# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/20 06:46:58*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR090130.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_SRR090130 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090130.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Apr 20 06:46:57 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR090130.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 18,568,594 |
| Mapped reads | 15,118,093 / 81.42% |
| Unmapped reads | 3,450,501 / 18.58% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 747 / 0% |
| Read min/max/mean length | 30 / 48 / 48 |
| Duplicated reads (estimated) | 2,587,421 / 13.93% |
| Duplication rate | 11.84% |
| Clipped reads | 1,644,543 / 8.86% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 208,432,199 / 29.36% |
| Number/percentage of C's | 146,772,730 / 20.67% |
| Number/percentage of T's | 202,627,807 / 28.54% |
| Number/percentage of G's | 152,042,146 / 21.42% |
| Number/percentage of N's | 36,245 / 0.01% |
| GC Percentage | 42.09% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.2294 |
| | |

| | |
|---|---|
| Standard Deviation | 1.5769 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.03 |

## 2.5. Mismatches and indels

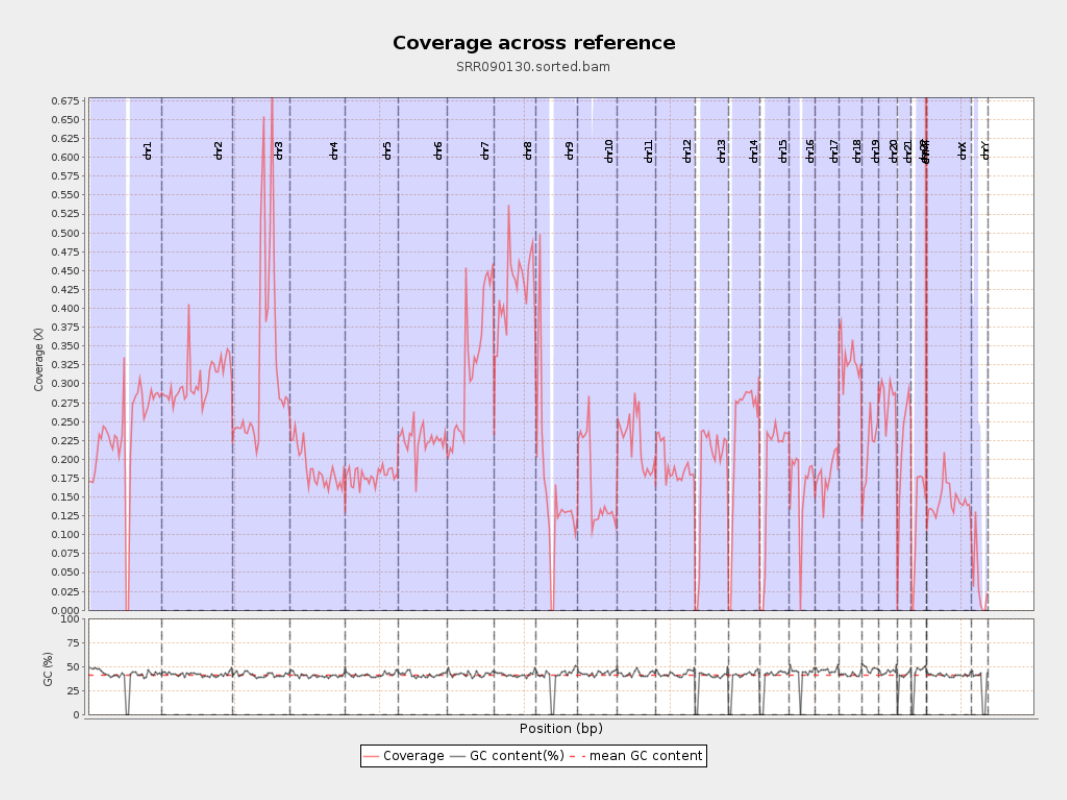
| | |
|---|---|
| General error rate | 0.49% |
| Mismatches | 3,472,615 |
| Insertions | 27,482 |
| Mapped reads with at least one insertion | 0.18% |
| Deletions | 87,509 |
| Mapped reads with at least one deletion | 0.58% |
| Homopolymer indels | 46.04% |

## 2.6. Chromosome stats

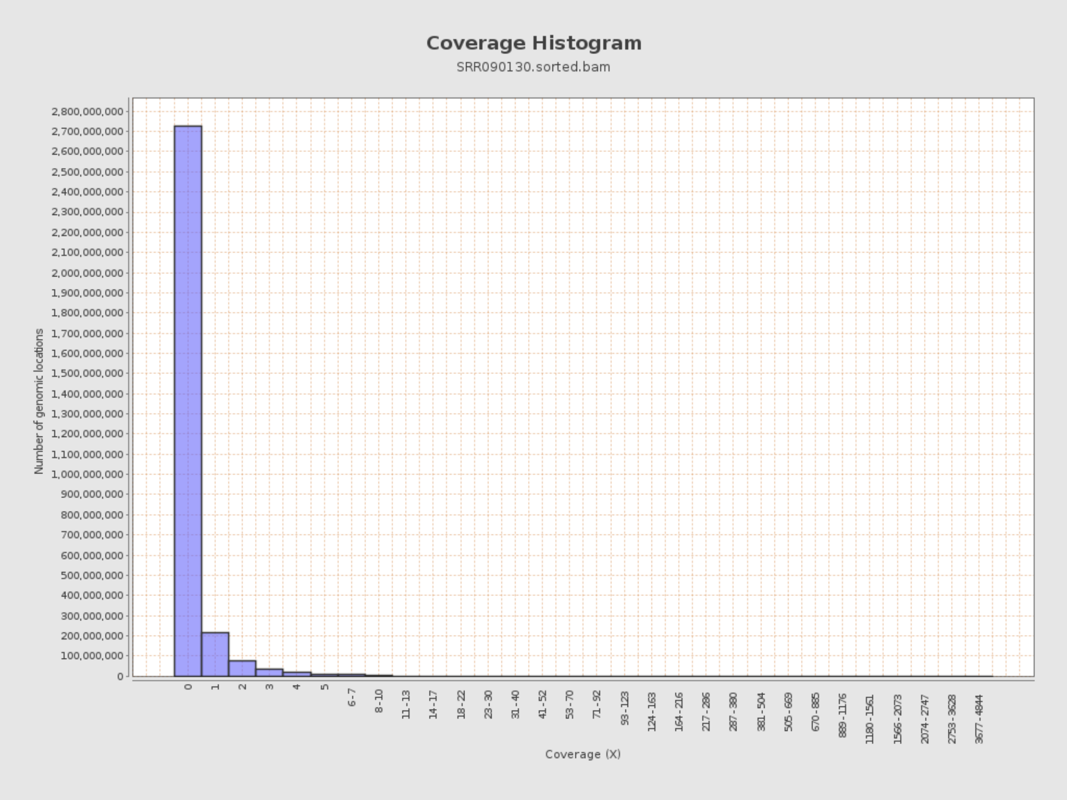
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 58037980 | 0.2328 | 2.8289 |
| chr2 | 243199373 | 73989371 | 0.3042 | 2.0258 |
| chr3 | 198022430 | 64252090 | 0.3245 | 1.028 |
| chr4 | 191154276 | 35934890 | 0.188 | 0.8094 |
| chr5 | 180915260 | 32163143 | 0.1778 | 0.7407 |
| chr6 | 171115067 | 38675874 | 0.226 | 0.9508 |
| chr7 | 159138663 | 51984696 | 0.3267 | 3.119 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 62400263 | 0.4263 | 2.2676 |
| chr9 | 141213431 | 21954608 | 0.1555 | 1.0843 |
| chr10 | 135534747 | 22153945 | 0.1635 | 1.1676 |
| chr11 | 135006516 | 29992586 | 0.2222 | 1.1548 |
| chr12 | 133851895 | 25668898 | 0.1918 | 0.8093 |
| chr13 | 115169878 | 21193015 | 0.184 | 0.7404 |
| chr14 | 107349540 | 25057663 | 0.2334 | 0.9 |
| chr15 | 102531392 | 18955190 | 0.1849 | 0.755 |
| chr16 | 90354753 | 14870038 | 0.1646 | 0.7751 |
| chr17 | 81195210 | 14510117 | 0.1787 | 0.8205 |
| chr18 | 78077248 | 26009639 | 0.3331 | 1.837 |
| chr19 | 59128983 | 12767219 | 0.2159 | 1.6961 |
| chr20 | 63025520 | 17561445 | 0.2786 | 0.9933 |
| chr21 | 48129895 | 10268073 | 0.2133 | 0.9713 |
| chr22 | 51304566 | 6201164 | 0.1209 | 0.6036 |
| chrMT | 16571 | 910824 | 54.9649 | 35.5075 |
| chrX | 155270560 | 22508875 | 0.145 | 0.9001 |
| chrY | 59373566 | 2023612 | 0.0341 | 1.3273 |

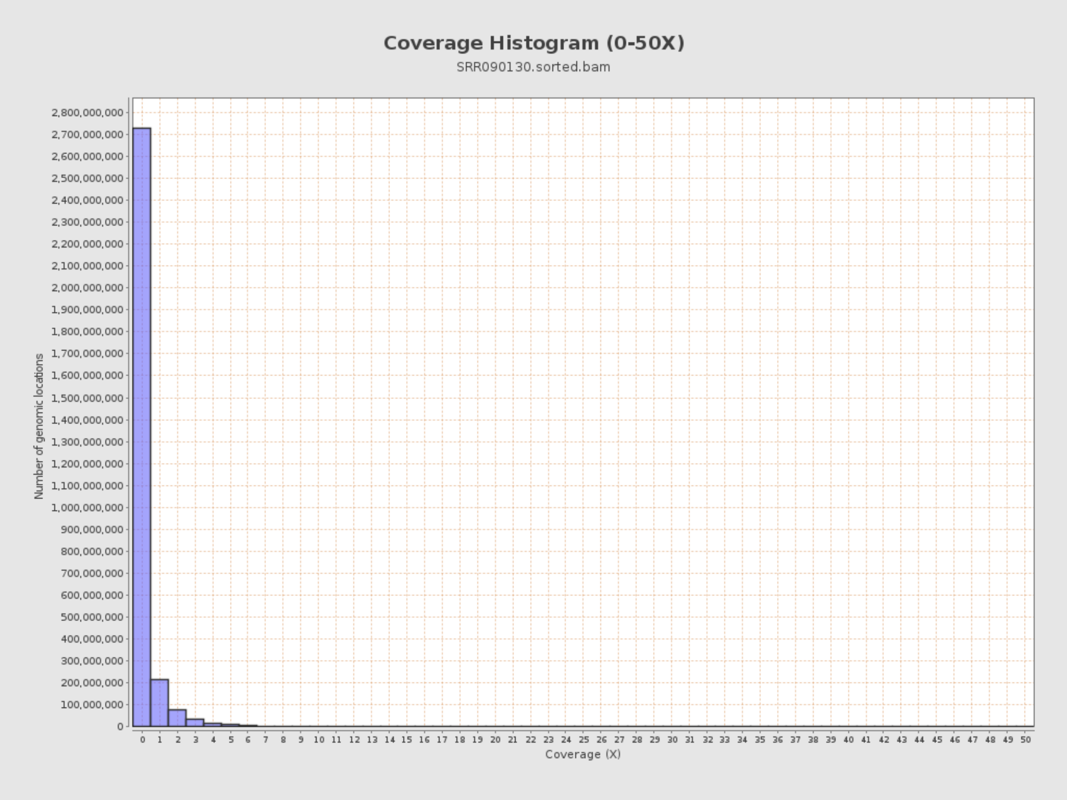
# 3. Results : Coverage across reference



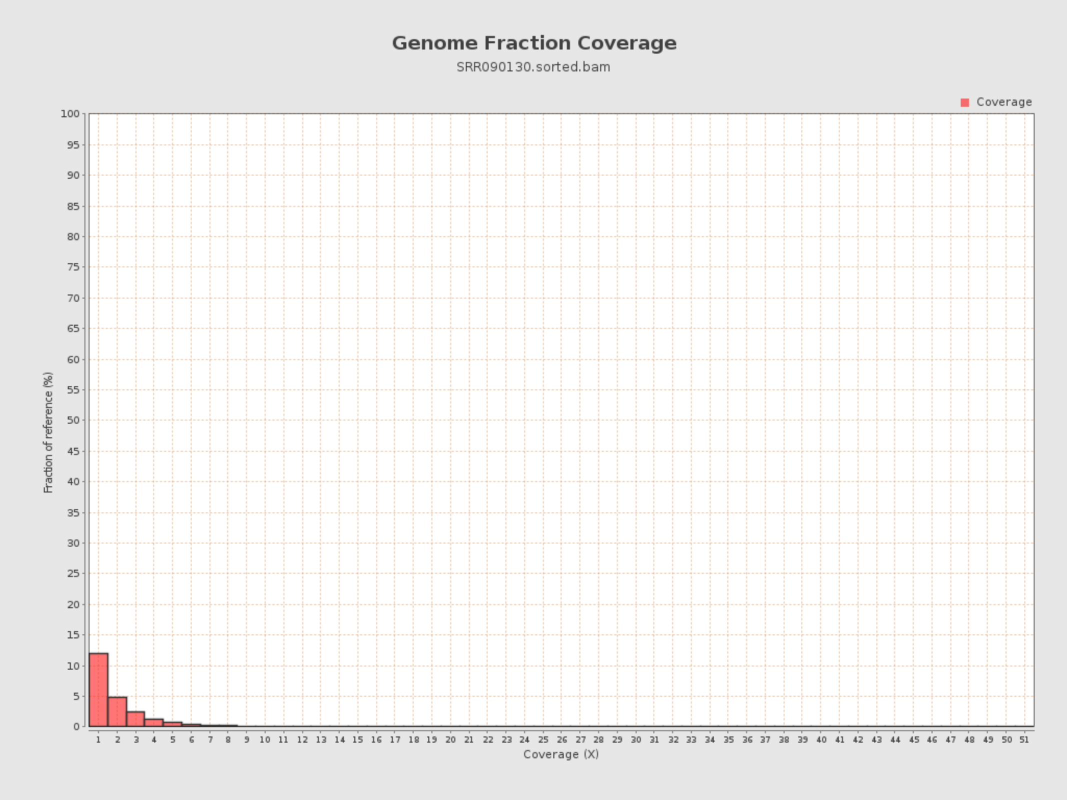
# 4. Results : Coverage Histogram



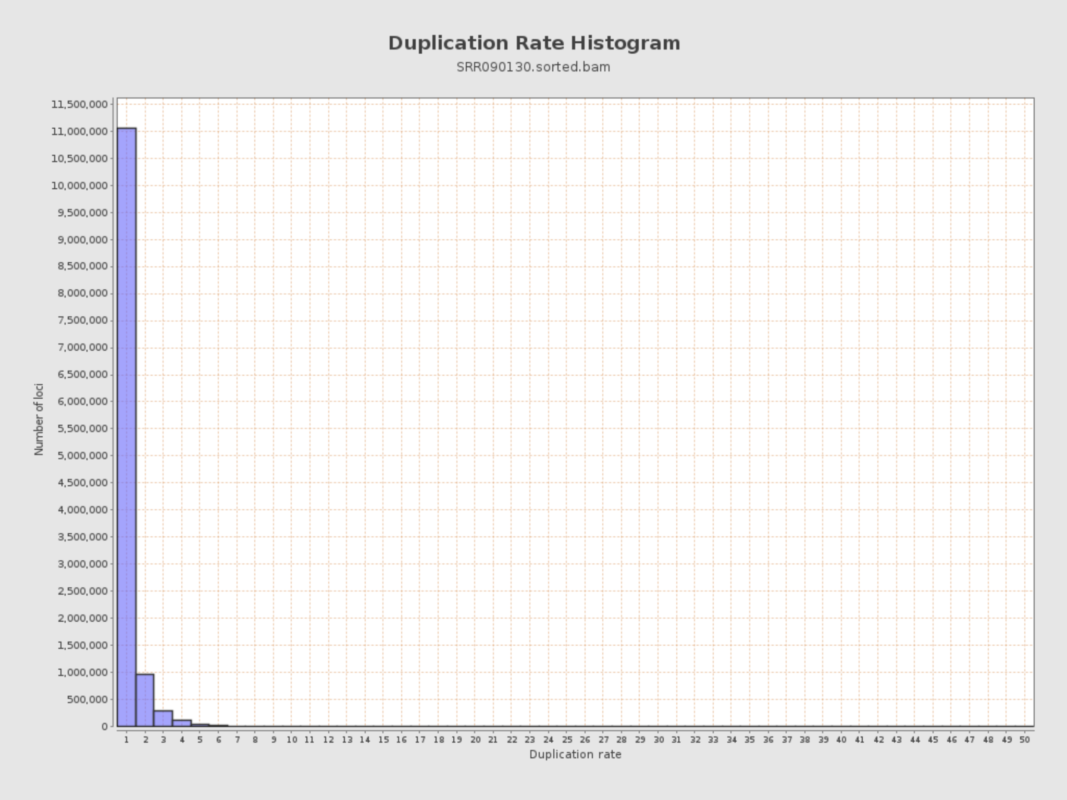
# 5. Results : Coverage Histogram (0-50X)



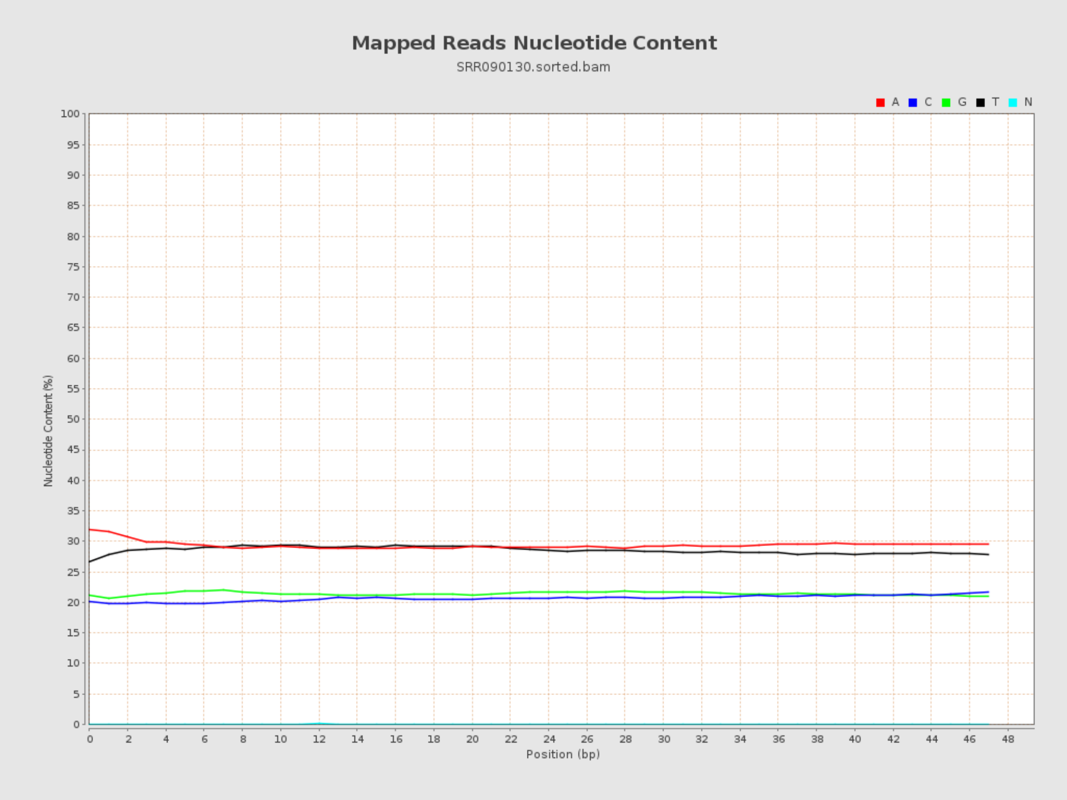
# 6. Results : Genome Fraction Coverage



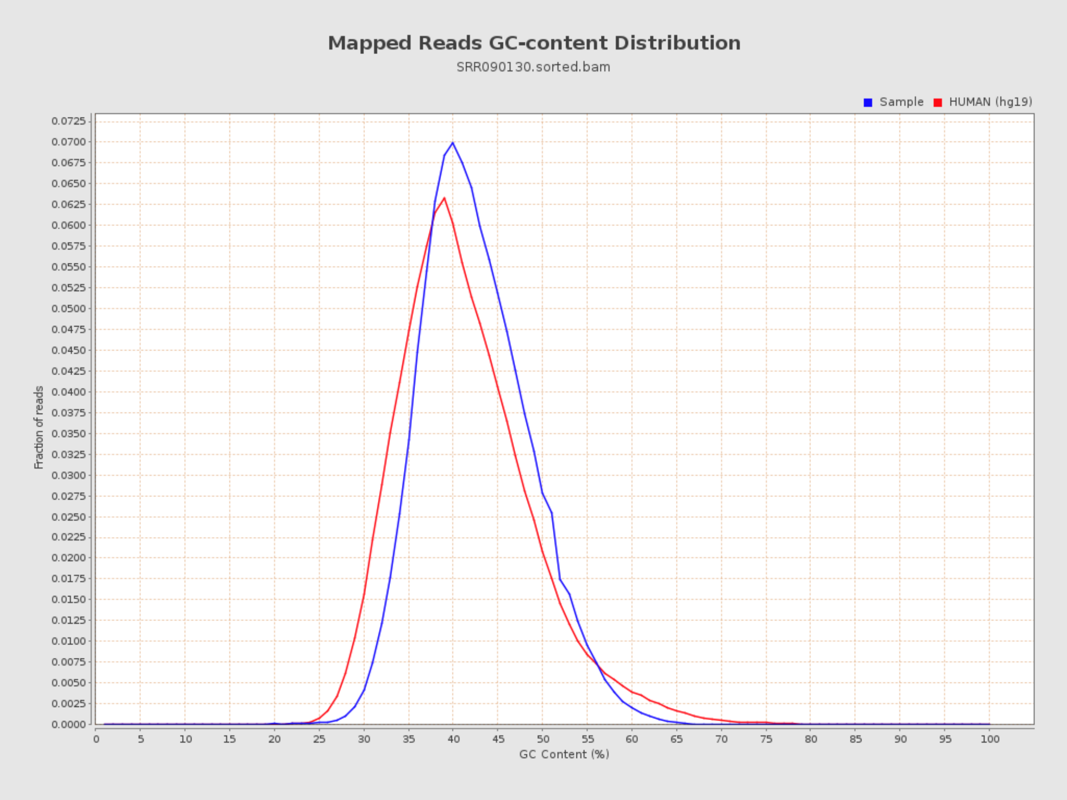
# 7. Results : Duplication Rate Histogram



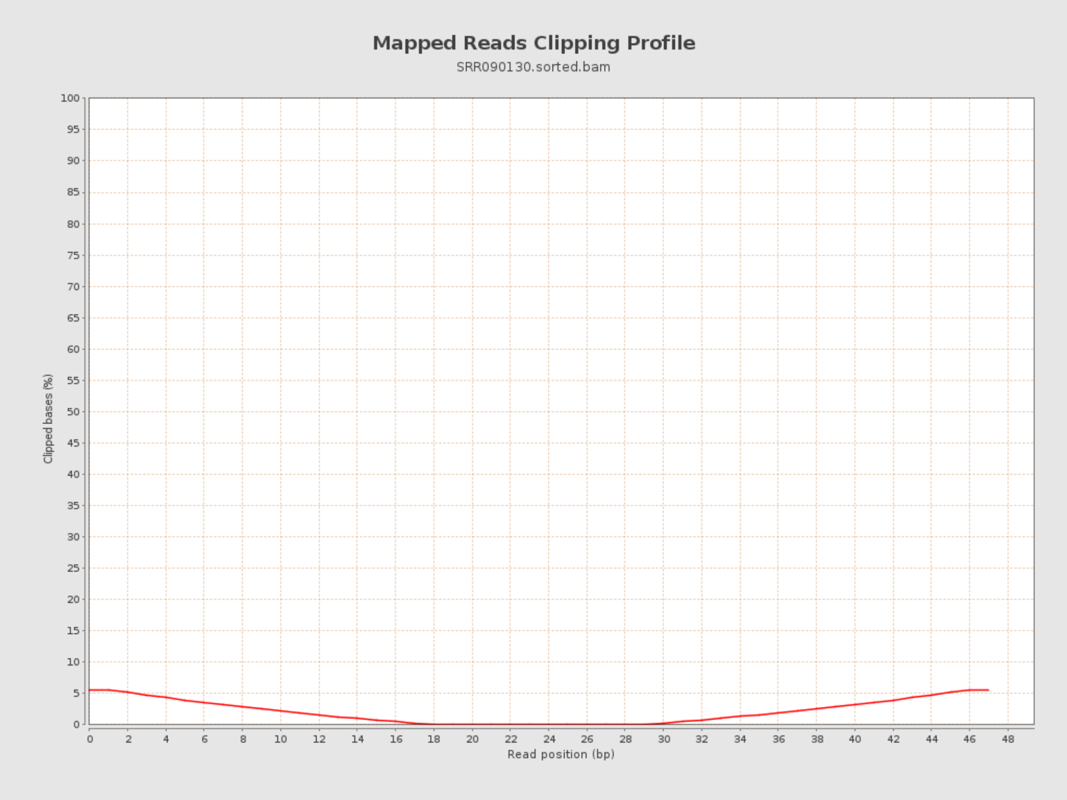
# 8. Results : Mapped Reads Nucleotide Content



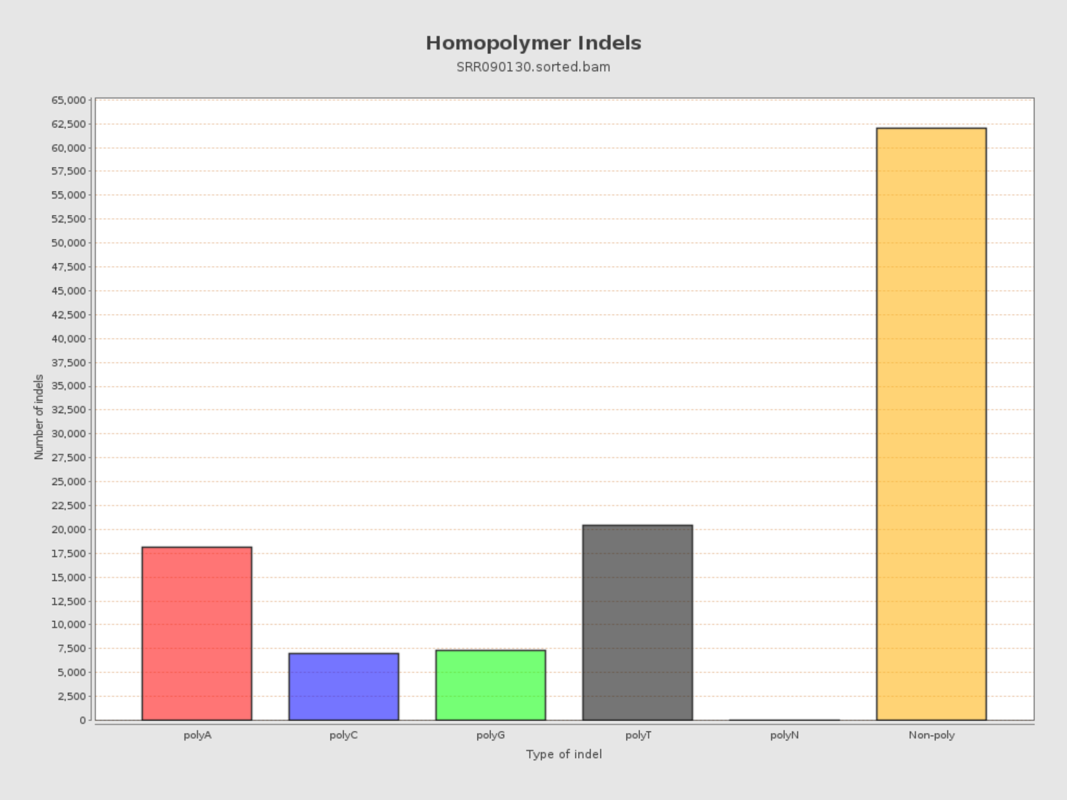
# 9. Results : Mapped Reads GC-content Distribution



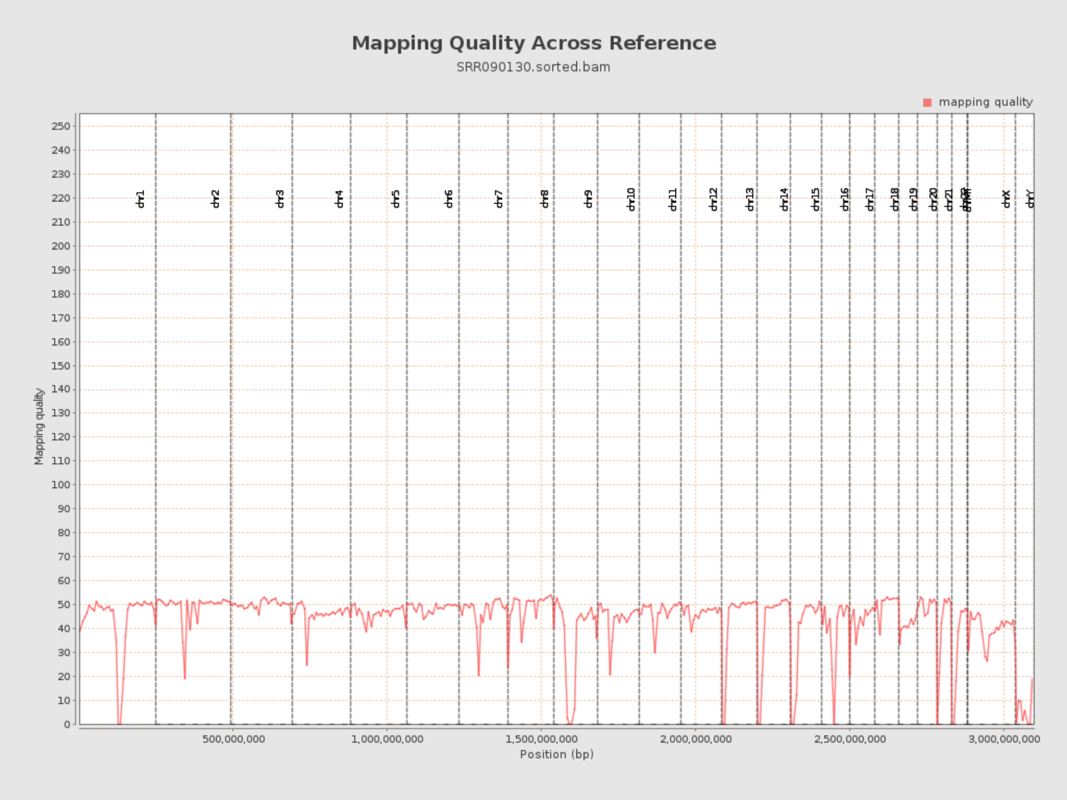
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram