# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 06:47:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818905.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_SRR1818905 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818905.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 06:47:22 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1818905.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,668,072 |
| Mapped reads | 1,639,940 / 98.31% |
| Unmapped reads | 28,132 / 1.69% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 23,767 / 1.42% |
| Read min/max/mean length | 30 / 101 / 101.55 |
| Duplicated reads (estimated) | 320,355 / 19.21% |
| Duplication rate | 16.27% |
| Clipped reads | 1,644,777 / 98.6% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 44,004,189 / 28.98% |
| Number/percentage of C's | 31,118,848 / 20.5% |
| Number/percentage of T's | 42,782,527 / 28.18% |
| Number/percentage of G's | 33,927,868 / 22.35% |
| Number/percentage of N's | 2,145 / 0% |
| GC Percentage | 42.84% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0491 |
| | |

| | |
|---|---|
| Standard Deviation | 0.631 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 49.22 |

## 2.5. Mismatches and indels

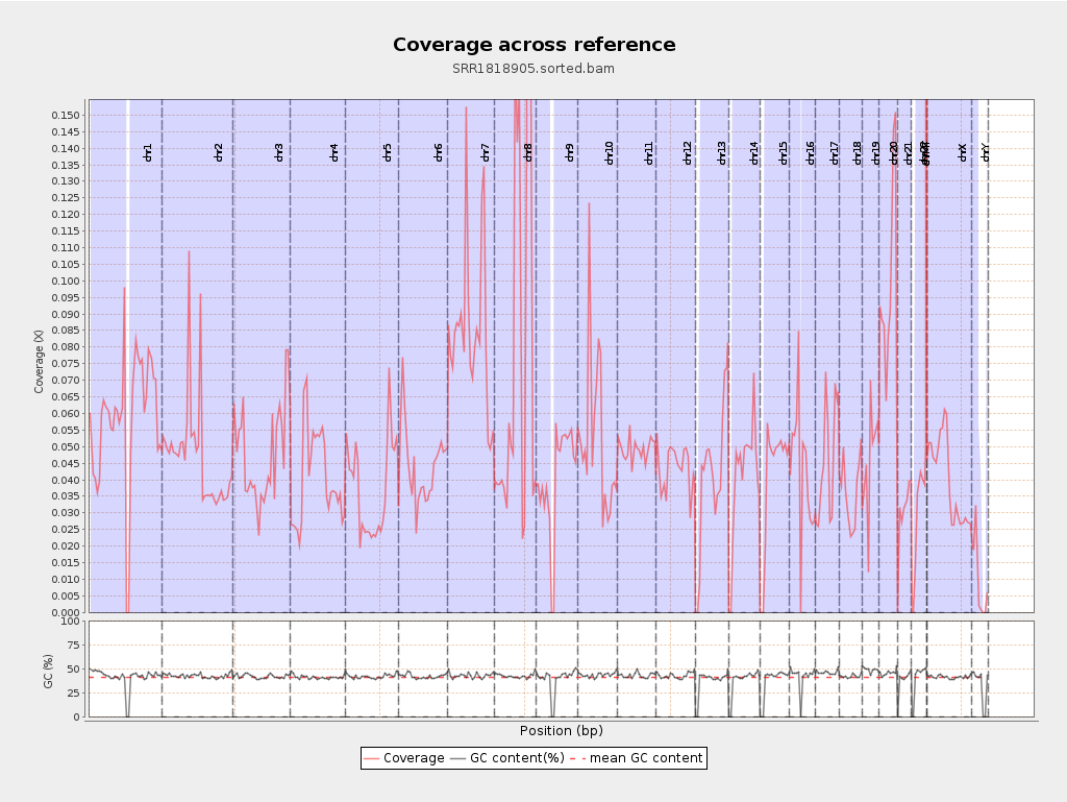
| | |
|---|---|
| General error rate | 0.65% |
| Mismatches | 929,900 |
| Insertions | 22,056 |
| Mapped reads with at least one insertion | 1.3% |
| Deletions | 50,023 |
| Mapped reads with at least one deletion | 2.97% |
| Homopolymer indels | 40.64% |

## 2.6. Chromosome stats

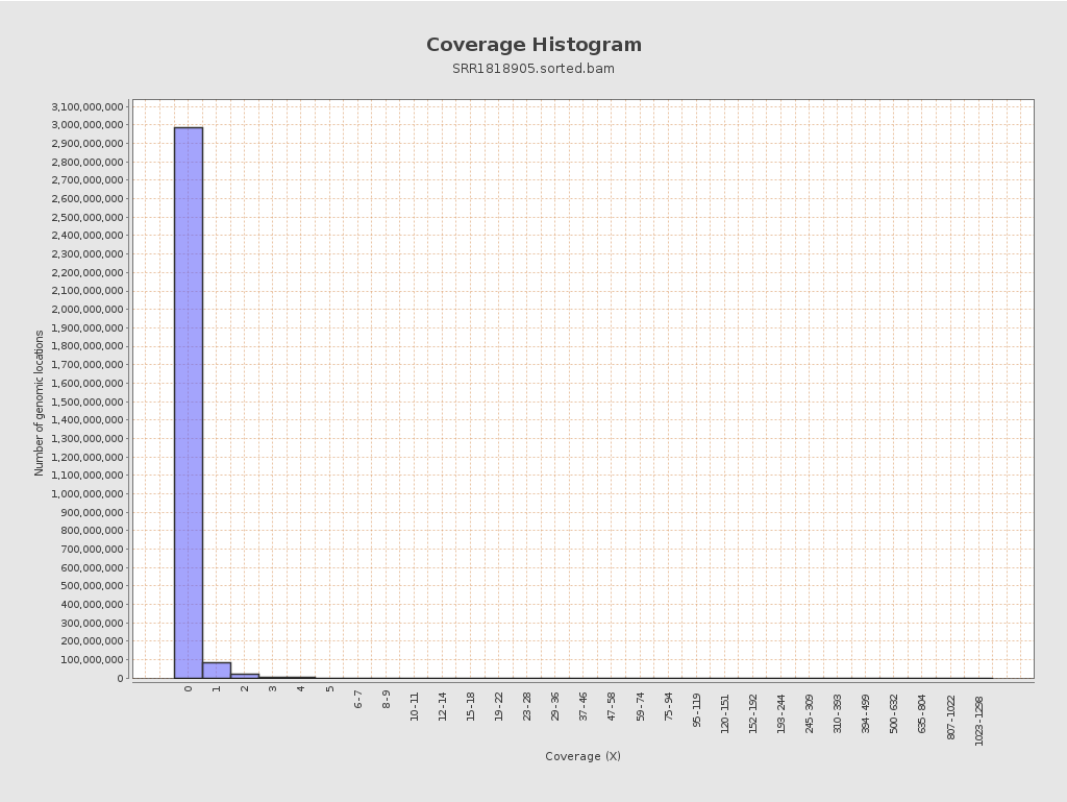
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 14509954 | 0.0582 | 0.9767 |
| chr2 | 243199373 | 11480333 | 0.0472 | 0.9117 |
| chr3 | 198022430 | 9452096 | 0.0477 | 0.2843 |
| chr4 | 191154276 | 7663315 | 0.0401 | 0.3506 |
| chr5 | 180915260 | 6727858 | 0.0372 | 0.2682 |
| chr6 | 171115067 | 7542141 | 0.0441 | 0.3049 |
| chr7 | 159138663 | 13627015 | 0.0856 | 1.3839 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 12953500 | 0.0885 | 0.5072 |
| chr9 | 141213431 | 5686356 | 0.0403 | 0.517 |
| chr10 | 135534747 | 7051129 | 0.052 | 0.8286 |
| chr11 | 135006516 | 6640999 | 0.0492 | 0.3648 |
| chr12 | 133851895 | 5868951 | 0.0438 | 0.2732 |
| chr13 | 115169878 | 4702948 | 0.0408 | 0.26 |
| chr14 | 107349540 | 4398990 | 0.041 | 0.2956 |
| chr15 | 102531392 | 4200172 | 0.041 | 0.2628 |
| chr16 | 90354753 | 3816867 | 0.0422 | 0.6459 |
| chr17 | 81195210 | 3797394 | 0.0468 | 0.3802 |
| chr18 | 78077248 | 2823687 | 0.0362 | 0.5938 |
| chr19 | 59128983 | 2718235 | 0.046 | 0.8615 |
| chr20 | 63025520 | 6246898 | 0.0991 | 0.4456 |
| chr21 | 48129895 | 1459797 | 0.0303 | 0.2827 |
| chr22 | 51304566 | 1426805 | 0.0278 | 0.2467 |
| chrMT | 16571 | 349141 | 21.0694 | 12.4377 |
| chrX | 155270560 | 6223205 | 0.0401 | 0.3155 |
| chrY | 59373566 | 566320 | 0.0095 | 0.7389 |

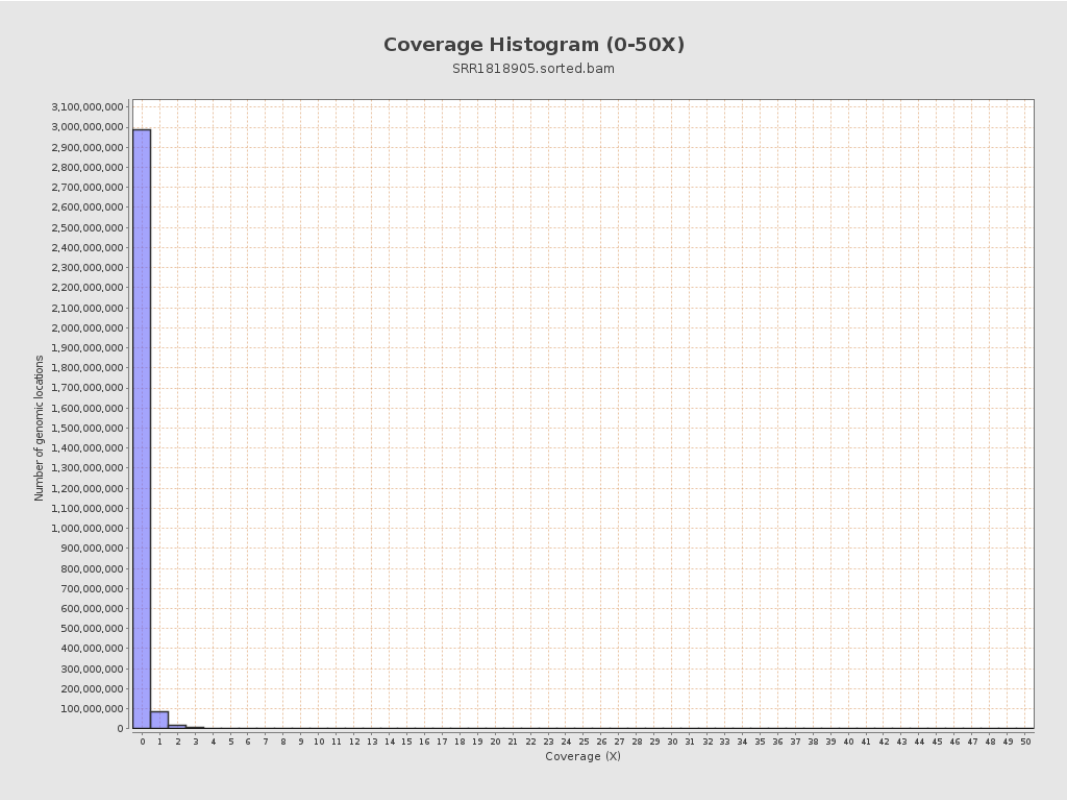
# 3. Results : Coverage across reference



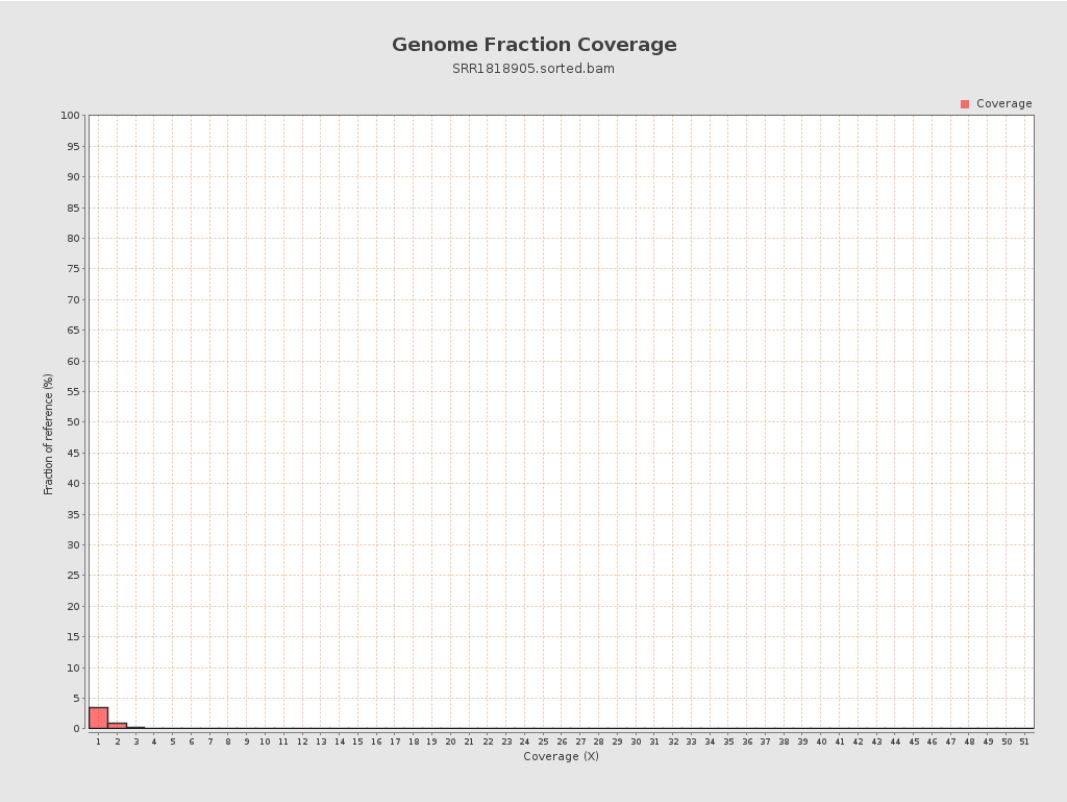
# 4. Results : Coverage Histogram



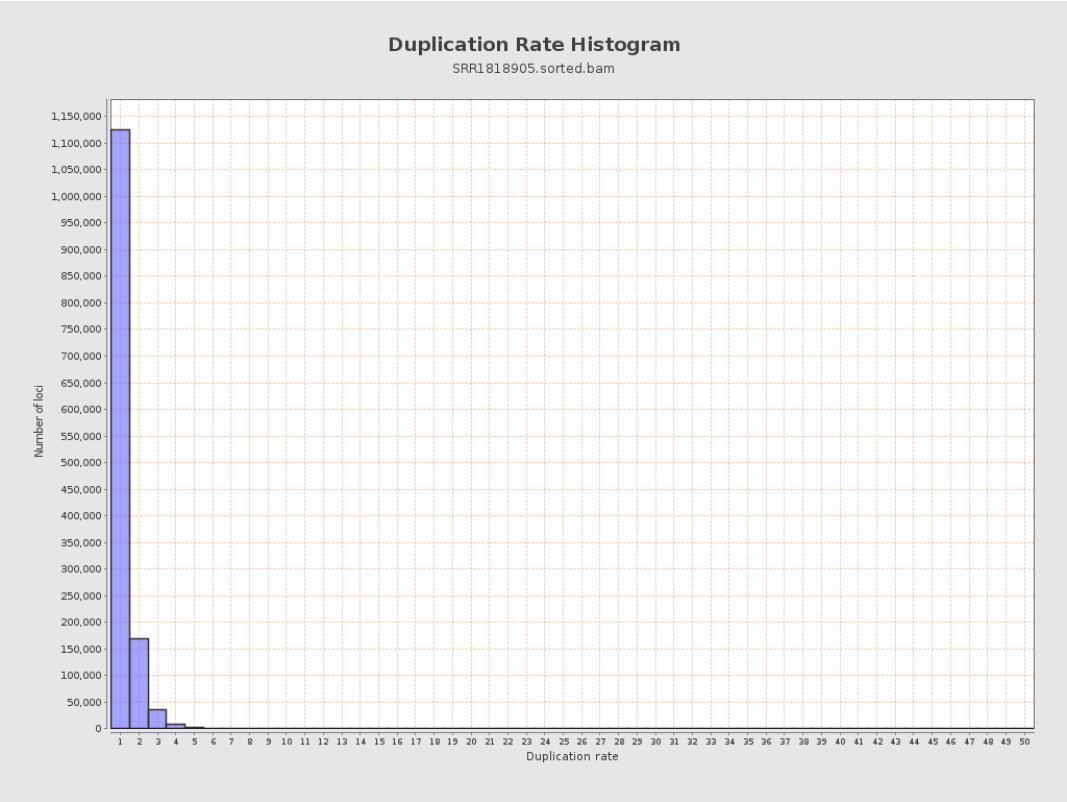
# 5. Results : Coverage Histogram (0-50X)



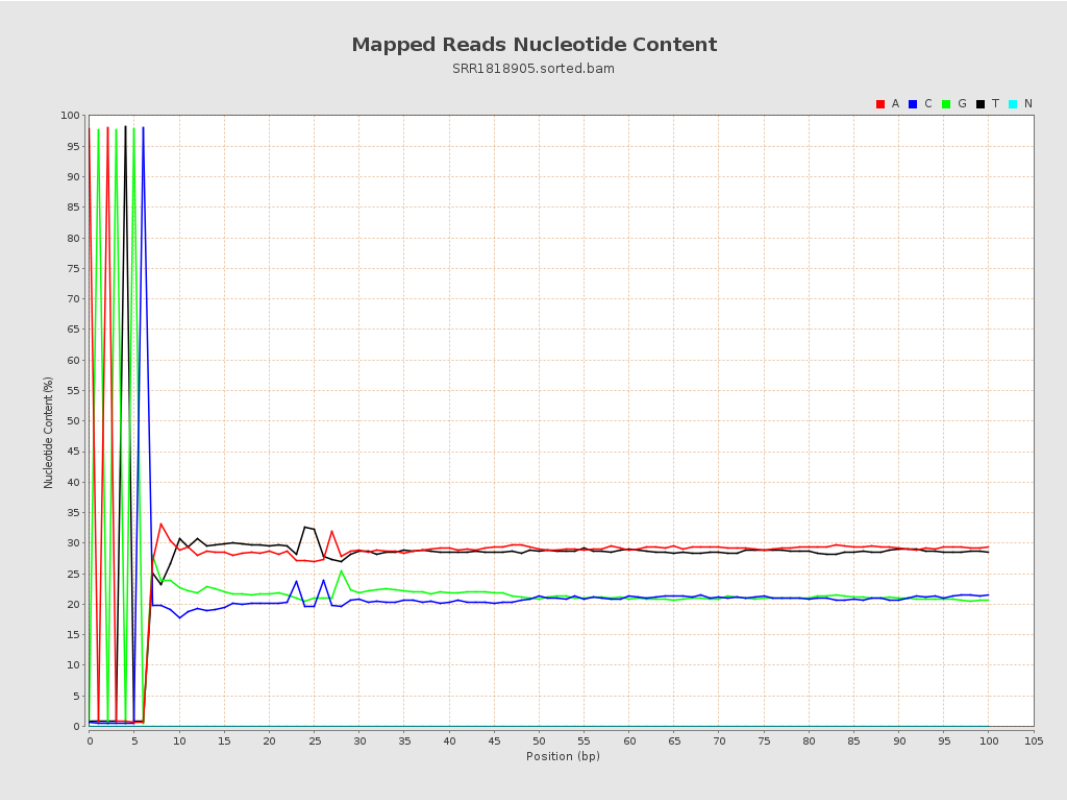
# 6. Results : Genome Fraction Coverage



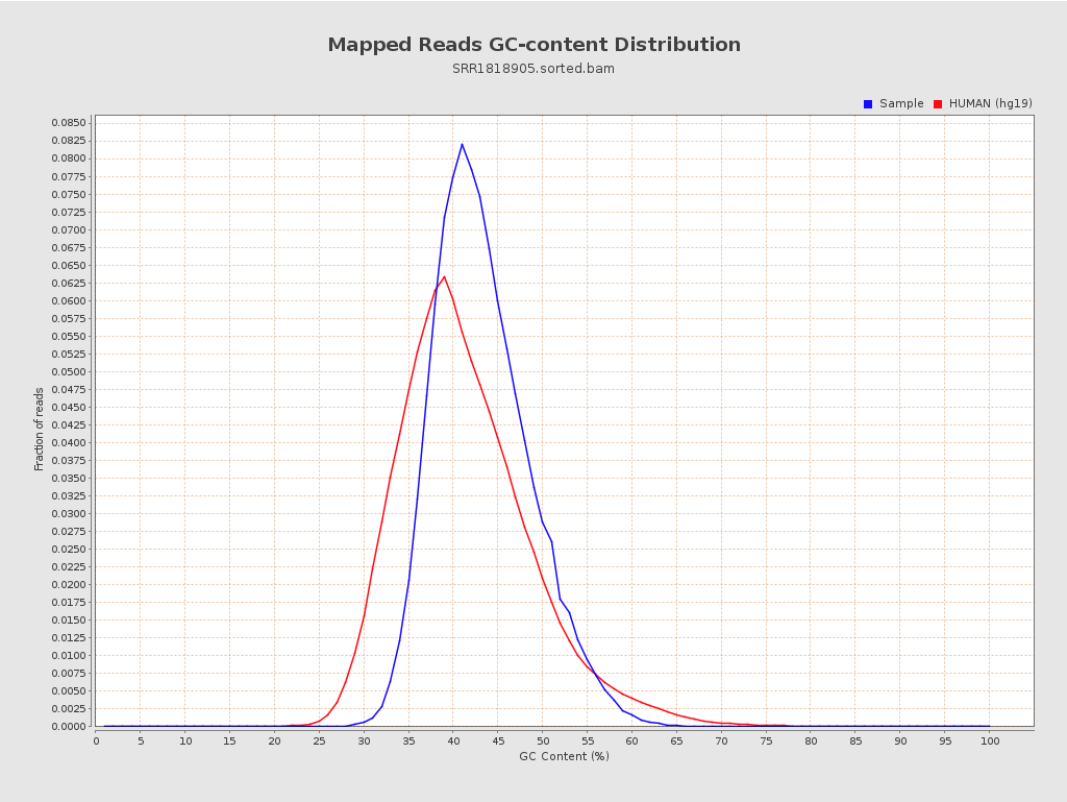
# 7. Results : Duplication Rate Histogram



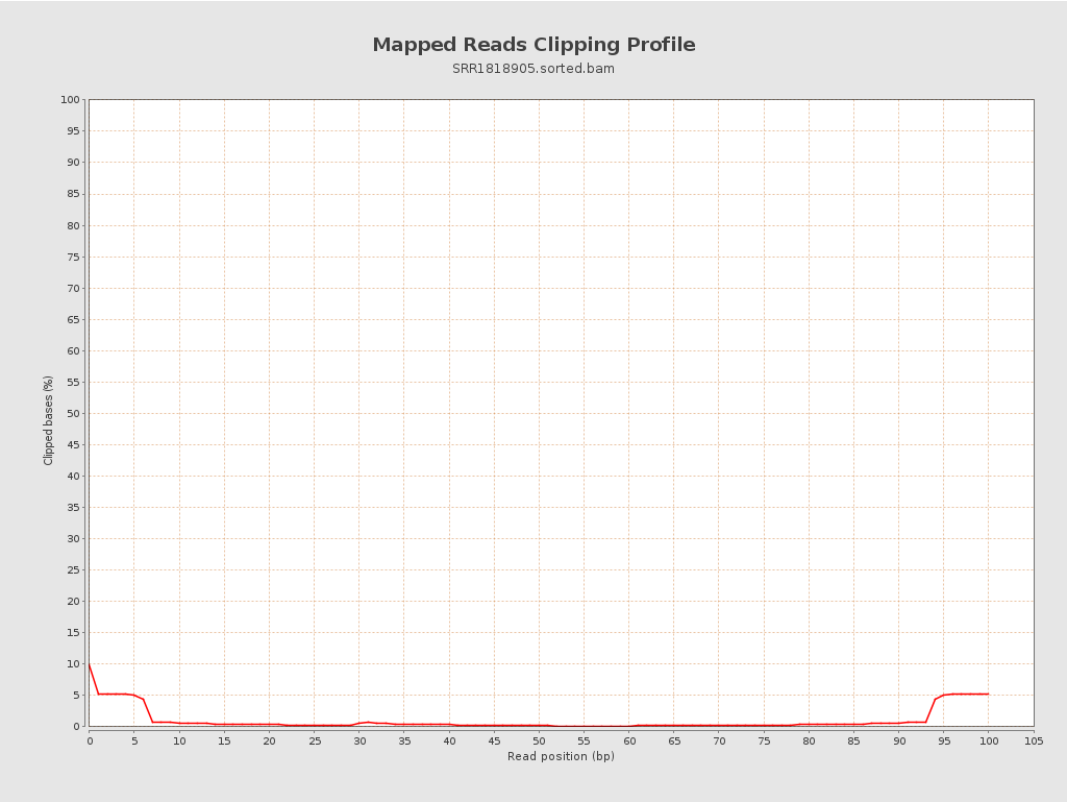
# 8. Results : Mapped Reads Nucleotide Content



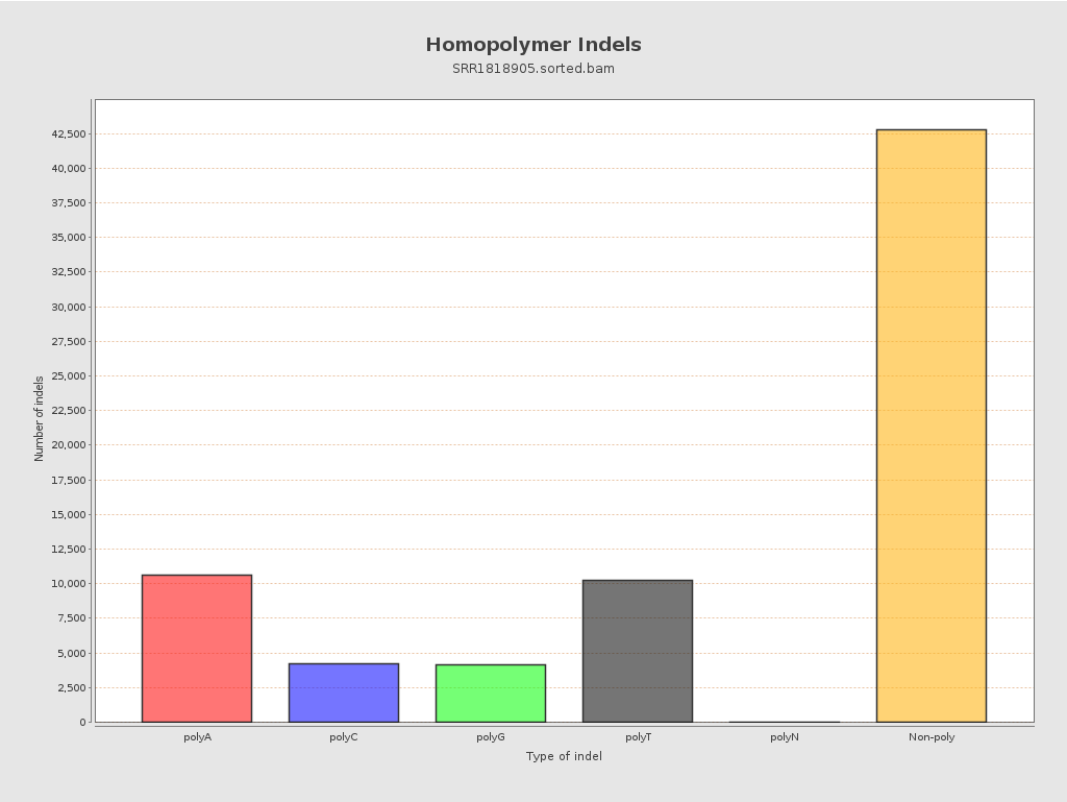
# 9. Results : Mapped Reads GC-content Distribution



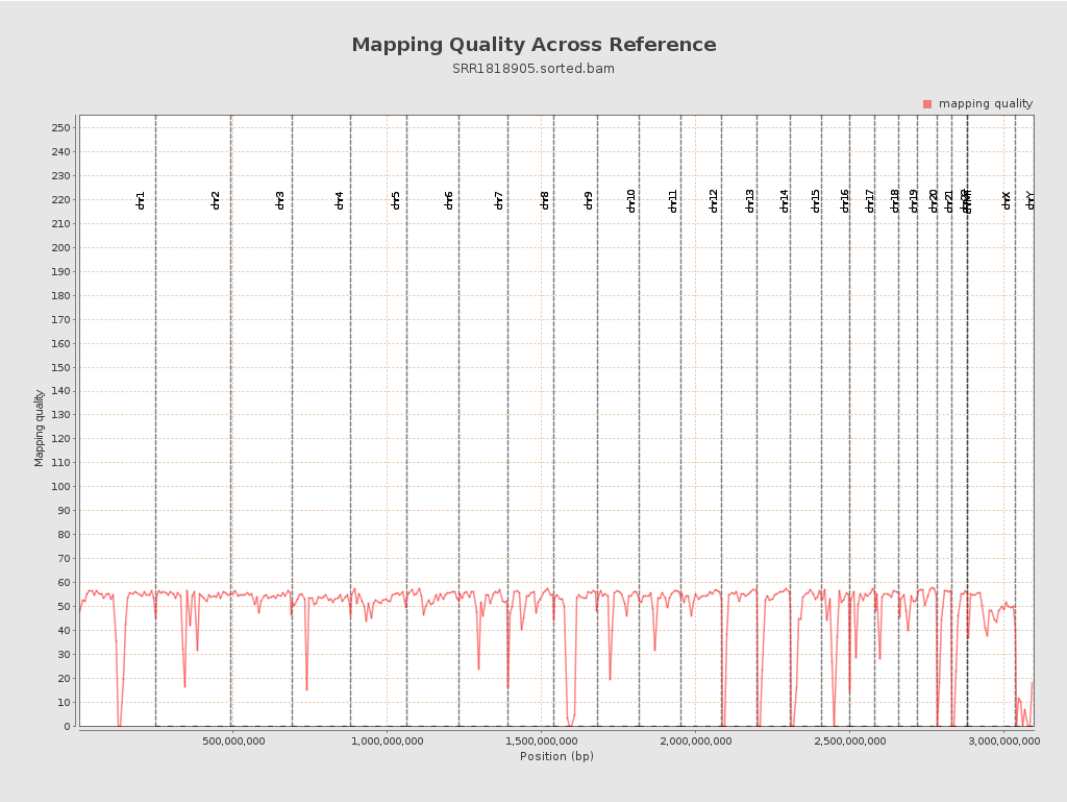
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram