# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 05:49:44*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080765.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_SRR3080765 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080765.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 05:49:43 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3080765.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 7,391,624 |
| Mapped reads | 3,491,994 / 47.24% |
| Unmapped reads | 3,899,630 / 52.76% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 26,791 / 0.36% |
| Read min/max/mean length | 30 / 66 / 66.12 |
| Duplicated reads (estimated) | 556,611 / 7.53% |
| Duplication rate | 12% |
| Clipped reads | 729,649 / 9.87% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 67,235,462 / 30.71% |
| Number/percentage of C's | 44,508,817 / 20.33% |
| Number/percentage of T's | 56,519,710 / 25.81% |
| Number/percentage of G's | 50,616,880 / 23.12% |
| Number/percentage of N's | 70,777 / 0.03% |
| GC Percentage | 43.45% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0708 |
| | |

| | |
|---|---|
| Standard Deviation | 0.659 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.61 |

## 2.5. Mismatches and indels

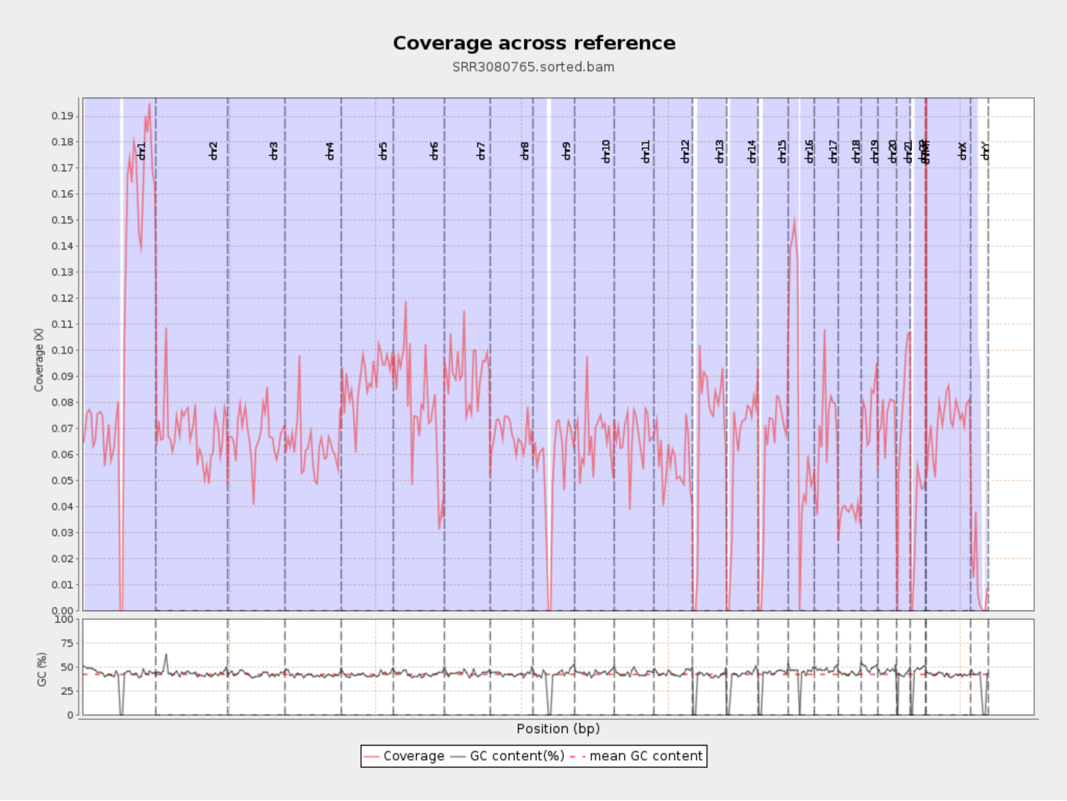
| | |
|---|---|
| General error rate | 0.95% |
| Mismatches | 2,057,032 |
| Insertions | 16,860 |
| Mapped reads with at least one insertion | 0.48% |
| Deletions | 40,677 |
| Mapped reads with at least one deletion | 1.15% |
| Homopolymer indels | 41.96% |

## 2.6. Chromosome stats

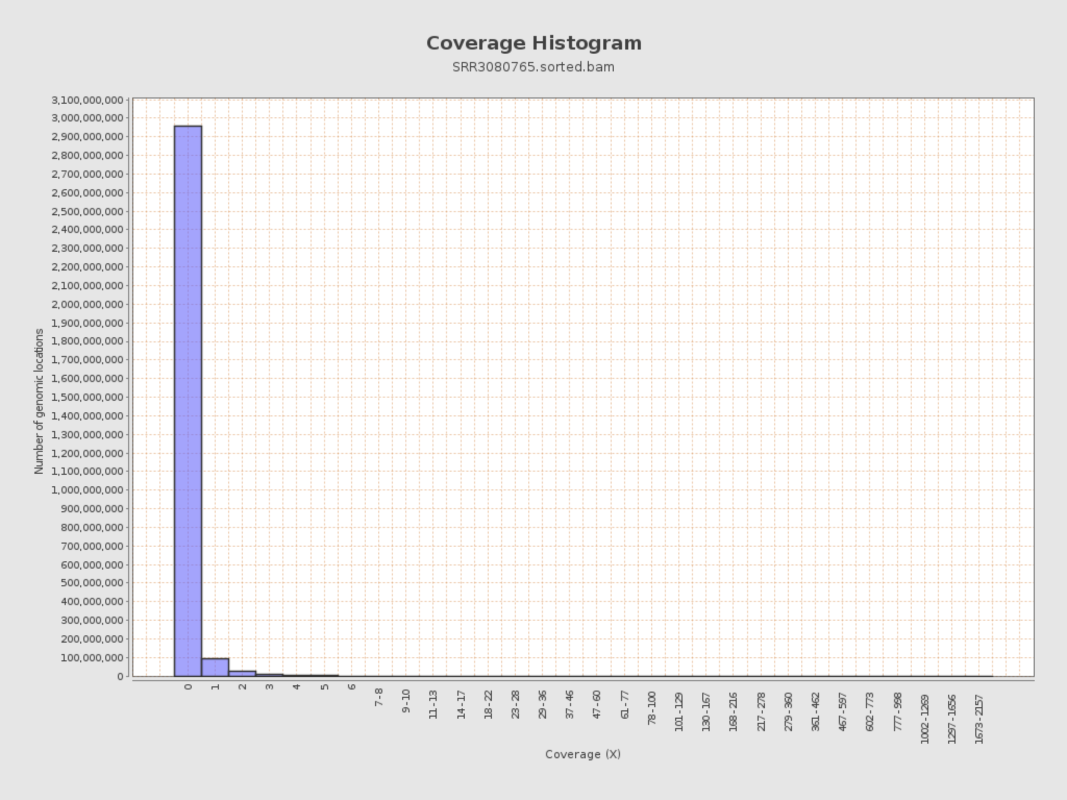
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 26757349 | 0.1074 | 0.6708 |
| chr2 | 243199373 | 16520807 | 0.0679 | 1.3677 |
| chr3 | 198022430 | 13291081 | 0.0671 | 0.402 |
| chr4 | 191154276 | 12038985 | 0.063 | 0.4422 |
| chr5 | 180915260 | 16072991 | 0.0888 | 0.469 |
| chr6 | 171115067 | 13336239 | 0.0779 | 1.1058 |
| chr7 | 159138663 | 14593137 | 0.0917 | 0.652 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 9956678 | 0.068 | 0.5944 |
| chr9 | 141213431 | 7753454 | 0.0549 | 0.3951 |
| chr10 | 135534747 | 8986175 | 0.0663 | 0.532 |
| chr11 | 135006516 | 8990562 | 0.0666 | 0.4756 |
| chr12 | 133851895 | 7717215 | 0.0577 | 0.4263 |
| chr13 | 115169878 | 8036225 | 0.0698 | 0.4151 |
| chr14 | 107349540 | 6600144 | 0.0615 | 0.5563 |
| chr15 | 102531392 | 6002307 | 0.0585 | 0.3914 |
| chr16 | 90354753 | 7114189 | 0.0787 | 0.4851 |
| chr17 | 81195210 | 5671189 | 0.0698 | 0.4354 |
| chr18 | 78077248 | 2944147 | 0.0377 | 0.4916 |
| chr19 | 59128983 | 4543360 | 0.0768 | 0.7657 |
| chr20 | 63025520 | 4679440 | 0.0742 | 0.4557 |
| chr21 | 48129895 | 3704643 | 0.077 | 0.5008 |
| chr22 | 51304566 | 1791761 | 0.0349 | 0.3056 |
| chrMT | 16571 | 45878 | 2.7686 | 3.7275 |
| chrX | 155270560 | 11243861 | 0.0724 | 0.4311 |
| chrY | 59373566 | 635964 | 0.0107 | 0.301 |

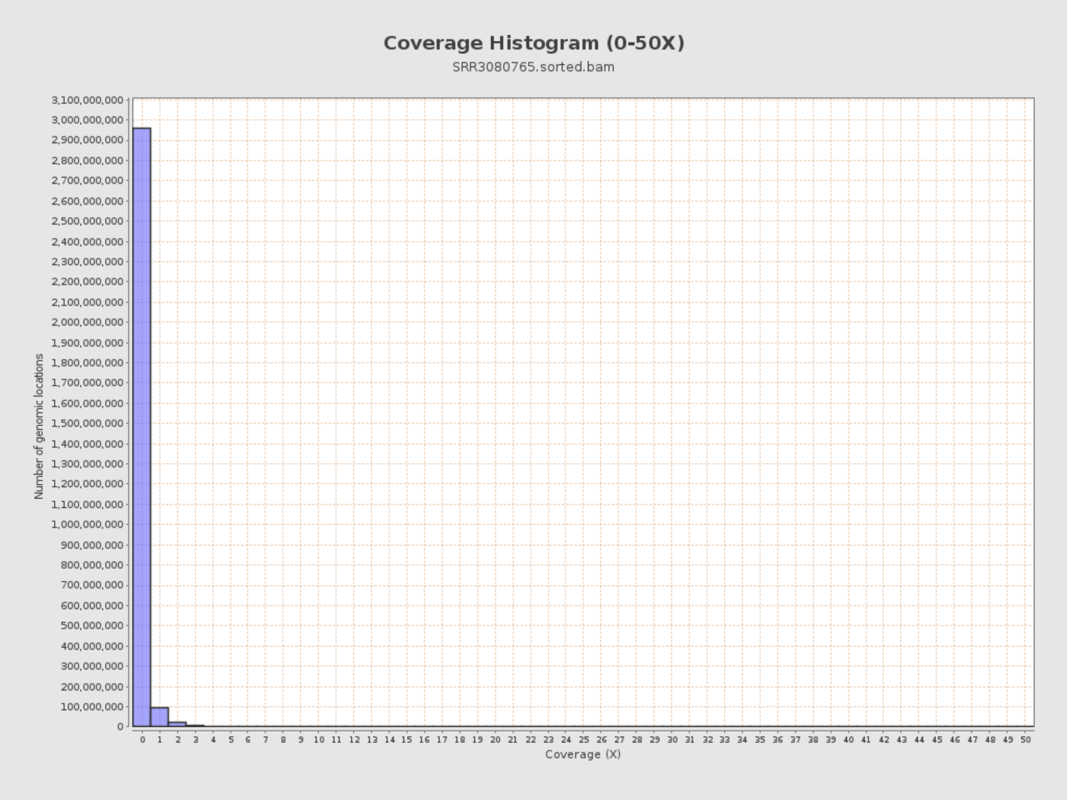
# 3. Results : Coverage across reference



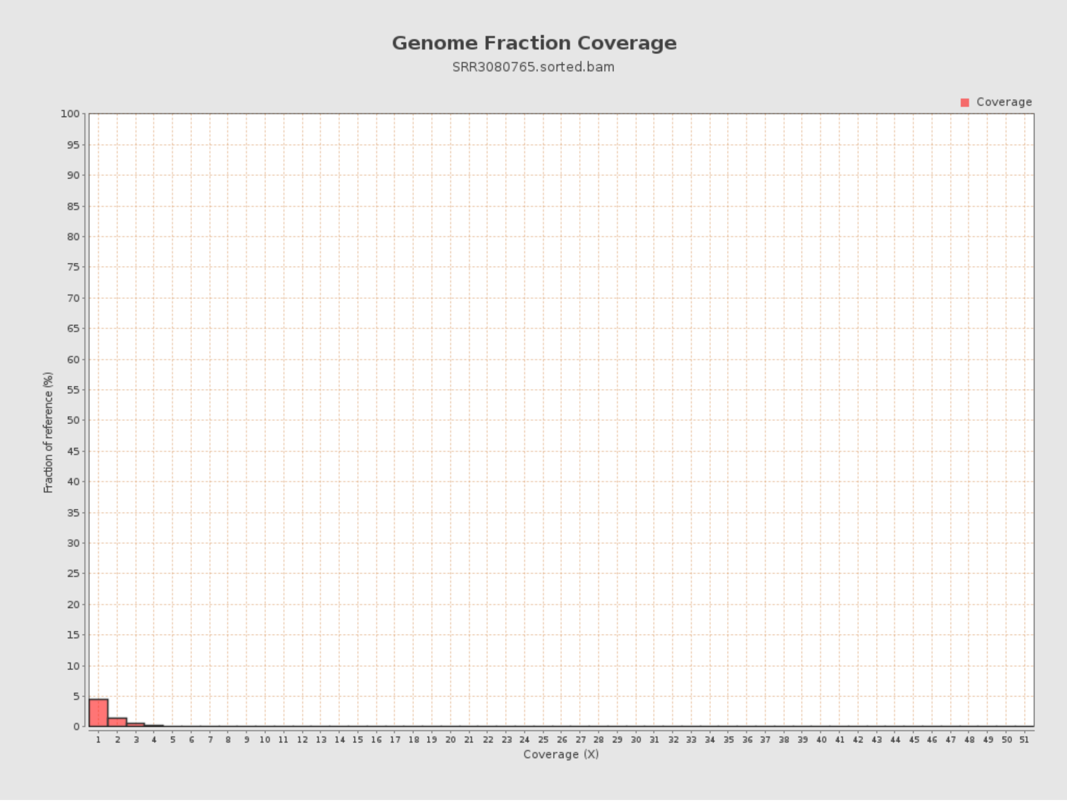
# 4. Results : Coverage Histogram



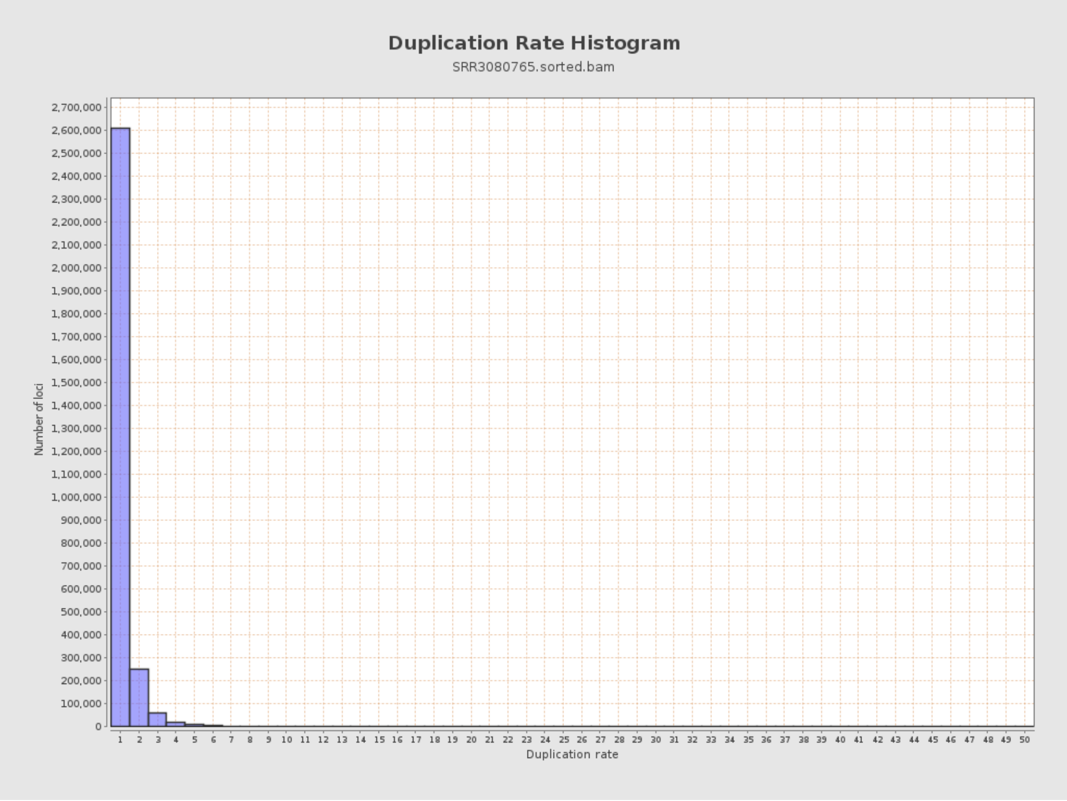
# 5. Results : Coverage Histogram (0-50X)



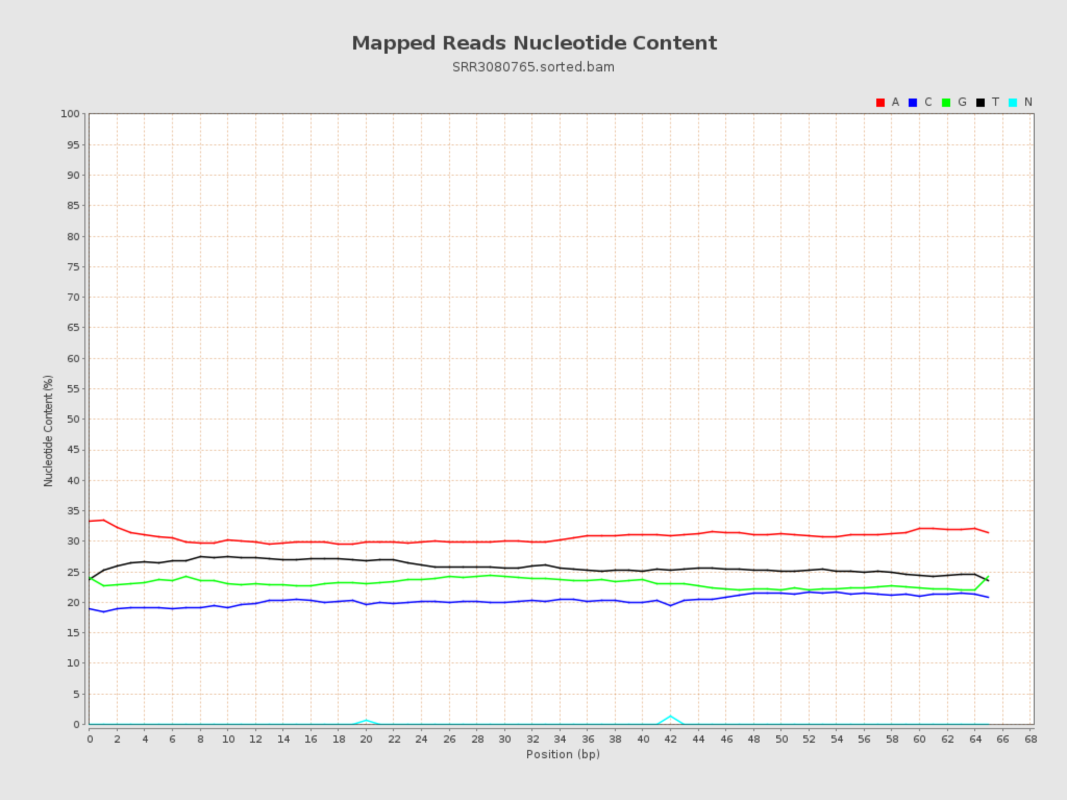
# 6. Results : Genome Fraction Coverage



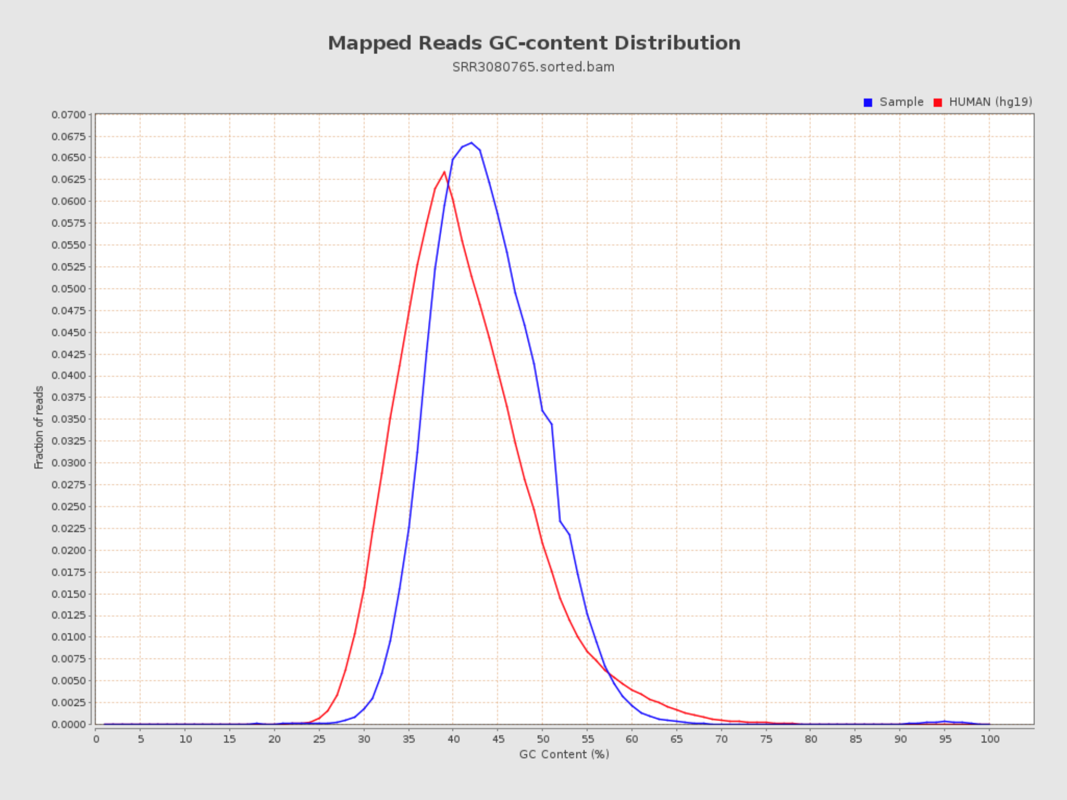
# 7. Results : Duplication Rate Histogram



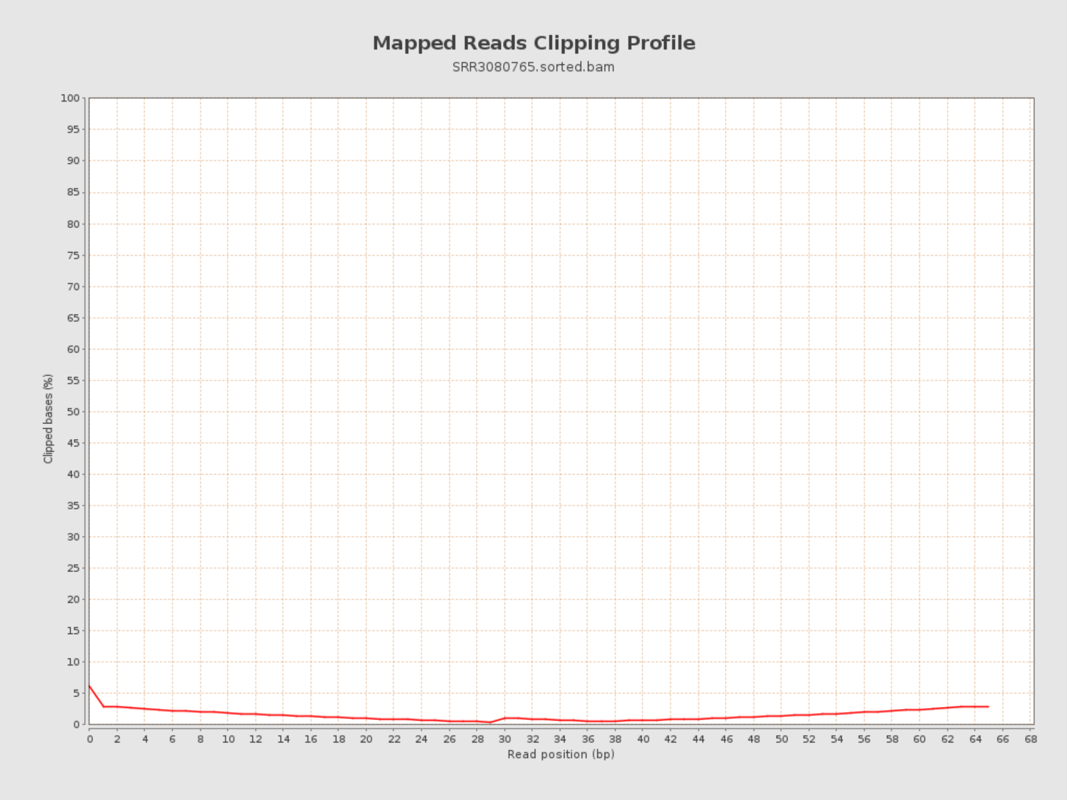
# 8. Results : Mapped Reads Nucleotide Content



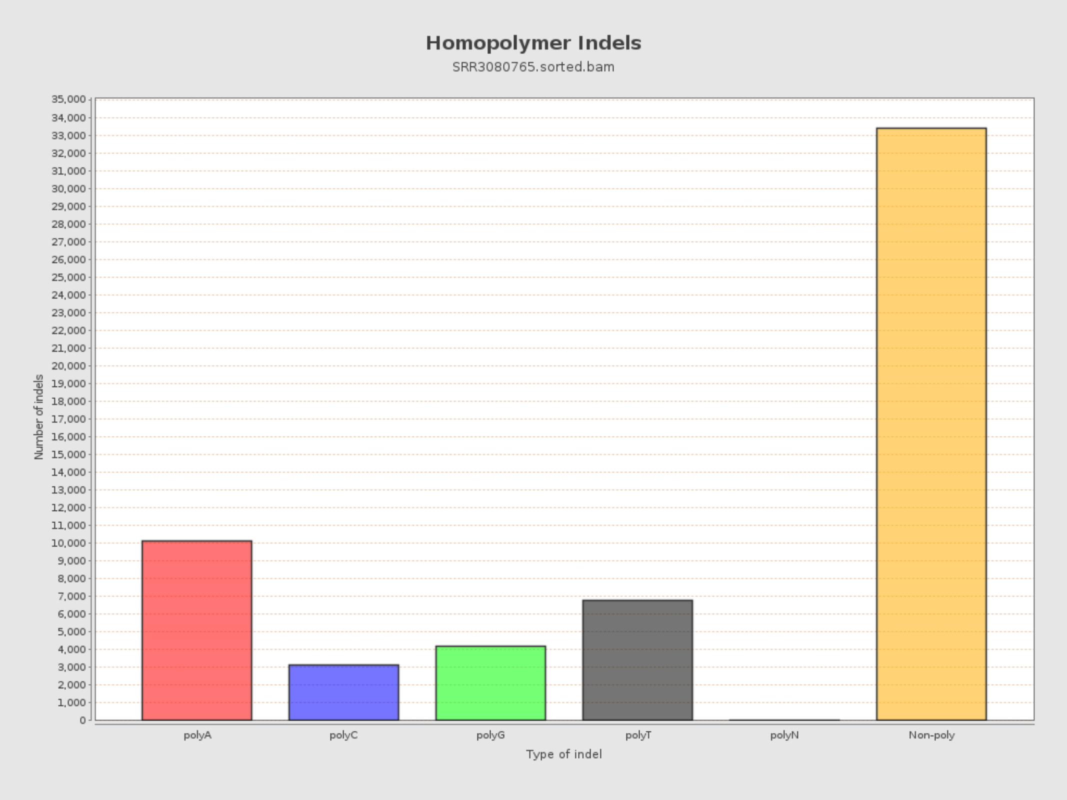
# 9. Results : Mapped Reads GC-content Distribution



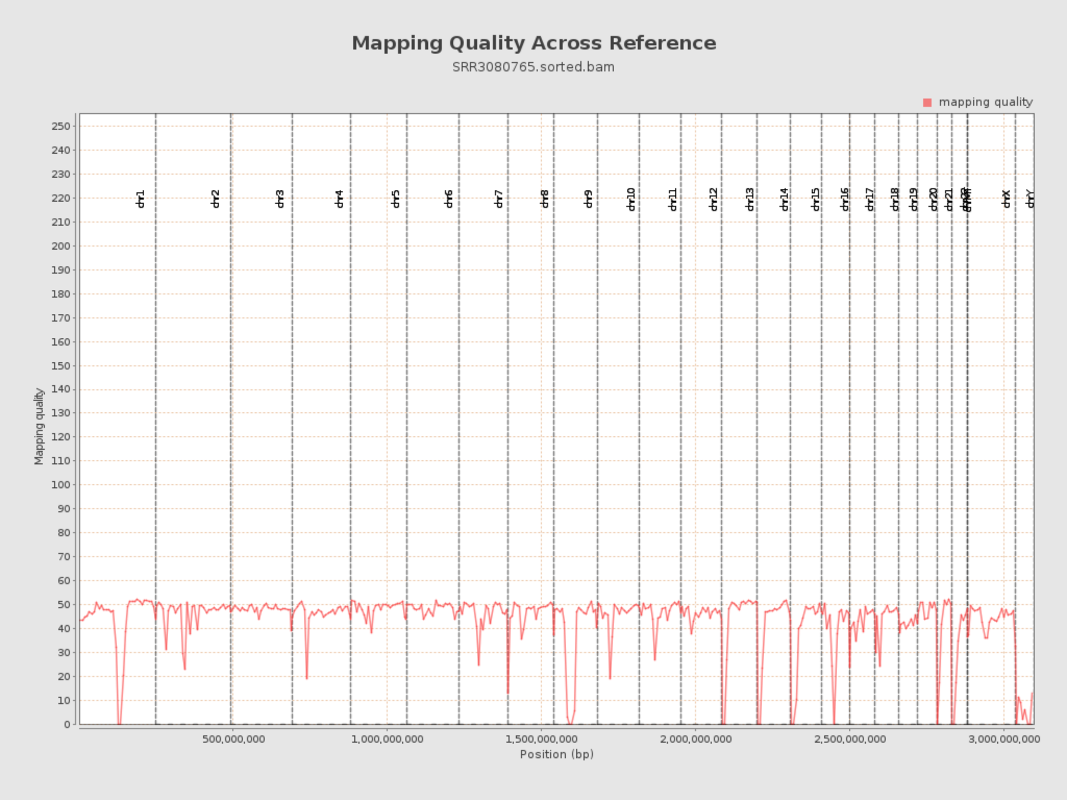
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram