# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 02:02:44*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083647.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_SRR3083647 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083647.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 02:02:44 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3083647.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,727,825 |
| Mapped reads | 1,347,846 / 78.01% |
| Unmapped reads | 379,979 / 21.99% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 8,111 / 0.47% |
| Read min/max/mean length | 30 / 76 / 76.16 |
| Duplicated reads (estimated) | 34,941 / 2.02% |
| Duplication rate | 2.11% |
| Clipped reads | 892,156 / 51.63% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 23,565,054 / 28.89% |
| Number/percentage of C's | 15,815,023 / 19.39% |
| Number/percentage of T's | 23,663,264 / 29.01% |
| Number/percentage of G's | 18,503,844 / 22.69% |
| Number/percentage of N's | 10,691 / 0.01% |
| GC Percentage | 42.08% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0264 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2374 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.59 |

## 2.5. Mismatches and indels

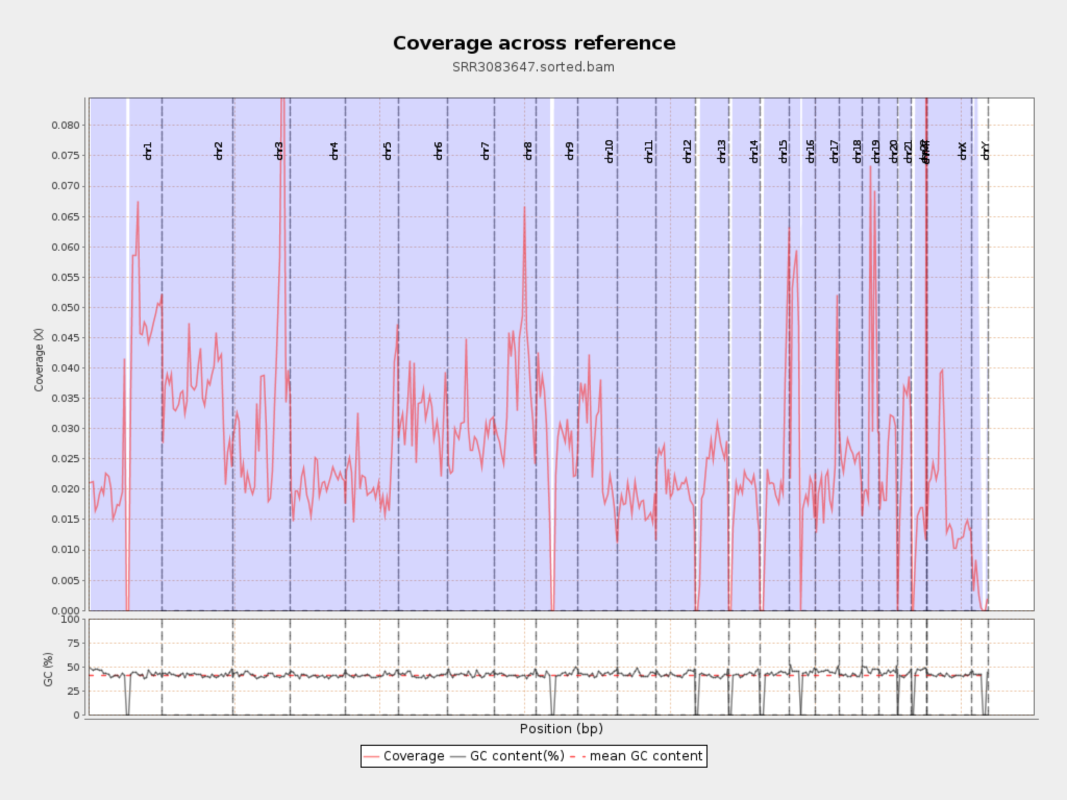
| | |
|---|---|
| General error rate | 0.88% |
| Mismatches | 707,901 |
| Insertions | 5,998 |
| Mapped reads with at least one insertion | 0.44% |
| Deletions | 16,705 |
| Mapped reads with at least one deletion | 1.23% |
| Homopolymer indels | 44.5% |

## 2.6. Chromosome stats

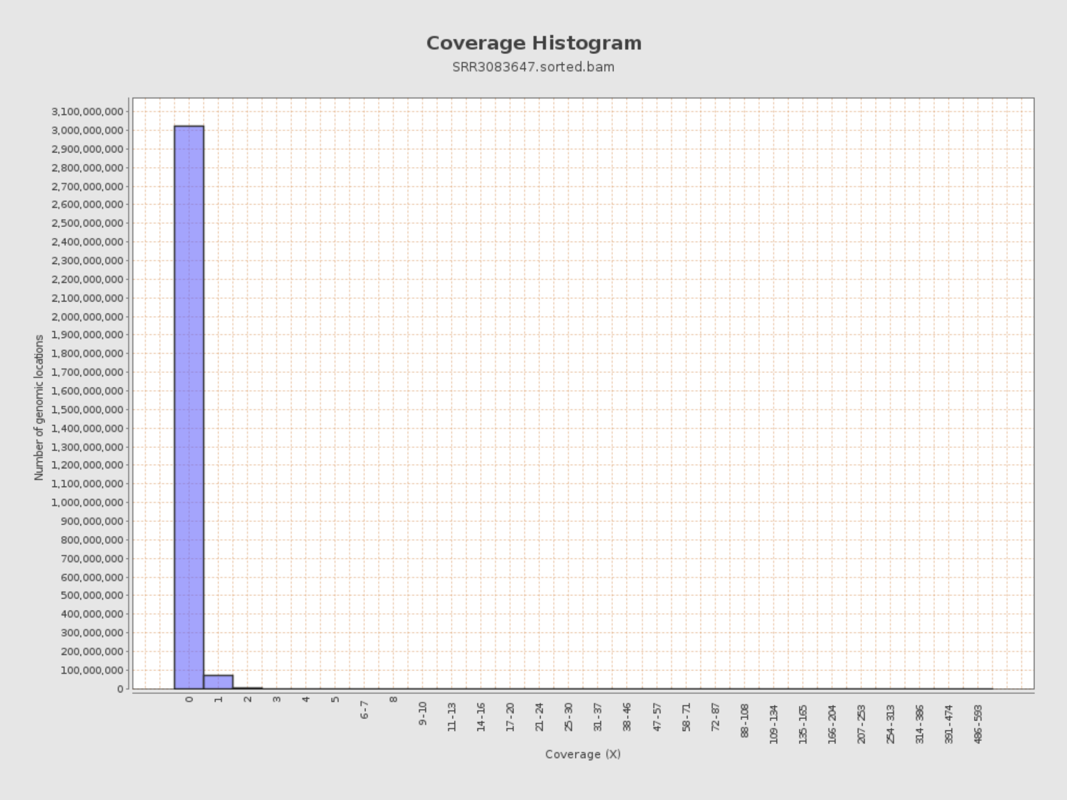
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7976340 | 0.032 | 0.4725 |
| chr2 | 243199373 | 8735505 | 0.0359 | 0.2362 |
| chr3 | 198022430 | 6782223 | 0.0342 | 0.1978 |
| chr4 | 191154276 | 3955574 | 0.0207 | 0.1541 |
| chr5 | 180915260 | 4169475 | 0.023 | 0.1618 |
| chr6 | 171115067 | 5499909 | 0.0321 | 0.2131 |
| chr7 | 159138663 | 4587941 | 0.0288 | 0.3044 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5540992 | 0.0379 | 0.2669 |
| chr9 | 141213431 | 3708348 | 0.0263 | 0.1957 |
| chr10 | 135534747 | 3780552 | 0.0279 | 0.2419 |
| chr11 | 135006516 | 2347571 | 0.0174 | 0.1609 |
| chr12 | 133851895 | 2852070 | 0.0213 | 0.1557 |
| chr13 | 115169878 | 2446092 | 0.0212 | 0.1534 |
| chr14 | 107349540 | 1857655 | 0.0173 | 0.1415 |
| chr15 | 102531392 | 2222321 | 0.0217 | 0.1577 |
| chr16 | 90354753 | 2653809 | 0.0294 | 0.1886 |
| chr17 | 81195210 | 1884427 | 0.0232 | 0.1686 |
| chr18 | 78077248 | 1990511 | 0.0255 | 0.3115 |
| chr19 | 59128983 | 2115045 | 0.0358 | 0.3399 |
| chr20 | 63025520 | 1541751 | 0.0245 | 0.1662 |
| chr21 | 48129895 | 1307491 | 0.0272 | 0.1772 |
| chr22 | 51304566 | 575350 | 0.0112 | 0.111 |
| chrMT | 16571 | 5984 | 0.3611 | 0.6221 |
| chrX | 155270560 | 2887305 | 0.0186 | 0.1518 |
| chrY | 59373566 | 160326 | 0.0027 | 0.0638 |

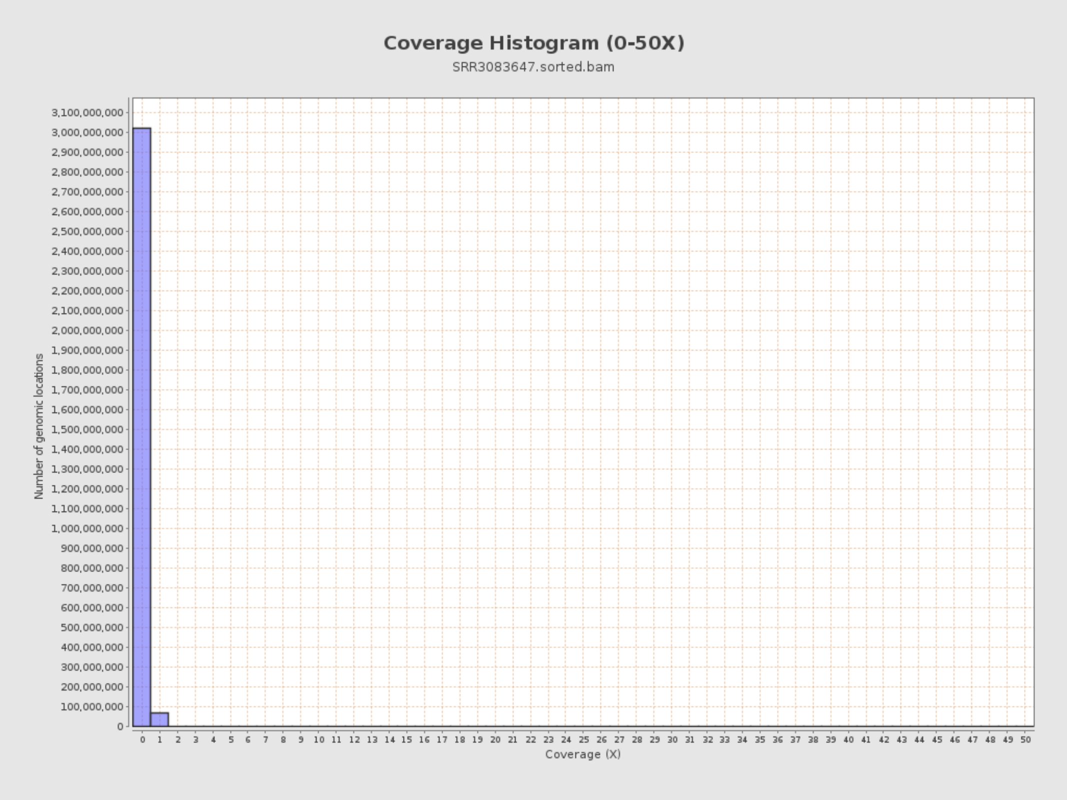
# 3. Results : Coverage across reference



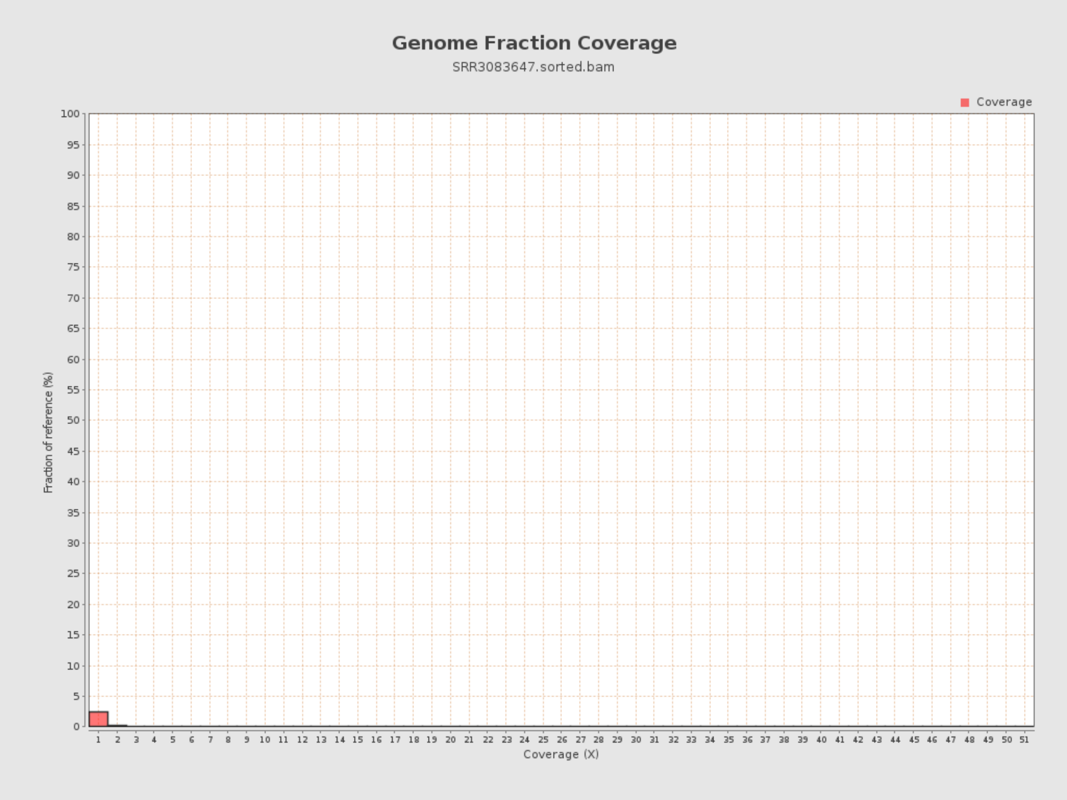
# 4. Results : Coverage Histogram



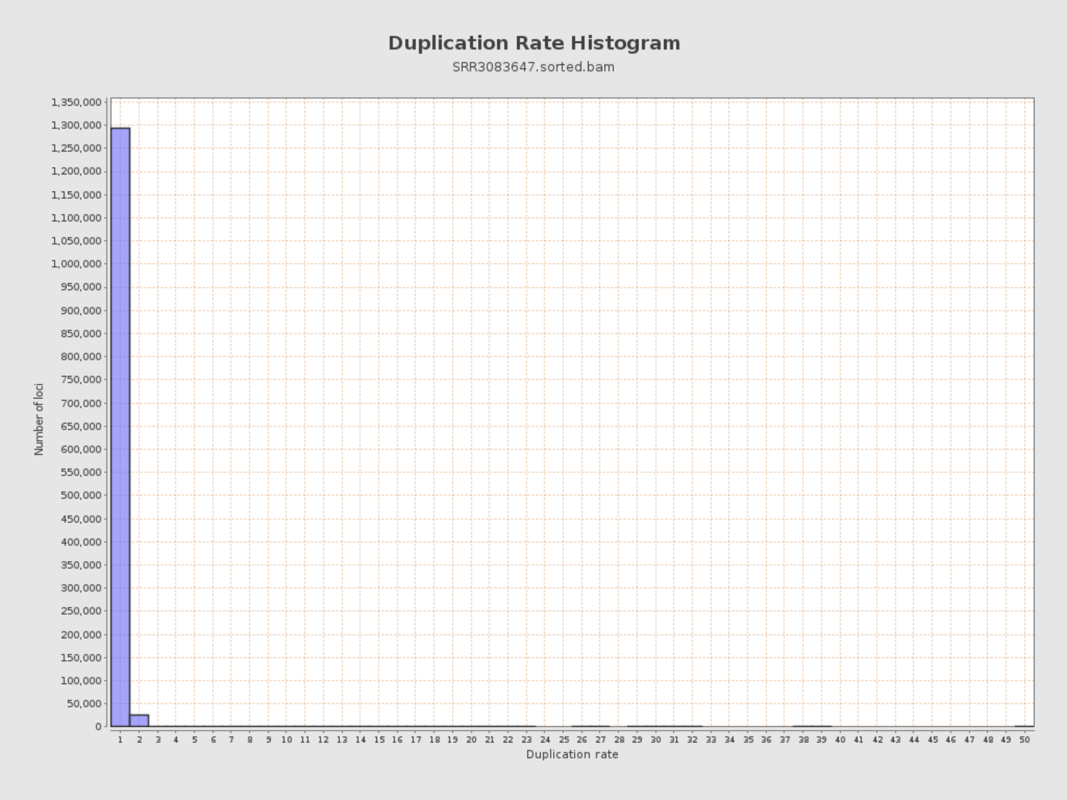
# 5. Results : Coverage Histogram (0-50X)



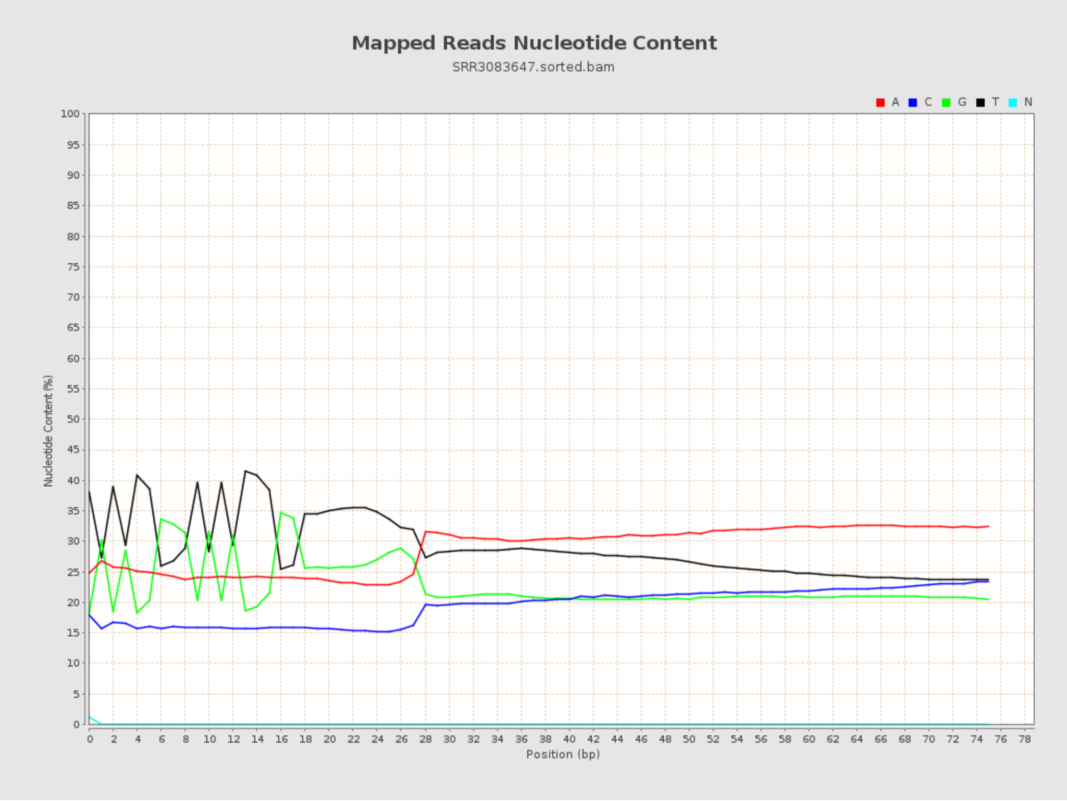
# 6. Results : Genome Fraction Coverage



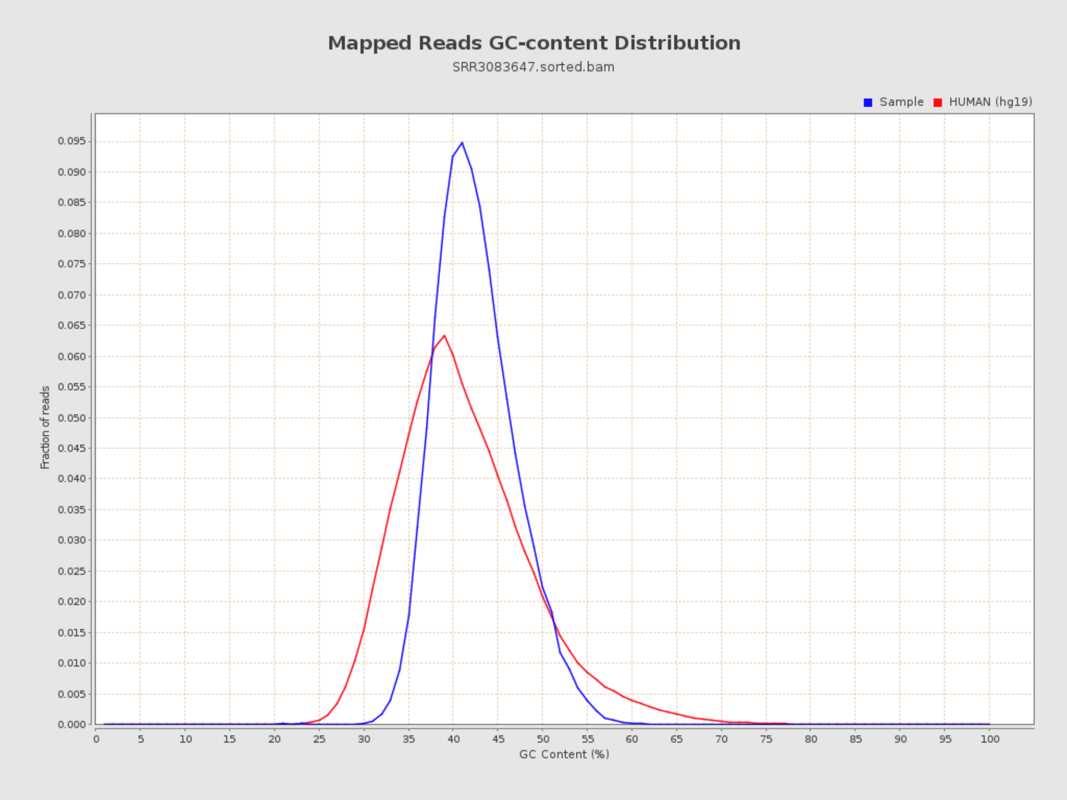
# 7. Results : Duplication Rate Histogram



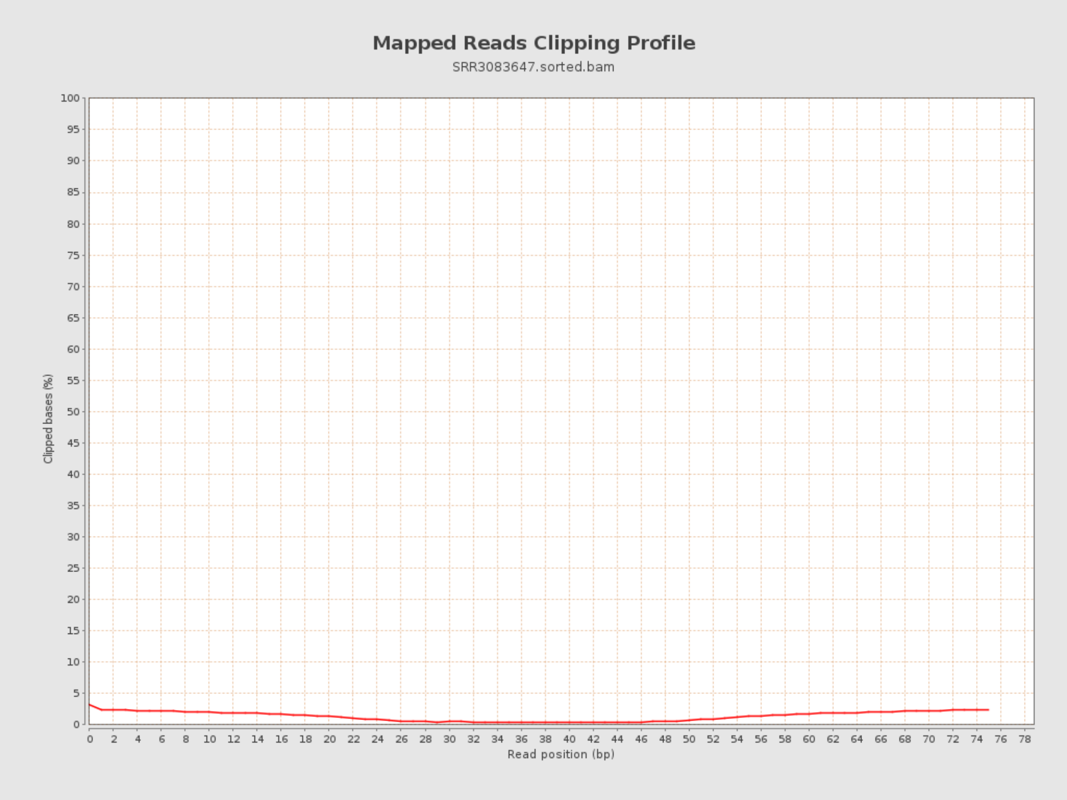
# 8. Results : Mapped Reads Nucleotide Content



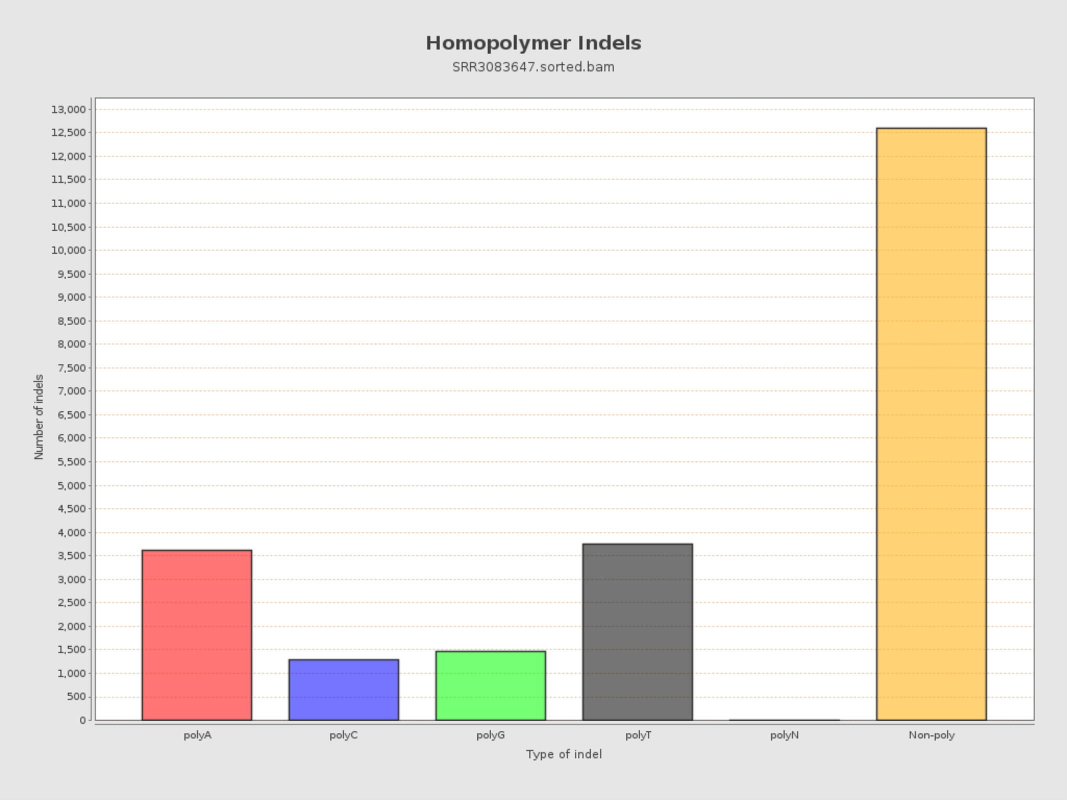
# 9. Results : Mapped Reads GC-content Distribution



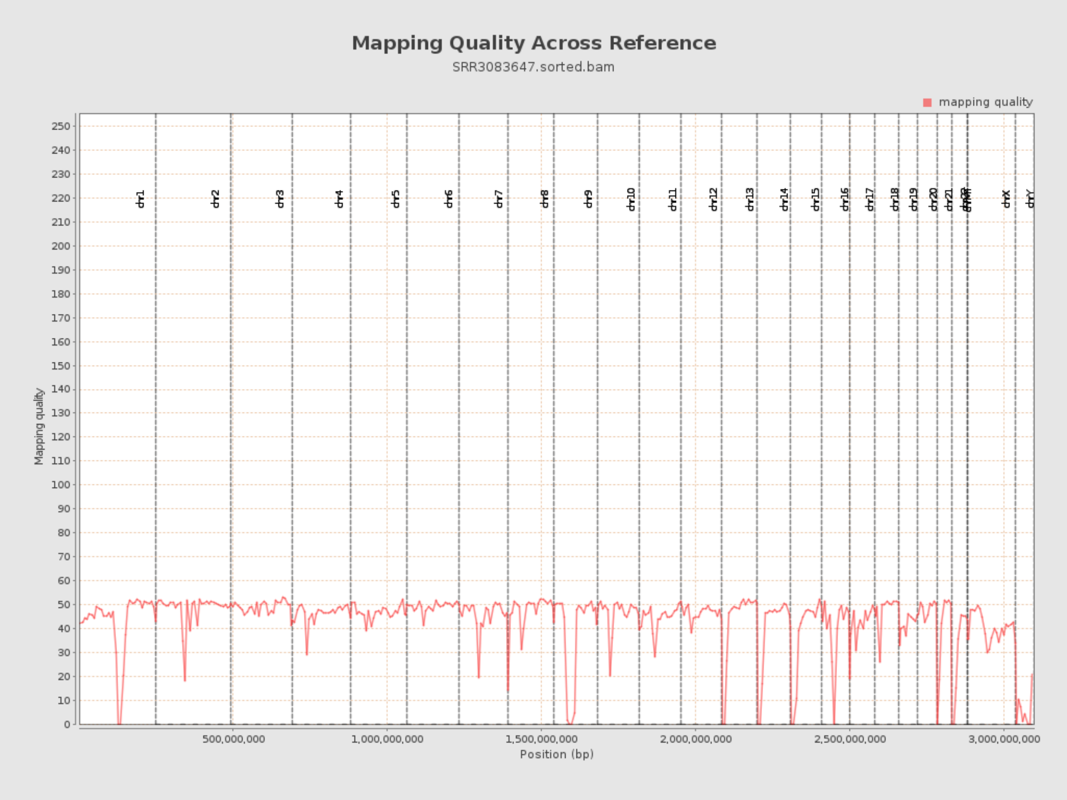
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram