# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 21:06:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084988.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_SRR3084988 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084988.fastq.gz` |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 21:06:52 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3084988.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,891,243 |
| Mapped reads | 2,622,223 / 90.7% |
| Unmapped reads | 269,020 / 9.3% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 23,551 / 0.81% |
| Read min/max/mean length | 30 / 76 / 76.28 |
| Duplicated reads (estimated) | 102,478 / 3.54% |
| Duplication rate | 2.97% |
| Clipped reads | 1,187,879 / 41.09% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 49,736,942 / 28.35% |
| Number/percentage of C's | 33,225,150 / 18.94% |
| Number/percentage of T's | 53,457,663 / 30.47% |
| Number/percentage of G's | 39,002,578 / 22.23% |
| Number/percentage of N's | 22,119 / 0.01% |
| GC Percentage | 41.17% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0567 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4502 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.11 |

## 2.5. Mismatches and indels

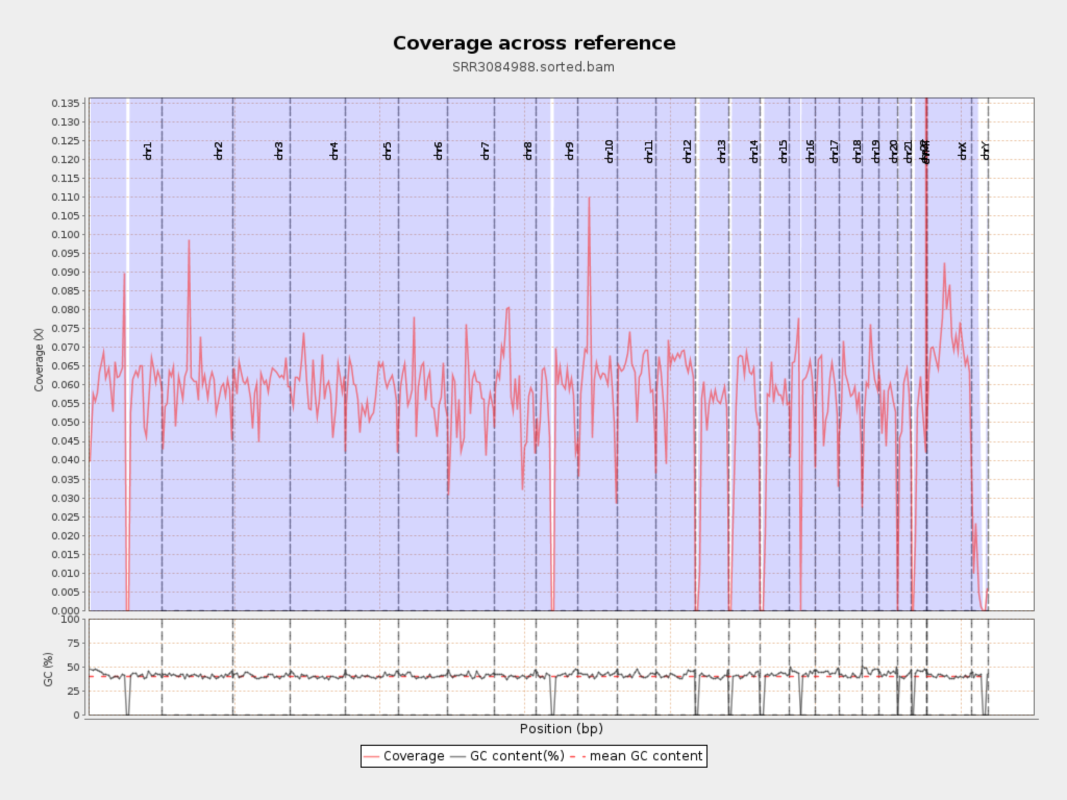
| | |
|---|---|
| General error rate | 0.86% |
| Mismatches | 1,474,499 |
| Insertions | 14,581 |
| Mapped reads with at least one insertion | 0.55% |
| Deletions | 42,022 |
| Mapped reads with at least one deletion | 1.59% |
| Homopolymer indels | 46.64% |

## 2.6. Chromosome stats

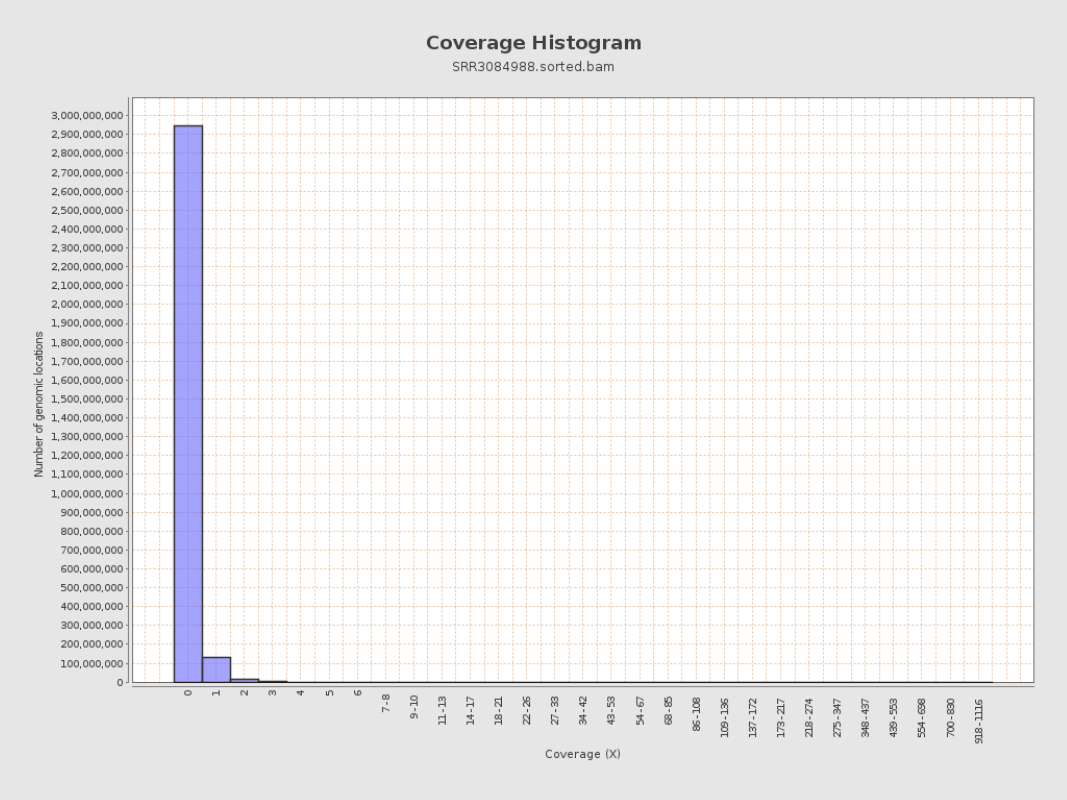
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 14263673 | 0.0572 | 0.7631 |
| chr2 | 243199373 | 14700110 | 0.0604 | 0.5509 |
| chr3 | 198022430 | 11980151 | 0.0605 | 0.2872 |
| chr4 | 191154276 | 11386456 | 0.0596 | 0.2906 |
| chr5 | 180915260 | 10504745 | 0.0581 | 0.2726 |
| chr6 | 171115067 | 10028485 | 0.0586 | 0.3467 |
| chr7 | 159138663 | 8789571 | 0.0552 | 0.3651 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8551988 | 0.0584 | 0.7428 |
| chr9 | 141213431 | 7276430 | 0.0515 | 0.4107 |
| chr10 | 135534747 | 8376666 | 0.0618 | 0.5783 |
| chr11 | 135006516 | 8473369 | 0.0628 | 0.444 |
| chr12 | 133851895 | 8481896 | 0.0634 | 0.2902 |
| chr13 | 115169878 | 5373159 | 0.0467 | 0.2427 |
| chr14 | 107349540 | 5506996 | 0.0513 | 0.2805 |
| chr15 | 102531392 | 4828966 | 0.0471 | 0.2491 |
| chr16 | 90354753 | 5218238 | 0.0578 | 0.3165 |
| chr17 | 81195210 | 4589677 | 0.0565 | 0.3104 |
| chr18 | 78077248 | 4522882 | 0.0579 | 0.7505 |
| chr19 | 59128983 | 3571973 | 0.0604 | 0.5772 |
| chr20 | 63025520 | 3354204 | 0.0532 | 0.2724 |
| chr21 | 48129895 | 2347038 | 0.0488 | 0.2745 |
| chr22 | 51304566 | 1891837 | 0.0369 | 0.218 |
| chrMT | 16571 | 32484 | 1.9603 | 1.7897 |
| chrX | 155270560 | 10988773 | 0.0708 | 0.3435 |
| chrY | 59373566 | 473018 | 0.008 | 0.152 |

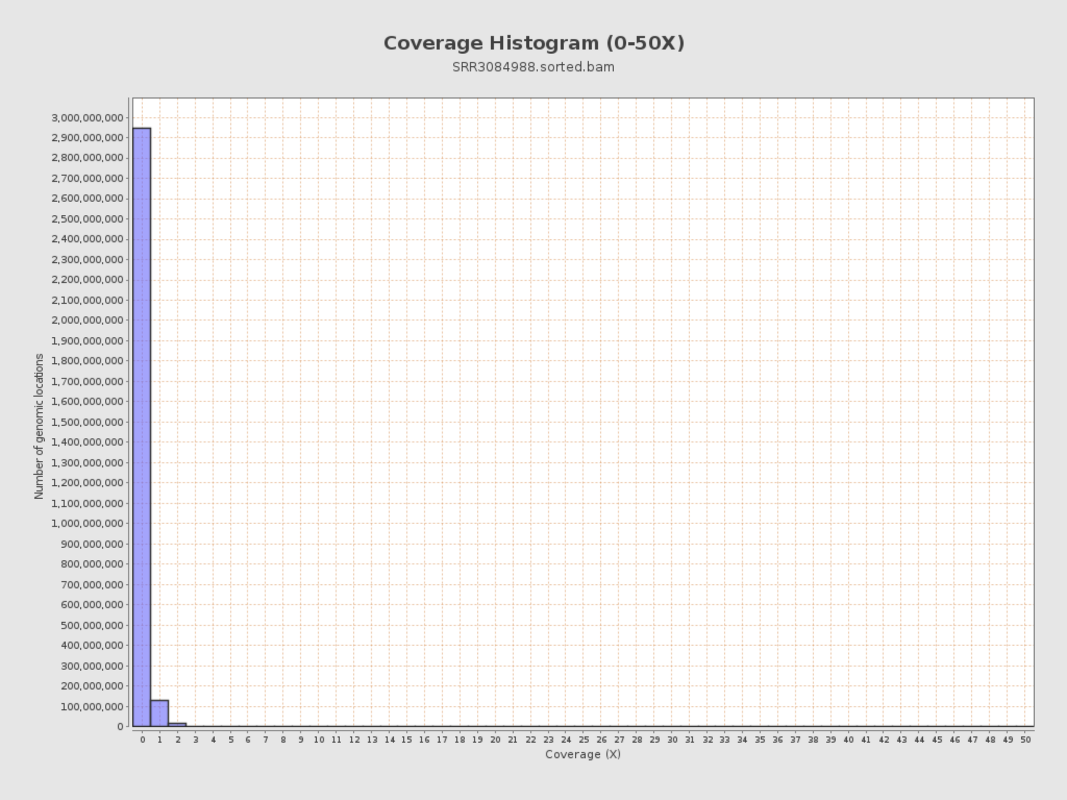
# 3. Results : Coverage across reference



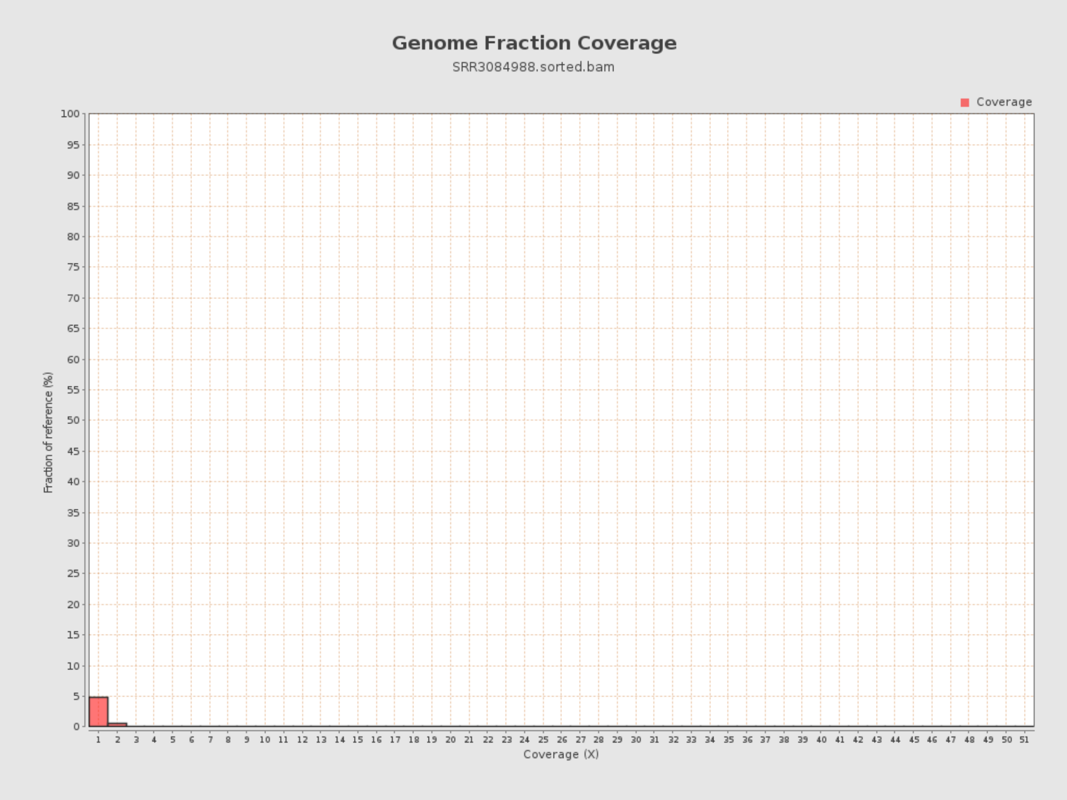
# 4. Results : Coverage Histogram



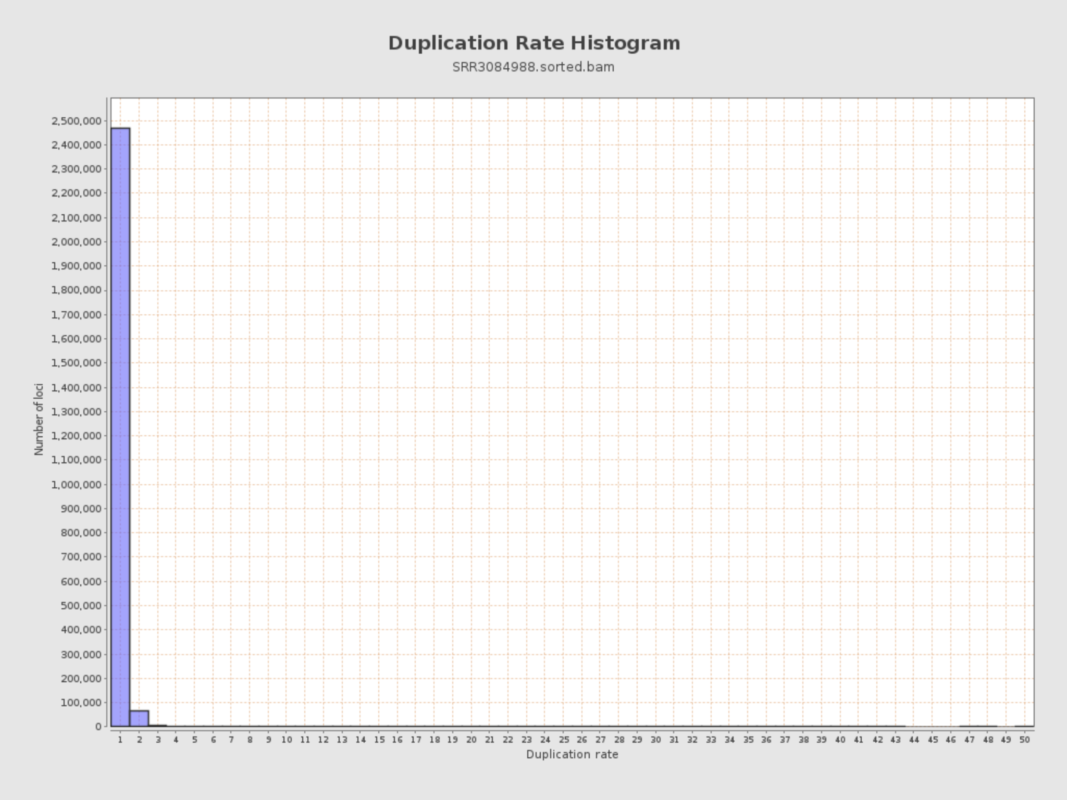
# 5. Results : Coverage Histogram (0-50X)



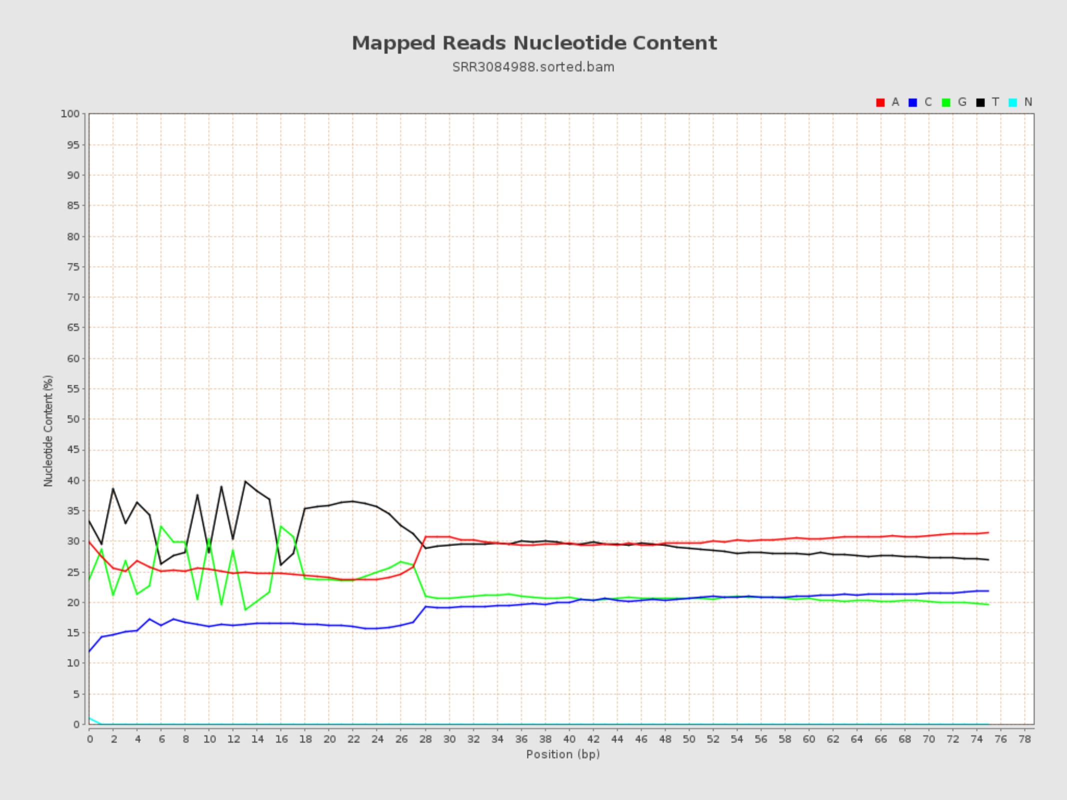
# 6. Results : Genome Fraction Coverage



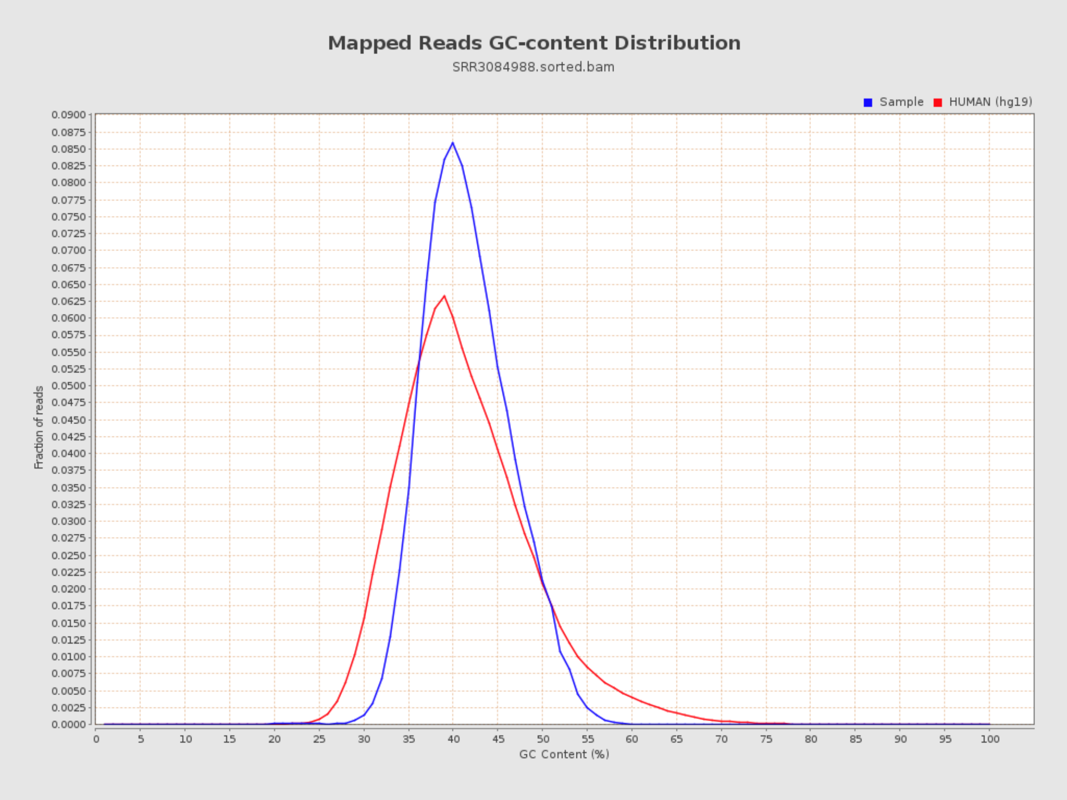
# 7. Results : Duplication Rate Histogram



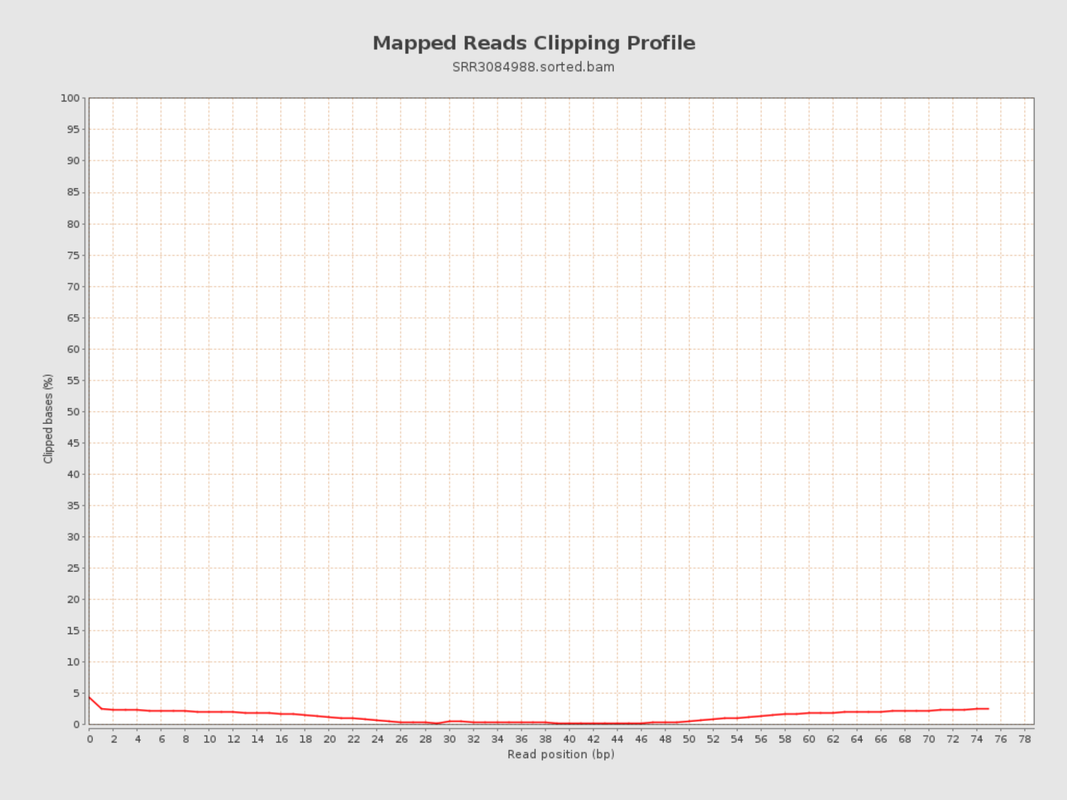
# 8. Results : Mapped Reads Nucleotide Content



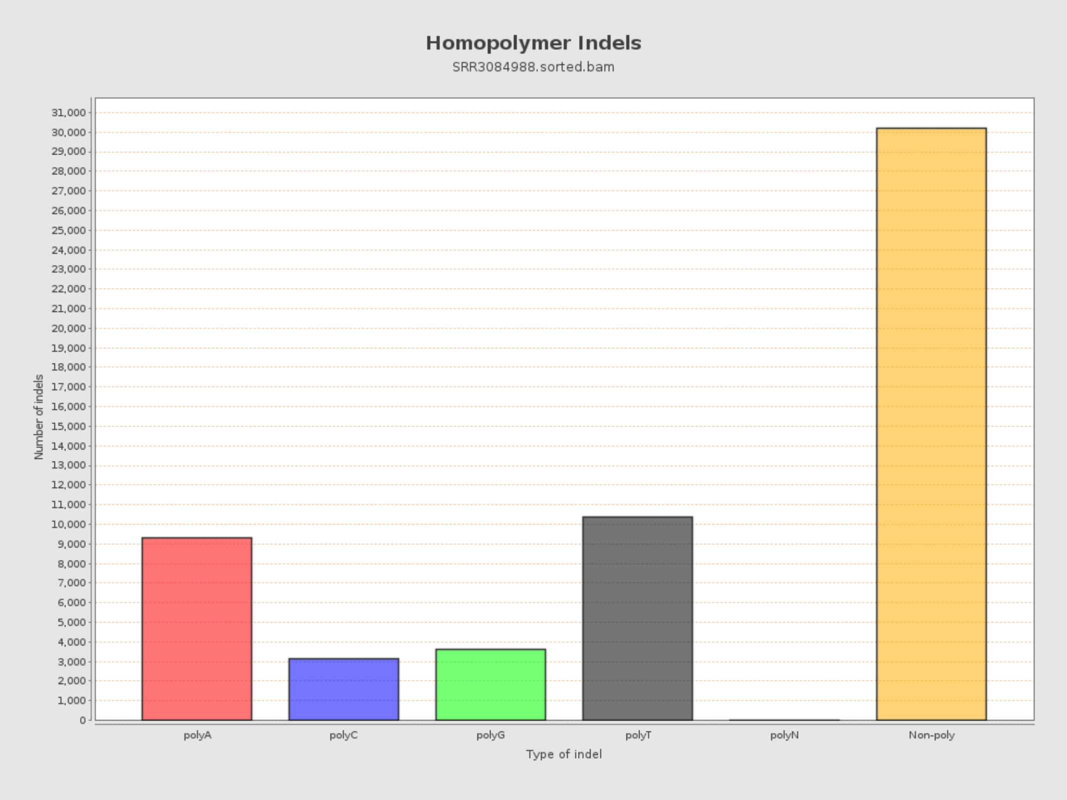
# 9. Results : Mapped Reads GC-content Distribution



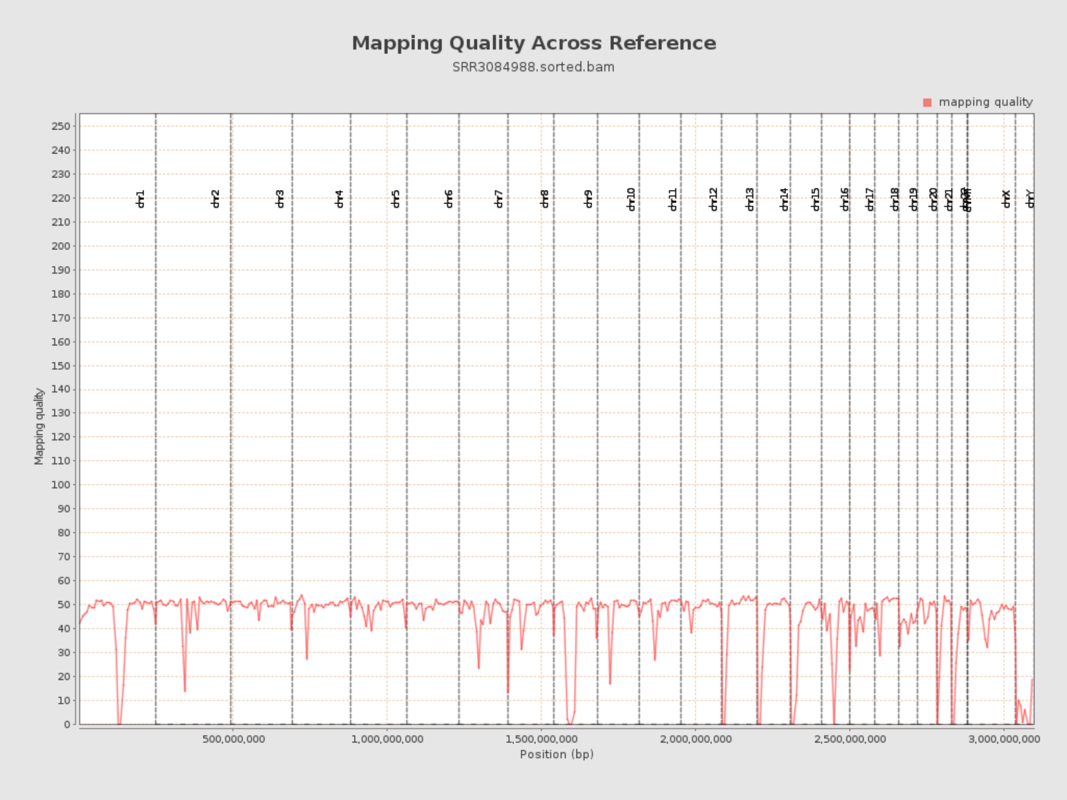
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram