1153330 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153330.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Dec 15 16:10:25 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1153330.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 56,190,624 |
| Mapped reads | 55,694,819 / 99.12% |
| Unmapped reads | 495,805 / 0.88% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 442,327 / 0.79% |
| Read min/max/mean length | 30 / 100 / 100.32 |
| Duplicated reads (estimated) | 29,929,029 / 53.26% |
| Duplication rate | 34.34% |
| Clipped reads | 7,457,826 / 13.27% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,459,549,114 / 27% |
| Number/percentage of C's | 1,236,430,953 / 22.87% |
| Number/percentage of T's | 1,490,436,308 / 27.57% |
| Number/percentage of G's | 1,218,260,557 / 22.53% |
| Number/percentage of N's | 1,593,075 / 0.03% |
| GC Percentage | 45.4% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 1.7467 |
| | |

| | |
|---|---|
| Standard Deviation | 18.9307 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 50.37 |

## 2.5. Mismatches and indels

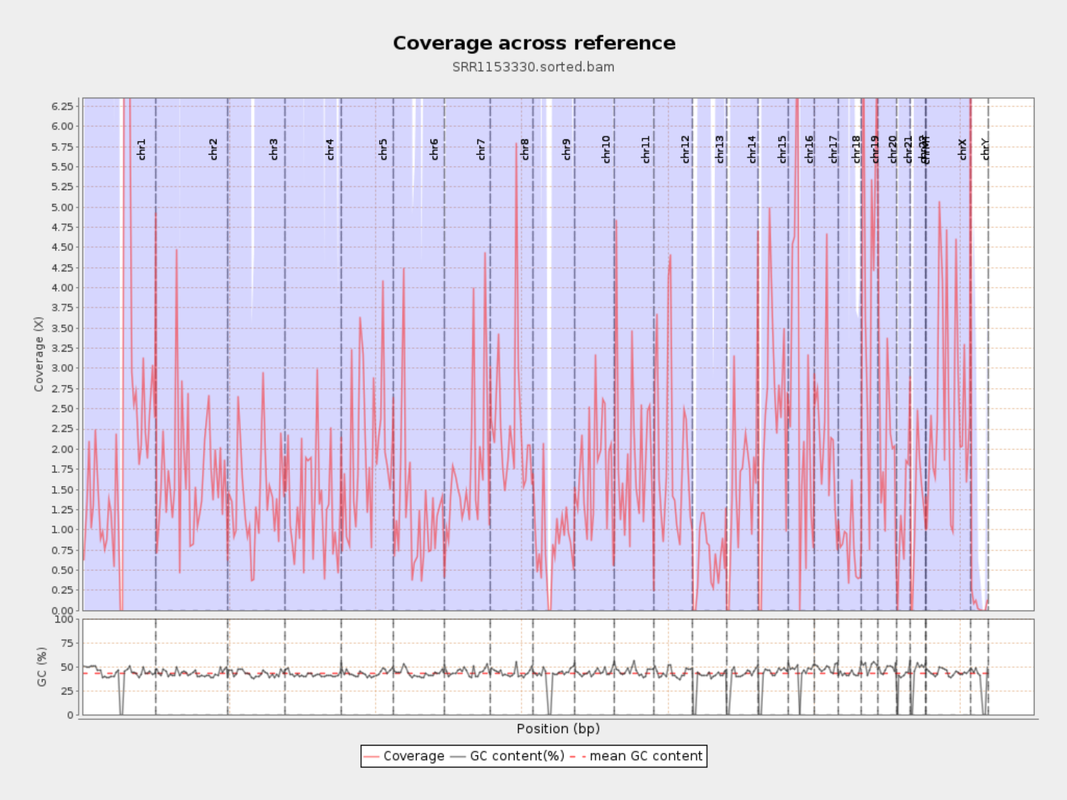
| | |
|---|---|
| General error rate | 0.3% |
| Mismatches | 15,534,493 |
| Insertions | 582,825 |
| Mapped reads with at least one insertion | 1.03% |
| Deletions | 439,169 |
| Mapped reads with at least one deletion | 0.78% |
| Homopolymer indels | 49.57% |

## 2.6. Chromosome stats

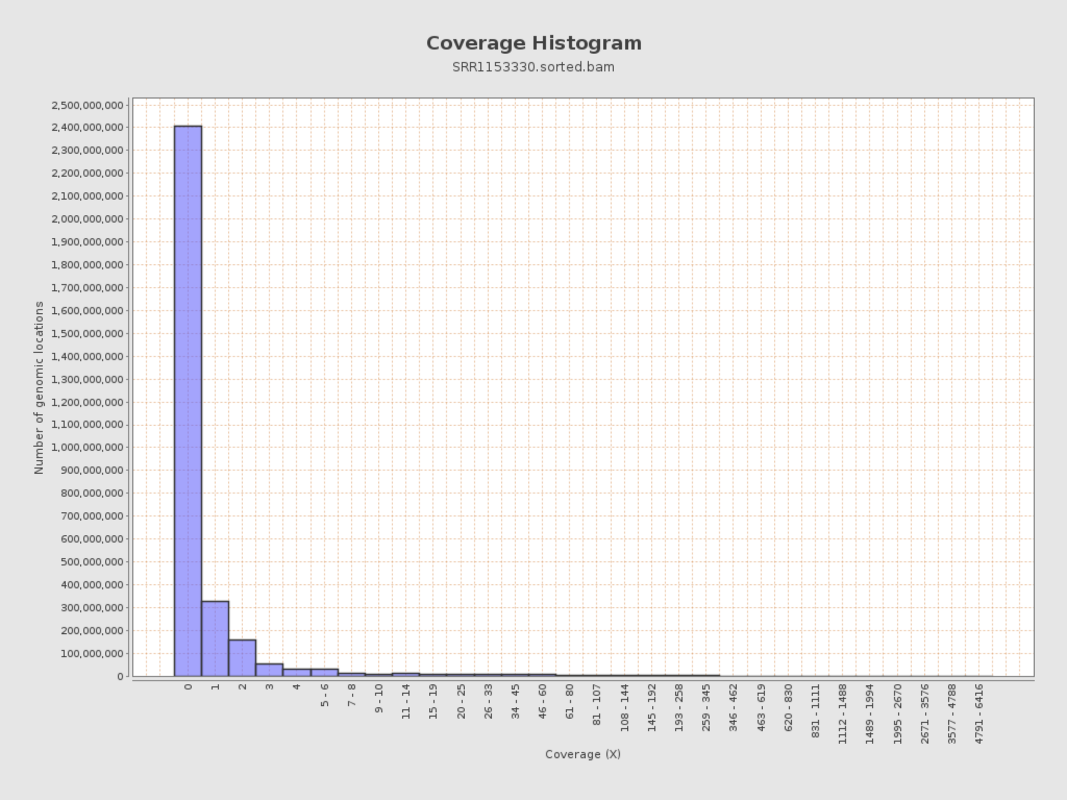
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 559269249 | 2.2438 | 22.1364 |
| chr2 | 243199373 | 408213603 | 1.6785 | 18.6132 |
| chr3 | 198022430 | 277478198 | 1.4012 | 13.5058 |
| chr4 | 191154276 | 253132579 | 1.3242 | 14.297 |
| chr5 | 180915260 | 354267646 | 1.9582 | 19.8523 |
| chr6 | 171115067 | 202709519 | 1.1846 | 13.6429 |
| chr7 | 159138663 | 273830197 | 1.7207 | 21.0734 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 338175064 | 2.3105 | 24.662 |
| chr9 | 141213431 | 115610788 | 0.8187 | 9.1875 |
| chr10 | 135534747 | 238332775 | 1.7585 | 16.4184 |
| chr11 | 135006516 | 256834120 | 1.9024 | 17.5307 |
| chr12 | 133851895 | 267525536 | 1.9987 | 16.8756 |
| chr13 | 115169878 | 73008794 | 0.6339 | 7.3678 |
| chr14 | 107349540 | 163784342 | 1.5257 | 14.2041 |
| chr15 | 102531392 | 240679258 | 2.3474 | 23.5534 |
| chr16 | 90354753 | 231354536 | 2.5605 | 26.818 |
| chr17 | 81195210 | 180379967 | 2.2216 | 20.144 |
| chr18 | 78077248 | 60685439 | 0.7772 | 8.6868 |
| chr19 | 59128983 | 249874715 | 4.2259 | 43.3937 |
| chr20 | 63025520 | 127582479 | 2.0243 | 17.2573 |
| chr21 | 48129895 | 60687913 | 1.2609 | 14.8796 |
| chr22 | 51304566 | 63854553 | 1.2446 | 12.2673 |
| chrMT | 16571 | 23419 | 1.4133 | 4.8114 |
| chrX | 155270560 | 405662502 | 2.6126 | 25.1229 |
| chrY | 59373566 | 4224605 | 0.0712 | 2.7024 |

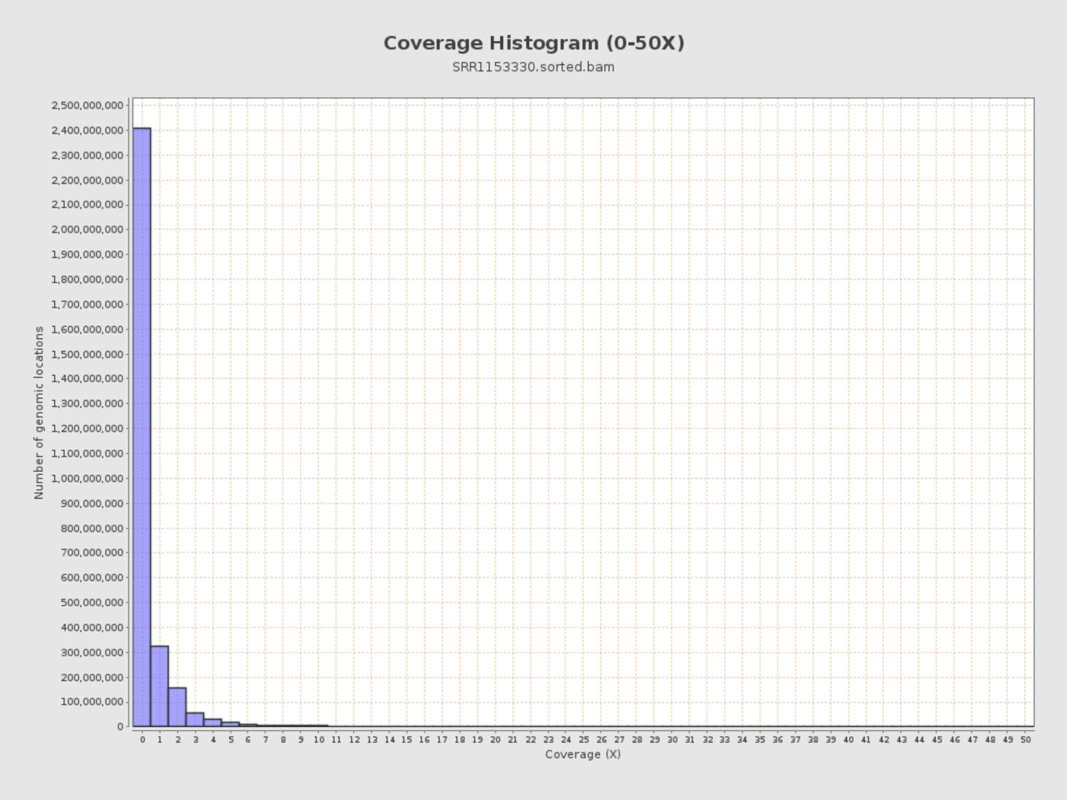
# 3. Results : Coverage across reference



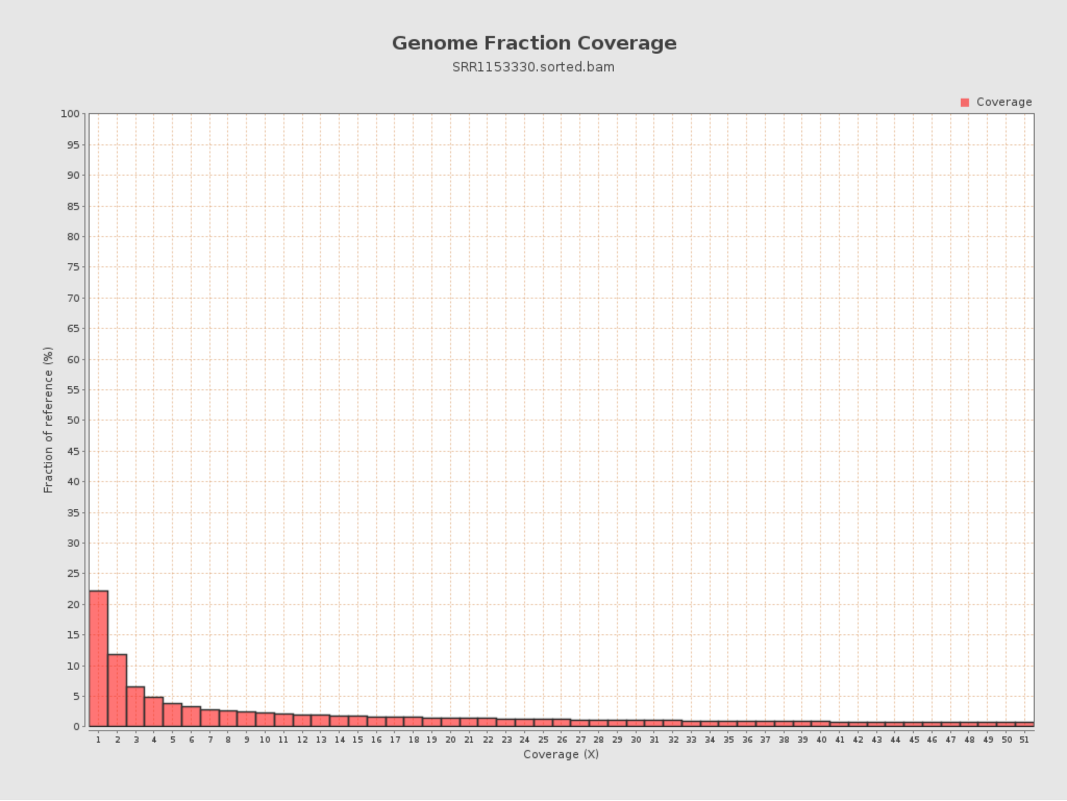
# 4. Results : Coverage Histogram



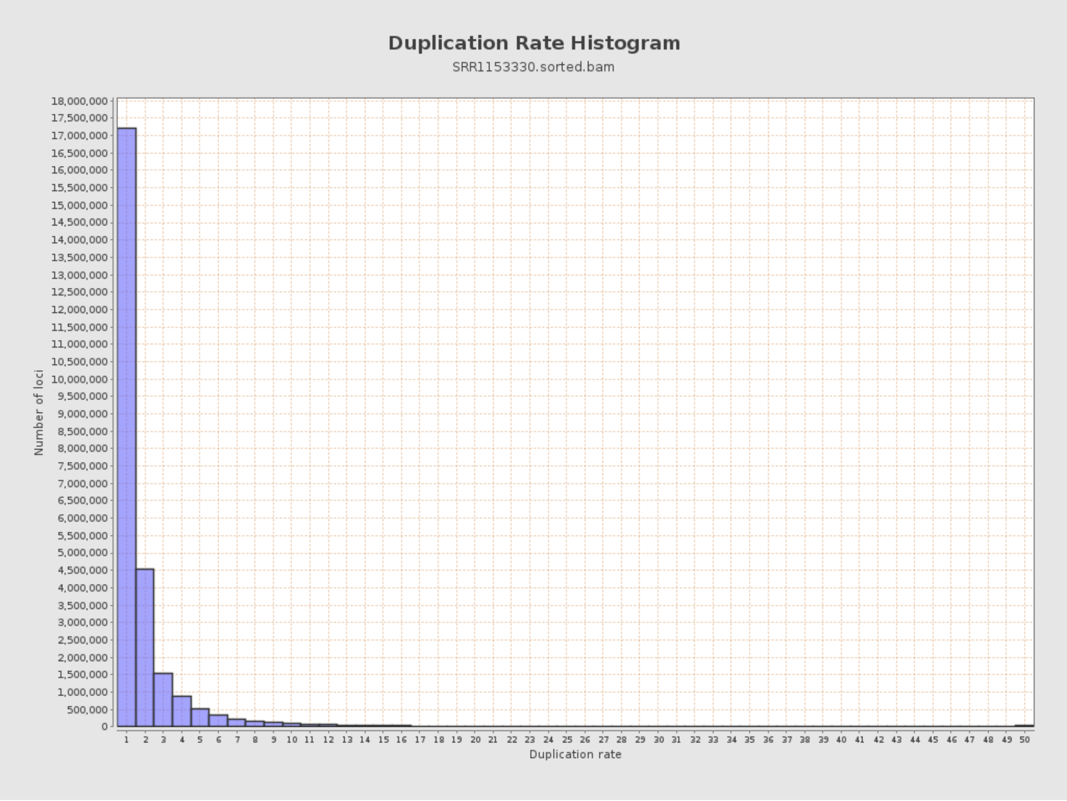
# 5. Results : Coverage Histogram (0-50X)



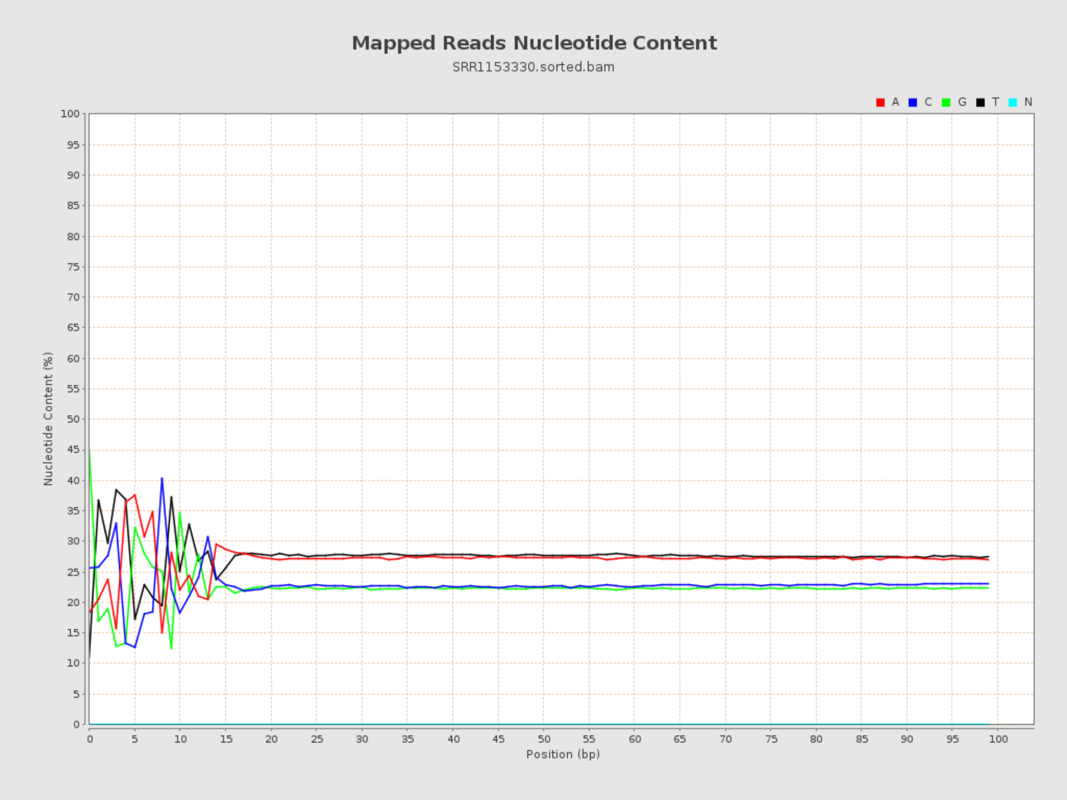
# 6. Results : Genome Fraction Coverage



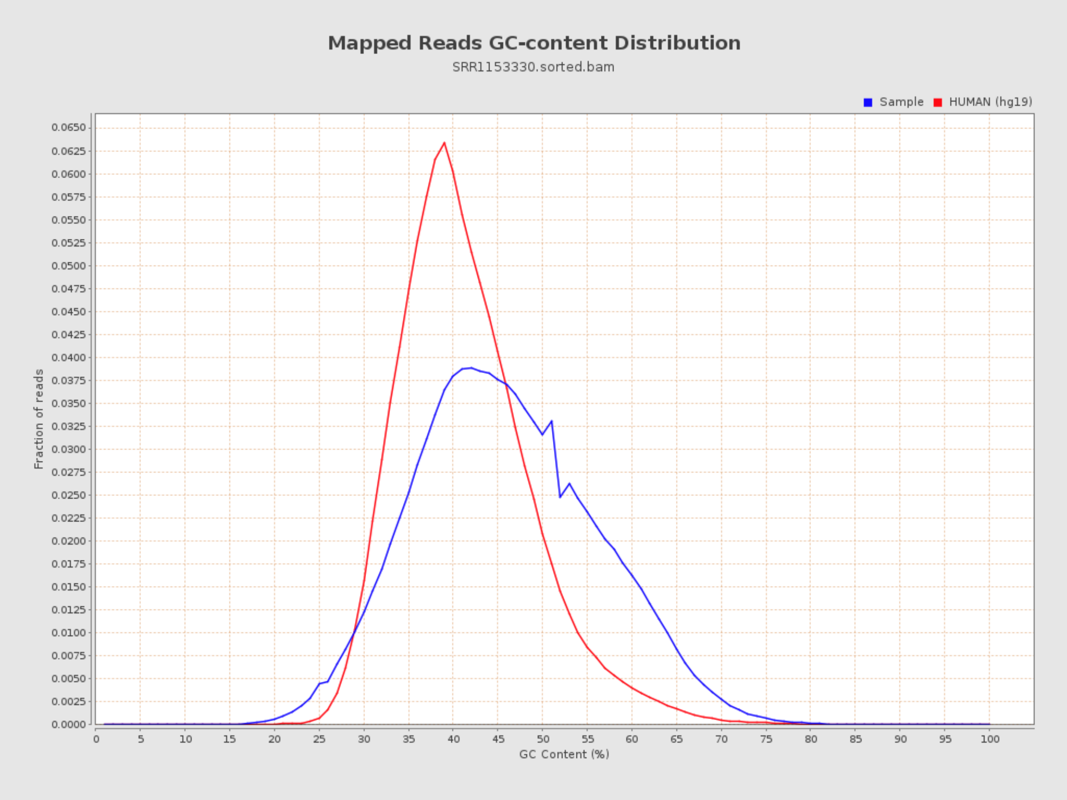
# 7. Results : Duplication Rate Histogram



# 8. Results : Mapped Reads Nucleotide Content

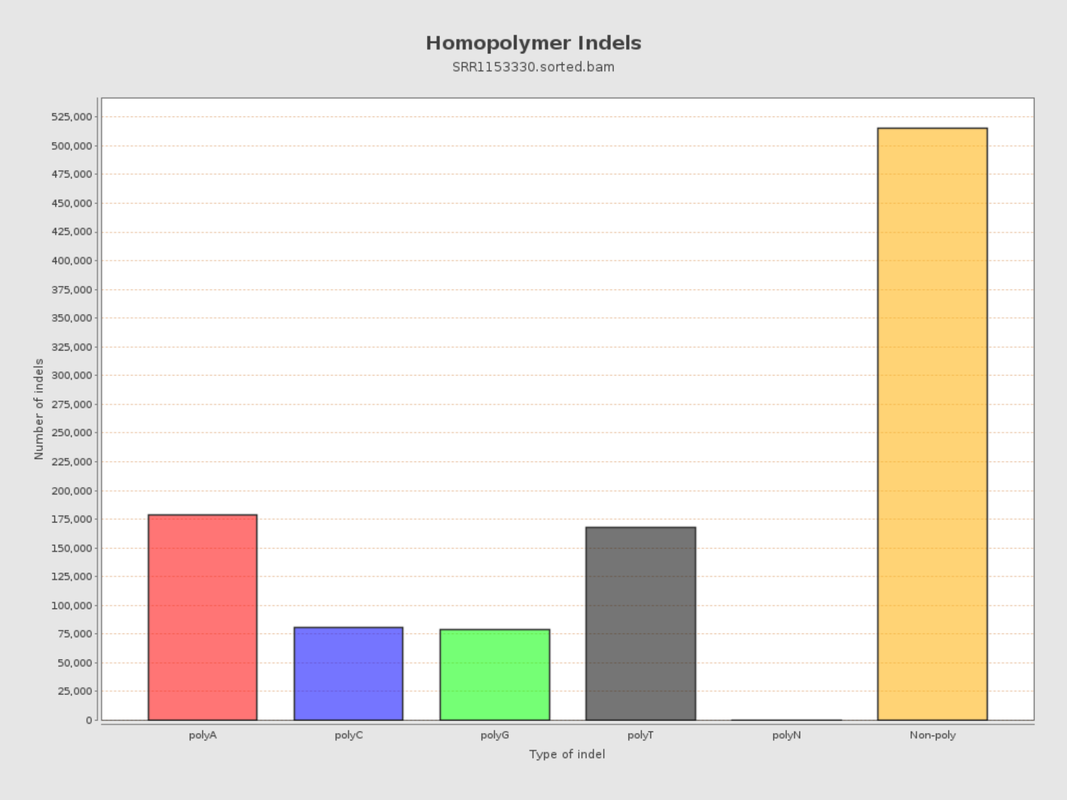


# 9. Results : Mapped Reads GC-content Distribution

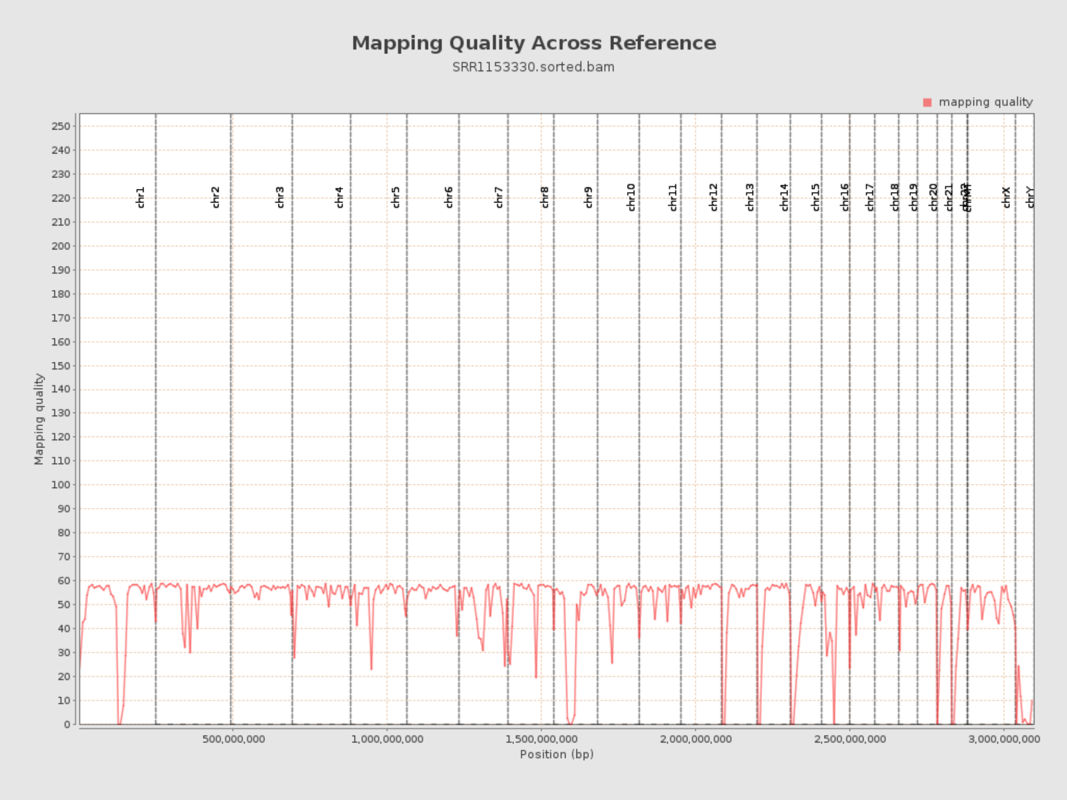


# 10. Results : Mapped Reads Clipping Profile

# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram