# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 20:25:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236097.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_SRR6236097 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236097.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 16 20:25:19 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6236097.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,646,204 |
| Mapped reads | 3,177,624 / 87.15% |
| Unmapped reads | 468,580 / 12.85% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 20,256 / 0.56% |
| Read min/max/mean length | 30 / 76 / 76.19 |
| Duplicated reads (estimated) | 182,298 / 5% |
| Duplication rate | 4.21% |
| Clipped reads | 1,690,430 / 46.36% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 57,896,395 / 28.16% |
| Number/percentage of C's | 36,947,893 / 17.97% |
| Number/percentage of T's | 65,604,020 / 31.91% |
| Number/percentage of G's | 45,041,584 / 21.91% |
| Number/percentage of N's | 76,301 / 0.04% |
| GC Percentage | 39.88% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0664 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6888 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.08 |

## 2.5. Mismatches and indels

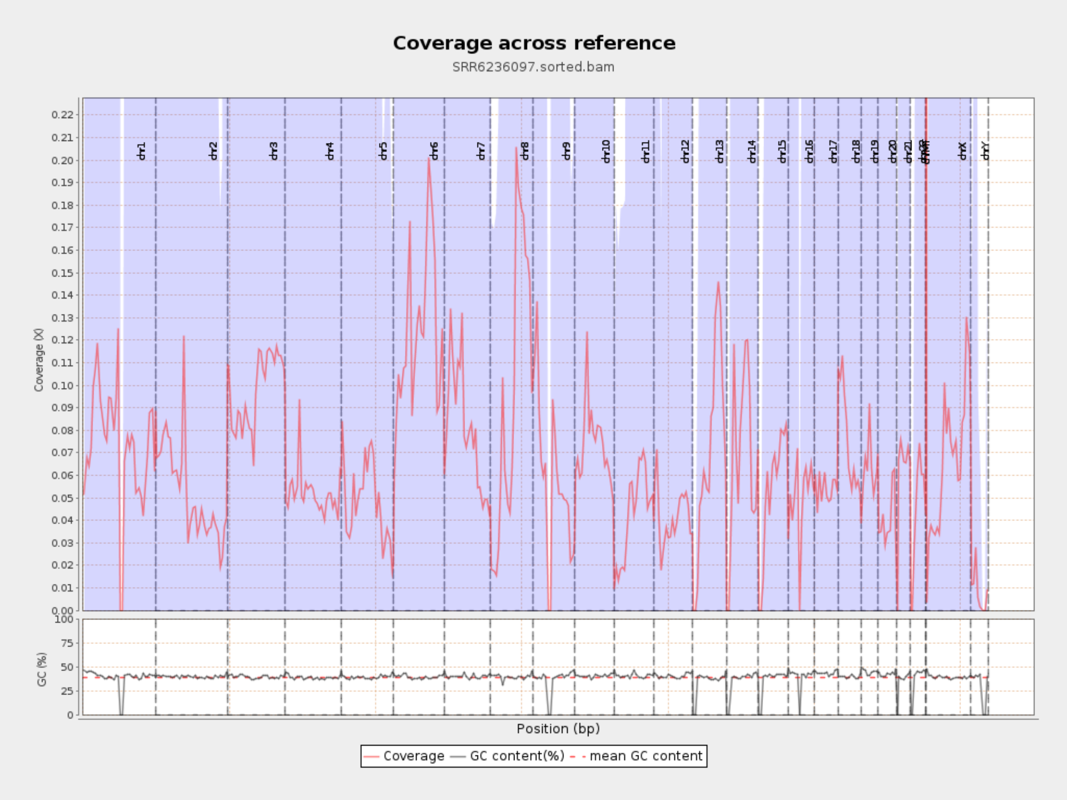
| | |
|---|---|
| General error rate | 0.92% |
| Mismatches | 1,859,245 |
| Insertions | 15,872 |
| Mapped reads with at least one insertion | 0.5% |
| Deletions | 62,990 |
| Mapped reads with at least one deletion | 1.96% |
| Homopolymer indels | 44.84% |

## 2.6. Chromosome stats

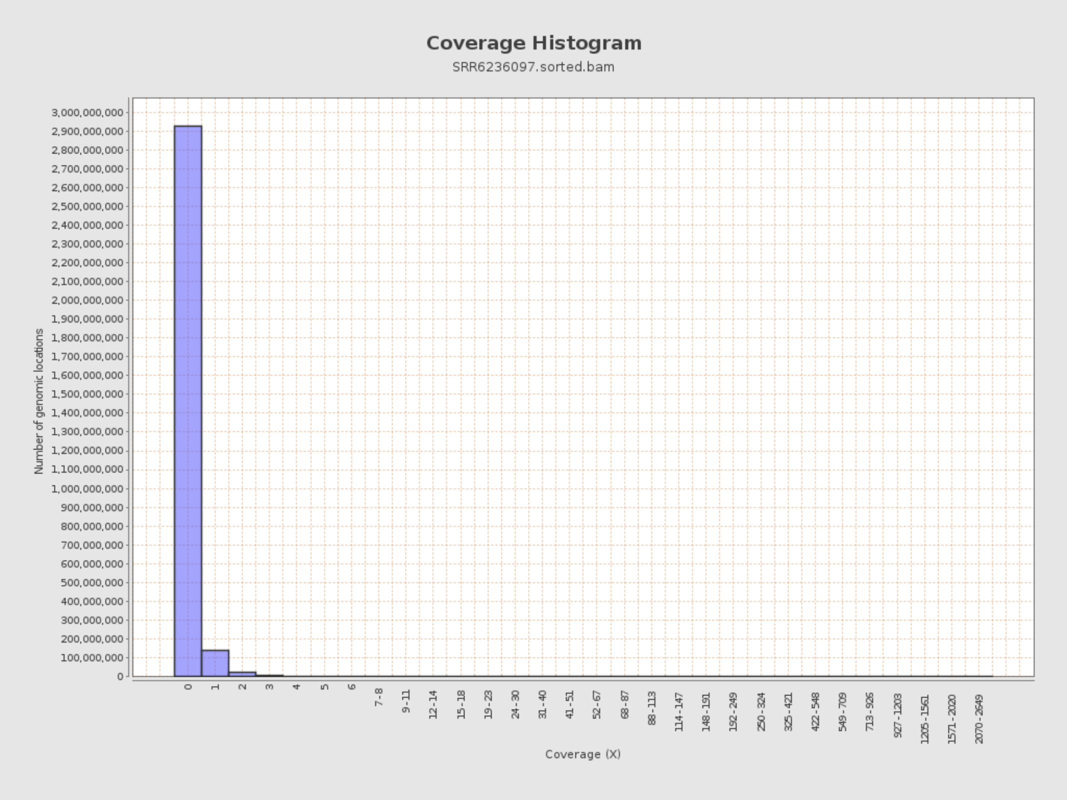
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 18186726 | 0.073 | 1.1077 |
| chr2 | 243199373 | 12690903 | 0.0522 | 0.753 |
| chr3 | 198022430 | 19389662 | 0.0979 | 0.3724 |
| chr4 | 191154276 | 9968799 | 0.0522 | 0.3245 |
| chr5 | 180915260 | 8870784 | 0.049 | 0.2686 |
| chr6 | 171115067 | 21431951 | 0.1252 | 0.5754 |
| chr7 | 159138663 | 12870135 | 0.0809 | 0.8241 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 14306482 | 0.0977 | 1.7233 |
| chr9 | 141213431 | 8346201 | 0.0591 | 0.5479 |
| chr10 | 135534747 | 9950232 | 0.0734 | 0.5427 |
| chr11 | 135006516 | 5845285 | 0.0433 | 0.4469 |
| chr12 | 133851895 | 5596628 | 0.0418 | 0.2766 |
| chr13 | 115169878 | 8166782 | 0.0709 | 0.3263 |
| chr14 | 107349540 | 7337651 | 0.0684 | 0.3436 |
| chr15 | 102531392 | 5384584 | 0.0525 | 0.283 |
| chr16 | 90354753 | 4426798 | 0.049 | 0.3402 |
| chr17 | 81195210 | 4378966 | 0.0539 | 0.3221 |
| chr18 | 78077248 | 5962307 | 0.0764 | 1.236 |
| chr19 | 59128983 | 3777871 | 0.0639 | 0.7732 |
| chr20 | 63025520 | 2636734 | 0.0418 | 0.2564 |
| chr21 | 48129895 | 3007985 | 0.0625 | 0.3419 |
| chr22 | 51304566 | 2303321 | 0.0449 | 0.2461 |
| chrMT | 16571 | 80812 | 4.8767 | 3.8064 |
| chrX | 155270560 | 10262292 | 0.0661 | 0.3699 |
| chrY | 59373566 | 494244 | 0.0083 | 0.2036 |

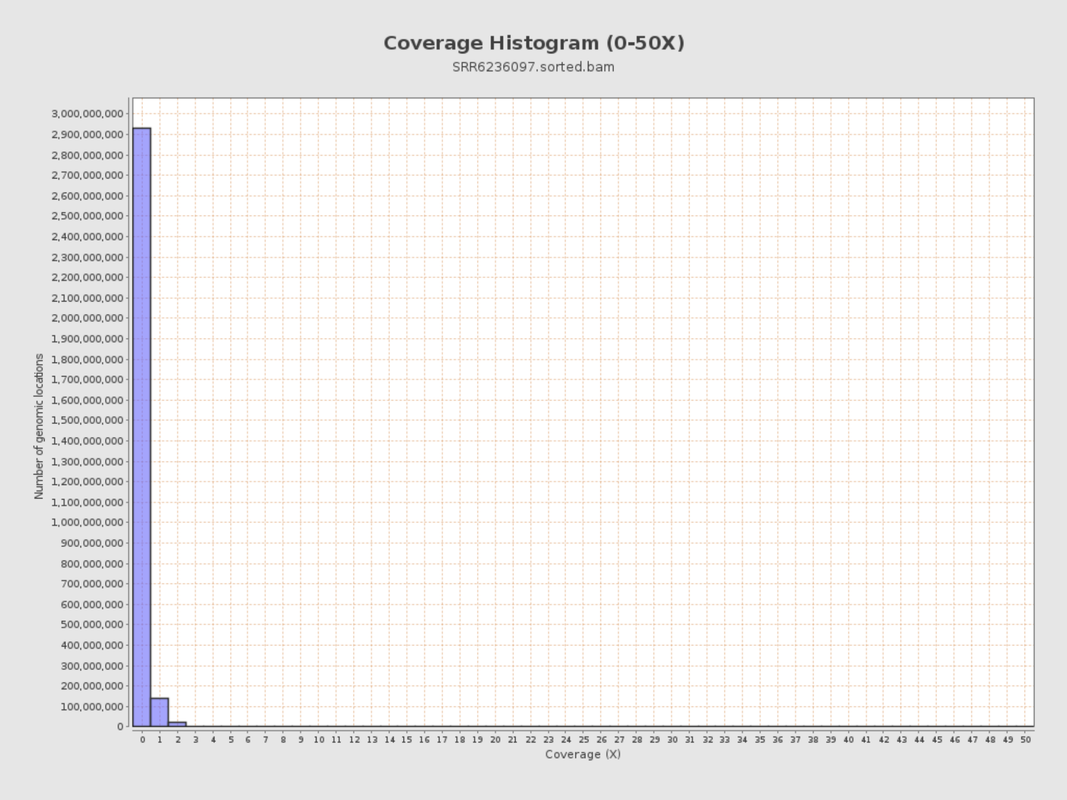
# 3. Results : Coverage across reference



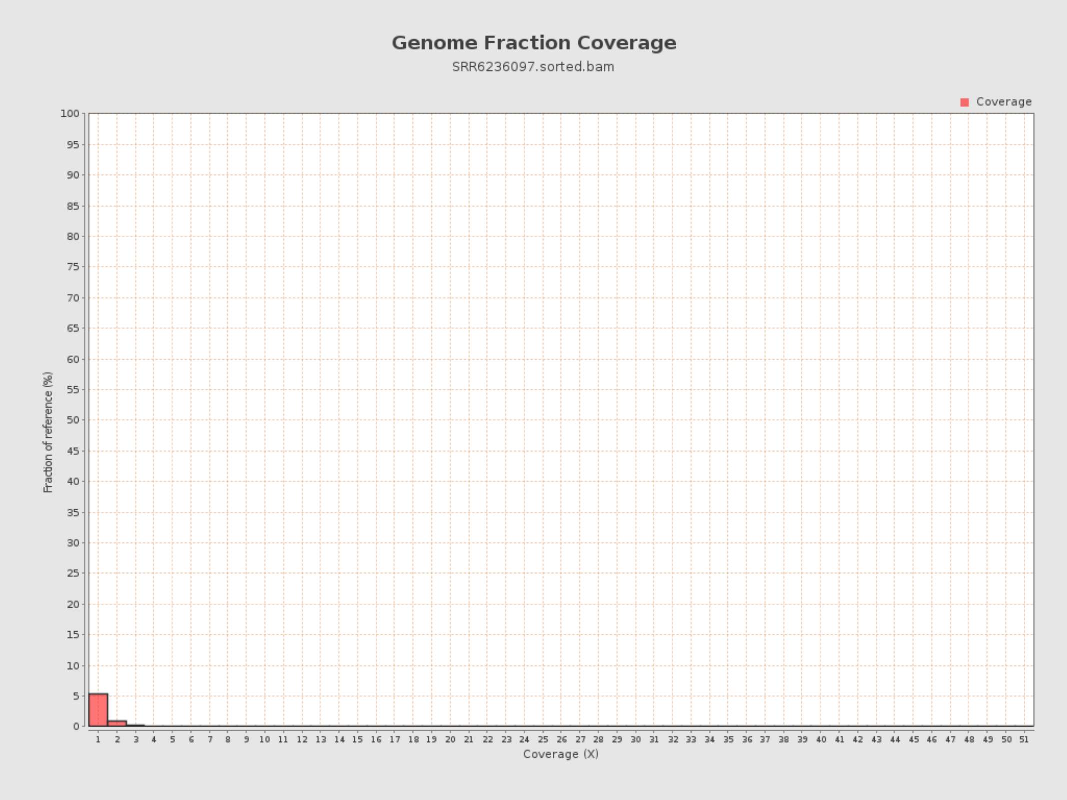
# 4. Results : Coverage Histogram



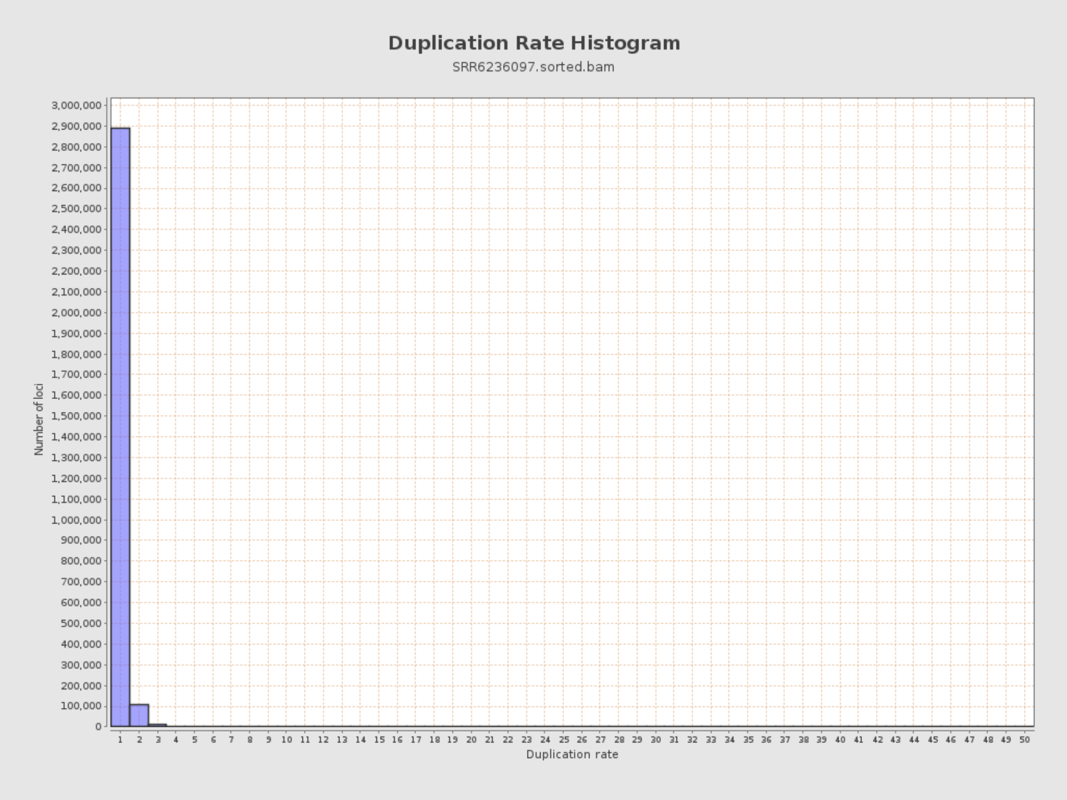
# 5. Results : Coverage Histogram (0-50X)



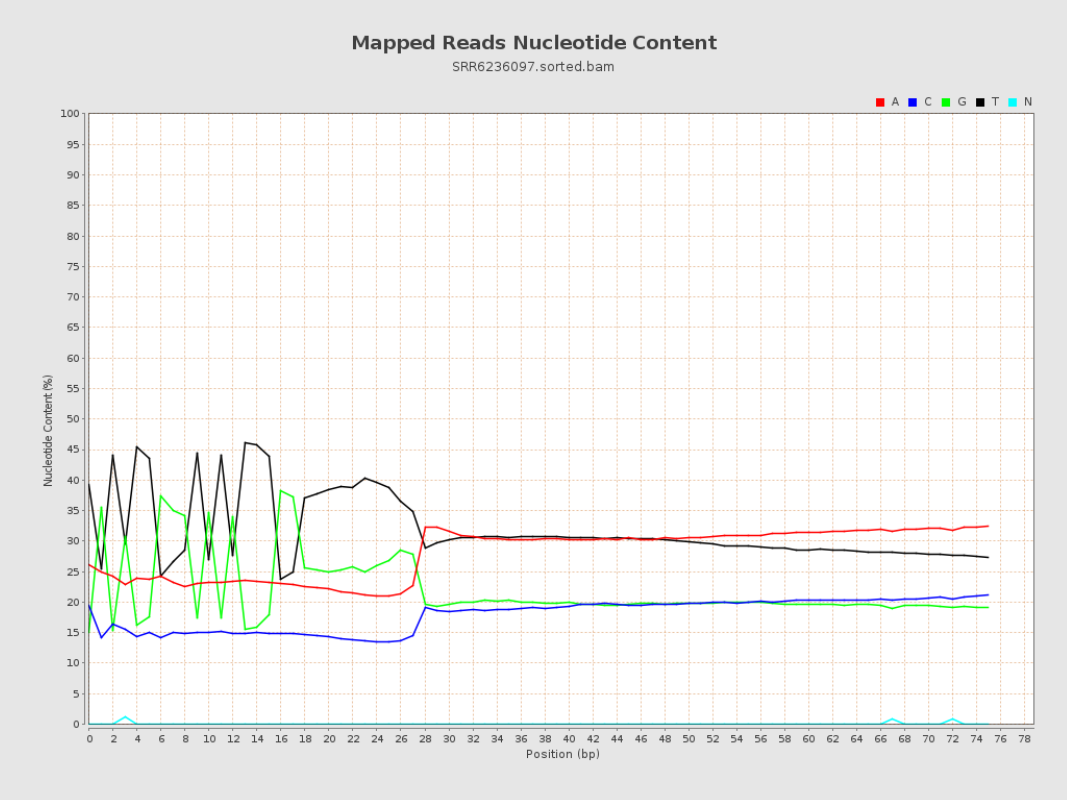
# 6. Results : Genome Fraction Coverage



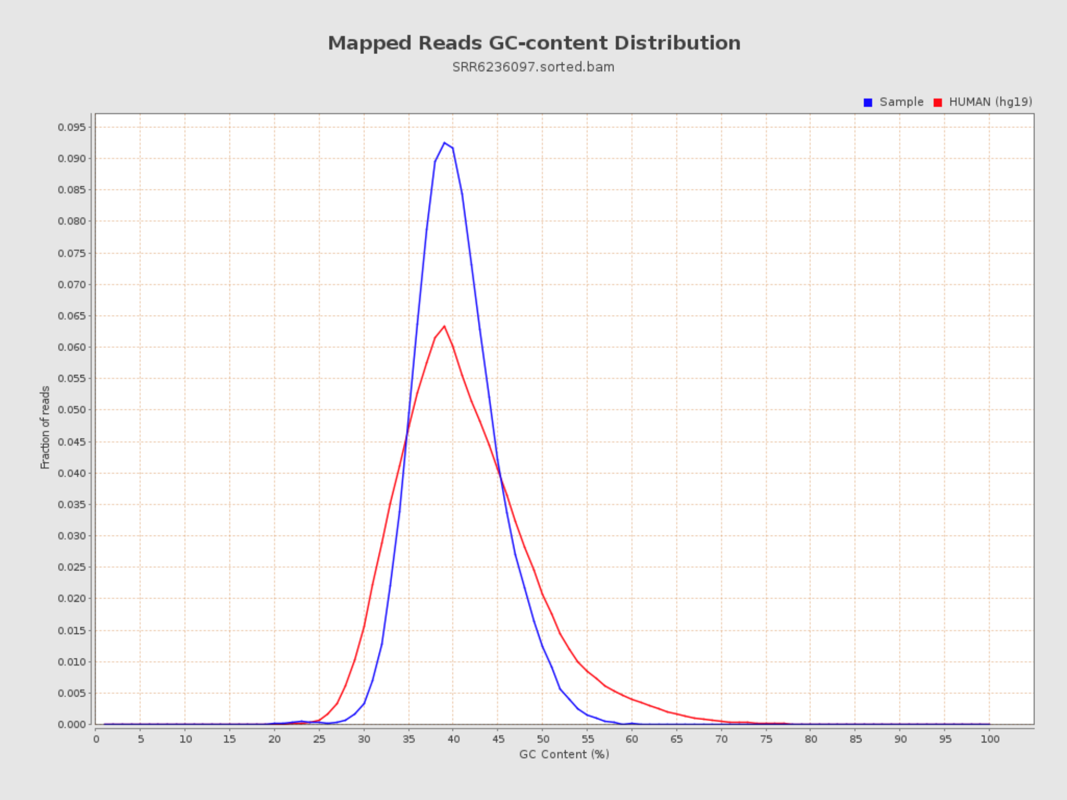
# 7. Results : Duplication Rate Histogram



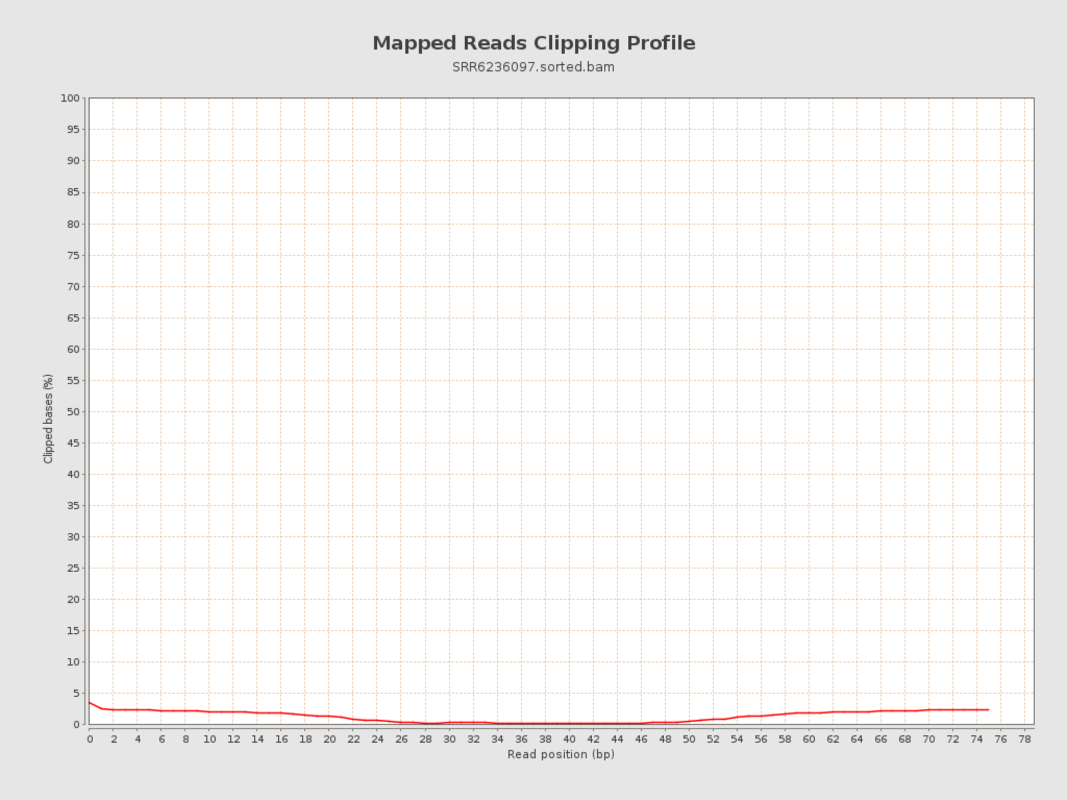
# 8. Results : Mapped Reads Nucleotide Content



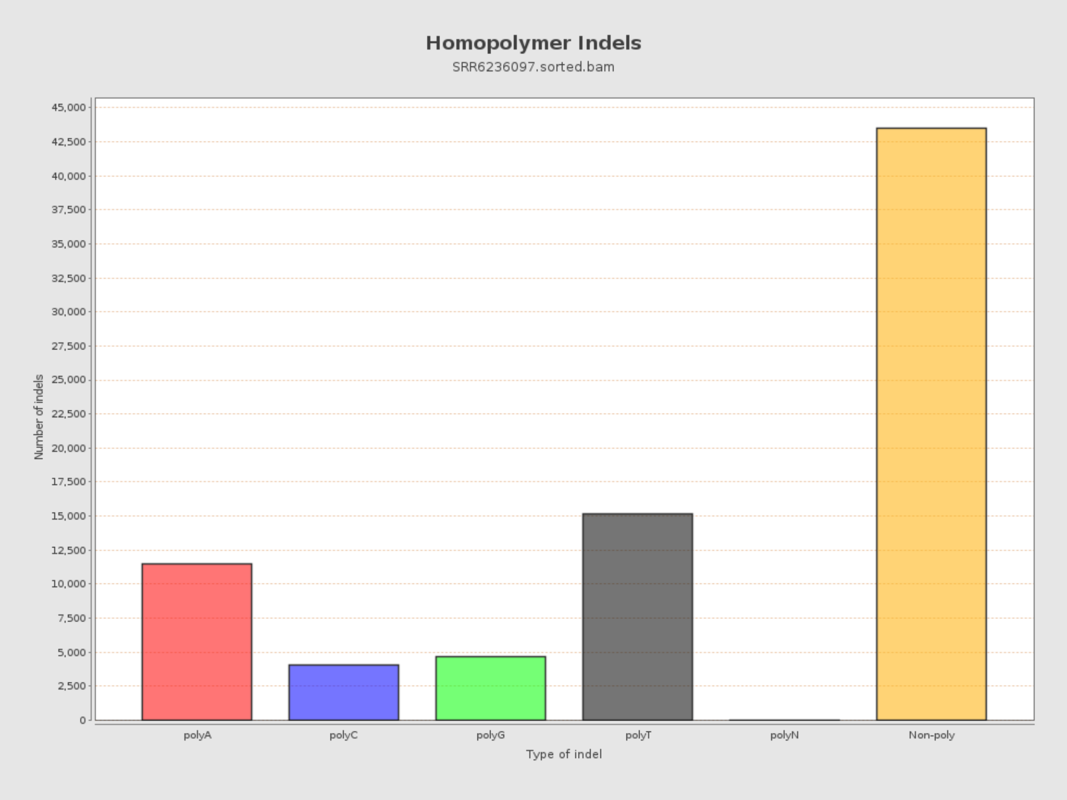
# 9. Results : Mapped Reads GC-content Distribution



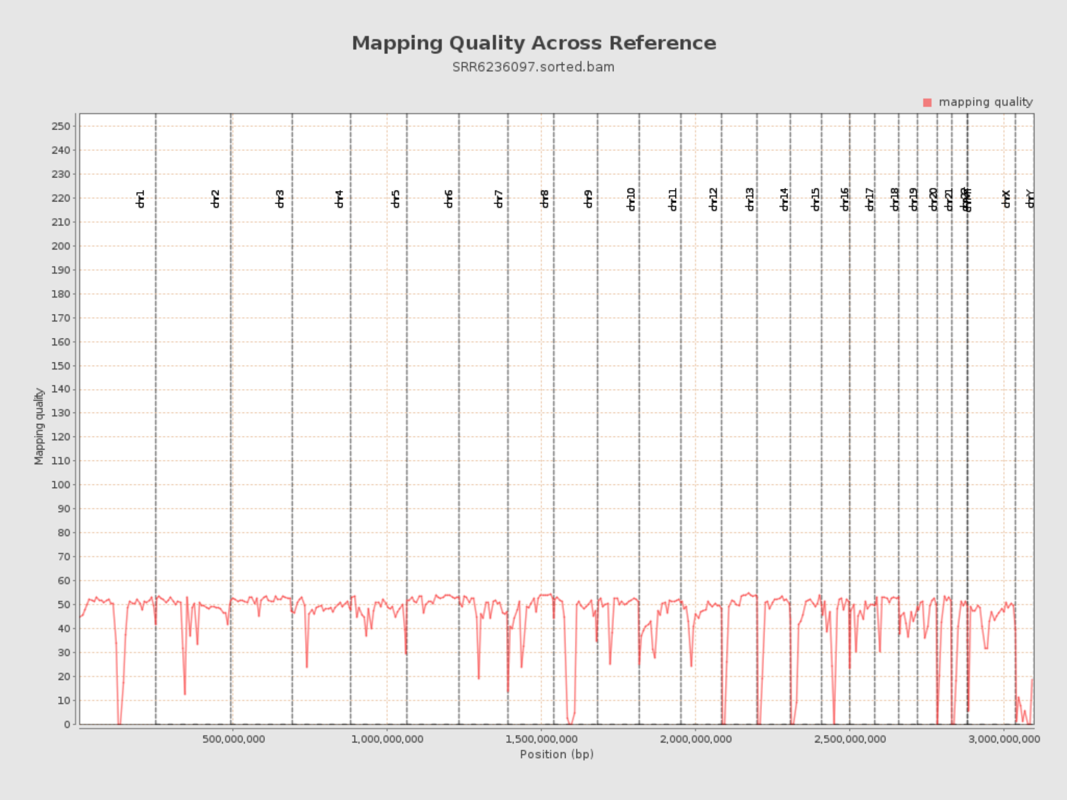
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram