# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 09:38:32*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008747.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_SRR6008747 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008747.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 14 09:38:31 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6008747.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,588,453 |
| Mapped reads | 1,173,068 / 73.85% |
| Unmapped reads | 415,385 / 26.15% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 8,240 / 0.52% |
| Read min/max/mean length | 30 / 76 / 76.18 |
| Duplicated reads (estimated) | 32,278 / 2.03% |
| Duplication rate | 2.18% |
| Clipped reads | 637,216 / 40.12% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 22,698,137 / 30.16% |
| Number/percentage of C's | 13,428,591 / 17.84% |
| Number/percentage of T's | 22,318,679 / 29.65% |
| Number/percentage of G's | 16,807,658 / 22.33% |
| Number/percentage of N's | 11,544 / 0.02% |
| GC Percentage | 40.17% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0243 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2238 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.47 |

## 2.5. Mismatches and indels

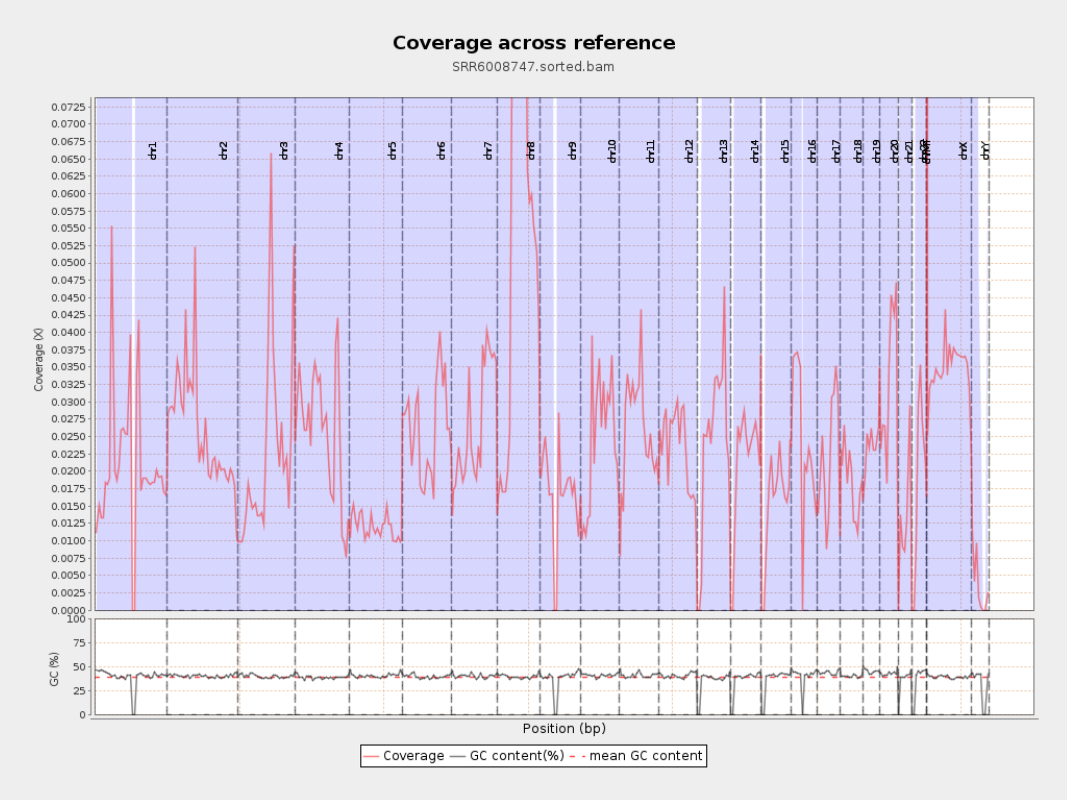
| | |
|---|---|
| General error rate | 0.94% |
| Mismatches | 694,866 |
| Insertions | 5,810 |
| Mapped reads with at least one insertion | 0.49% |
| Deletions | 24,365 |
| Mapped reads with at least one deletion | 2.05% |
| Homopolymer indels | 47.09% |

## 2.6. Chromosome stats

| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5161292 | 0.0207 | 0.3212 |
| chr2 | 243199373 | 6326695 | 0.026 | 0.2778 |
| chr3 | 198022430 | 4443238 | 0.0224 | 0.1695 |
| chr4 | 191154276 | 4928970 | 0.0258 | 0.1841 |
| chr5 | 180915260 | 2184595 | 0.0121 | 0.1193 |
| chr6 | 171115067 | 4506633 | 0.0263 | 0.1958 |
| chr7 | 159138663 | 4255832 | 0.0267 | 0.239 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8373872 | 0.0572 | 0.3372 |
| chr9 | 141213431 | 2347946 | 0.0166 | 0.2131 |
| chr10 | 135534747 | 3266187 | 0.0241 | 0.2305 |
| chr11 | 135006516 | 3560094 | 0.0264 | 0.2138 |
| chr12 | 133851895 | 3154581 | 0.0236 | 0.1716 |
| chr13 | 115169878 | 2804976 | 0.0244 | 0.1775 |
| chr14 | 107349540 | 2266516 | 0.0211 | 0.1669 |
| chr15 | 102531392 | 1585772 | 0.0155 | 0.1384 |
| chr16 | 90354753 | 2168612 | 0.024 | 0.1881 |
| chr17 | 81195210 | 1796769 | 0.0221 | 0.1877 |
| chr18 | 78077248 | 1430126 | 0.0183 | 0.3367 |
| chr19 | 59128983 | 1409067 | 0.0238 | 0.2251 |
| chr20 | 63025520 | 2066569 | 0.0328 | 0.2046 |
| chr21 | 48129895 | 644234 | 0.0134 | 0.1355 |
| chr22 | 51304566 | 977951 | 0.0191 | 0.1542 |
| chrMT | 16571 | 16055 | 0.9689 | 1.3172 |
| chrX | 155270560 | 5420771 | 0.0349 | 0.2249 |
| chrY | 59373566 | 205604 | 0.0035 | 0.0829 |

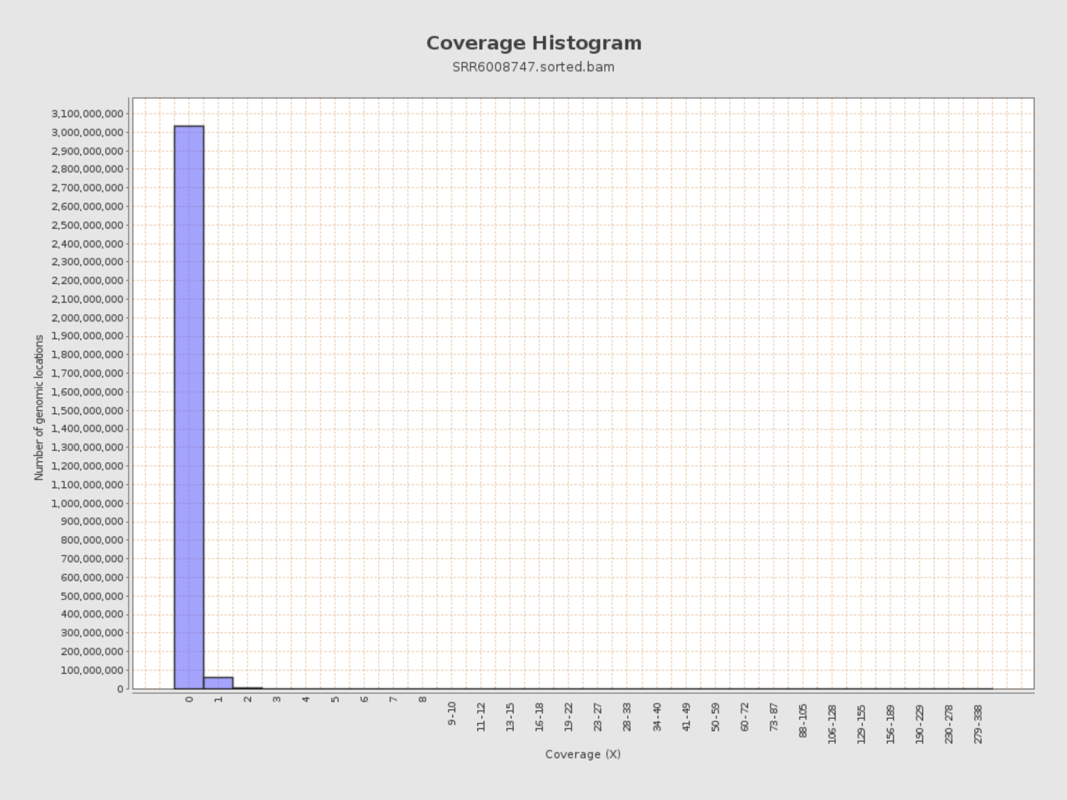
# 3. Results : Coverage across reference



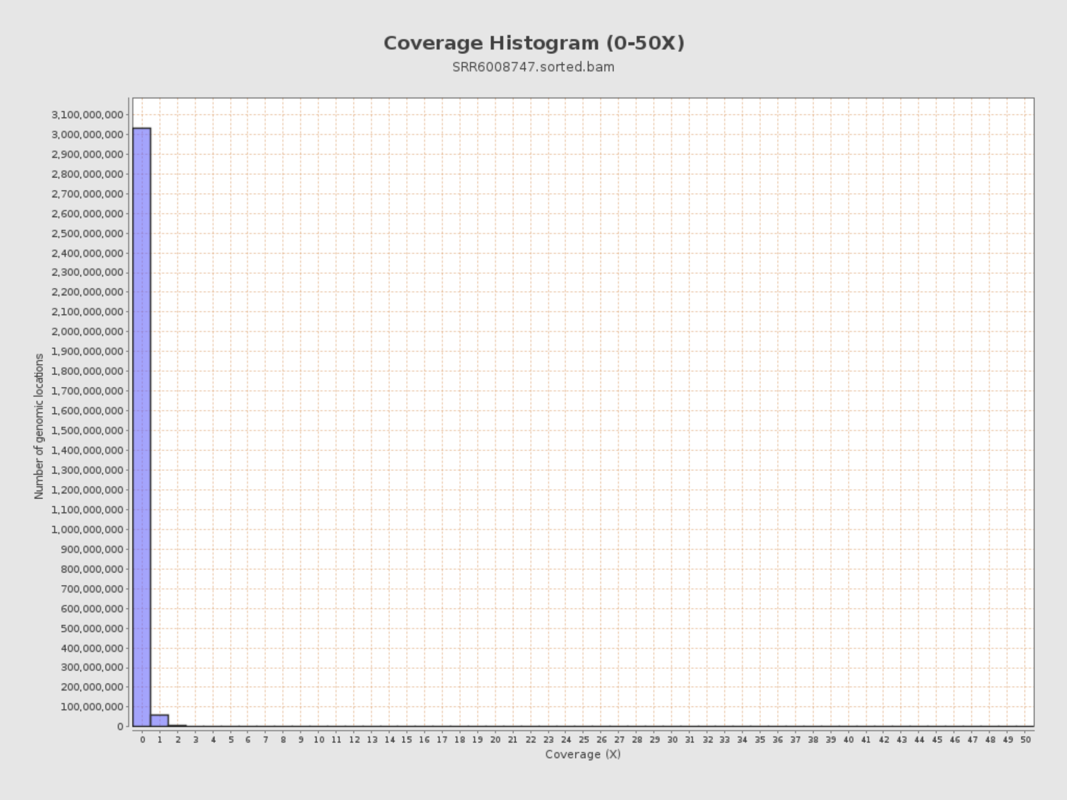
Coverage across reference

SRR6008747.sorted.bam

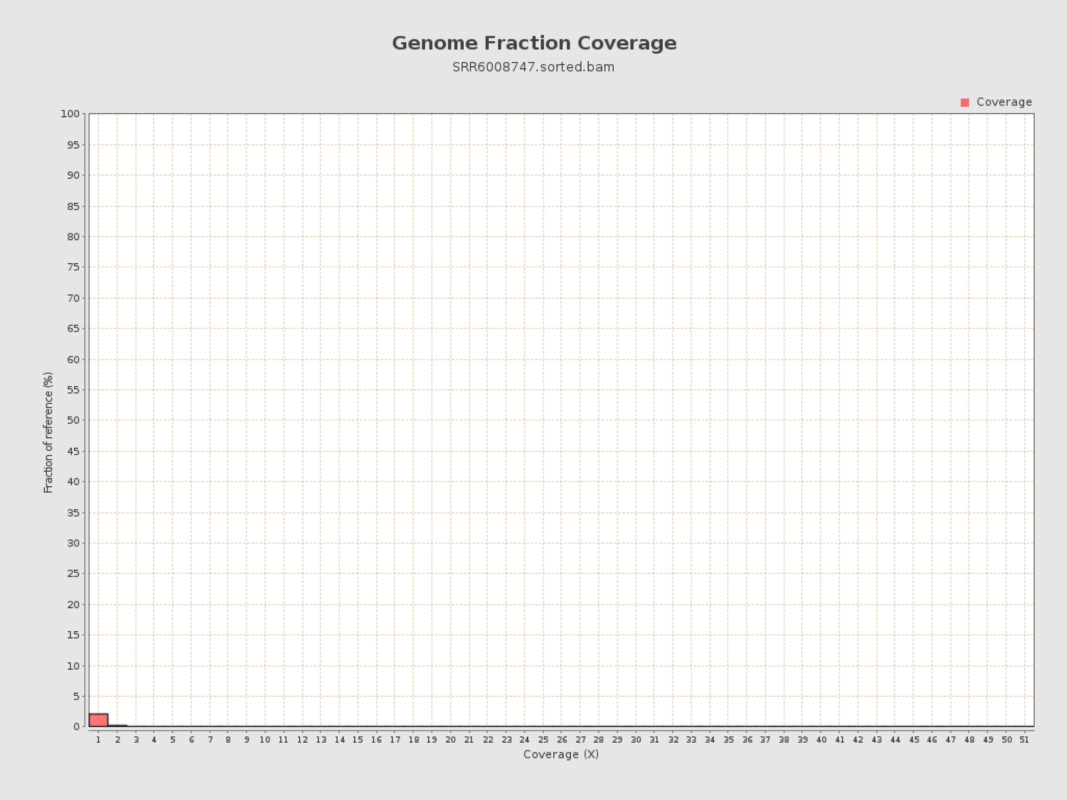
# 4. Results : Coverage Histogram



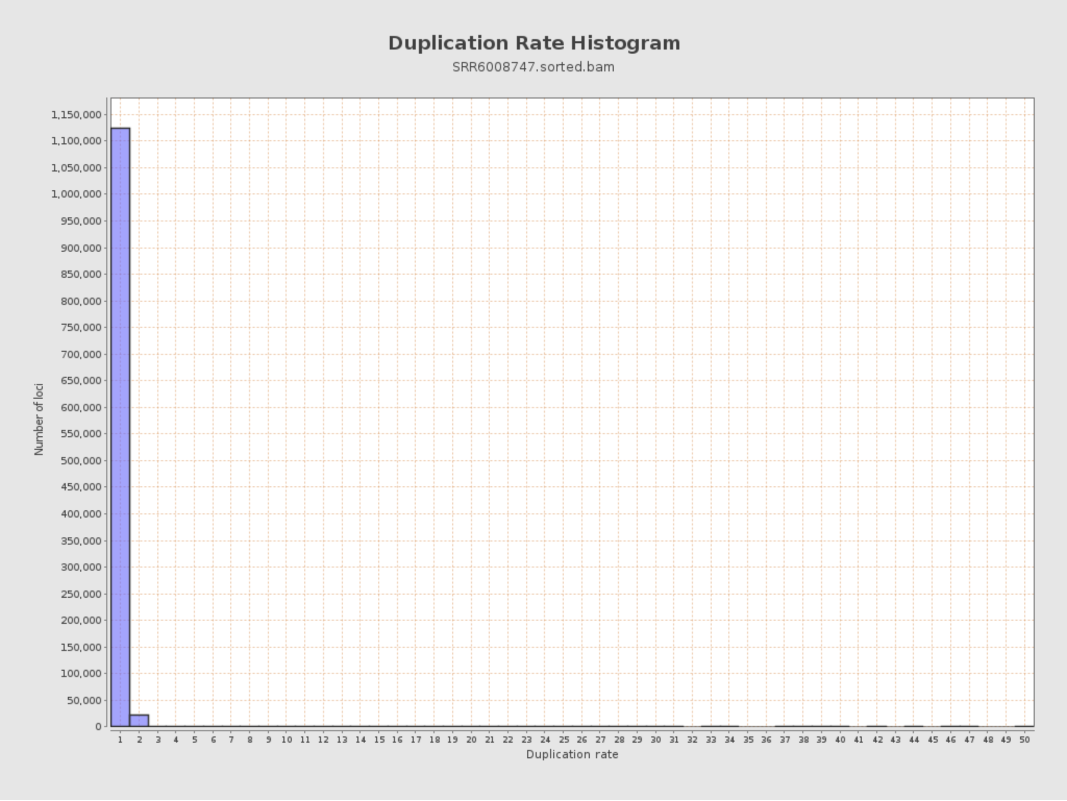
# 5. Results : Coverage Histogram (0-50X)



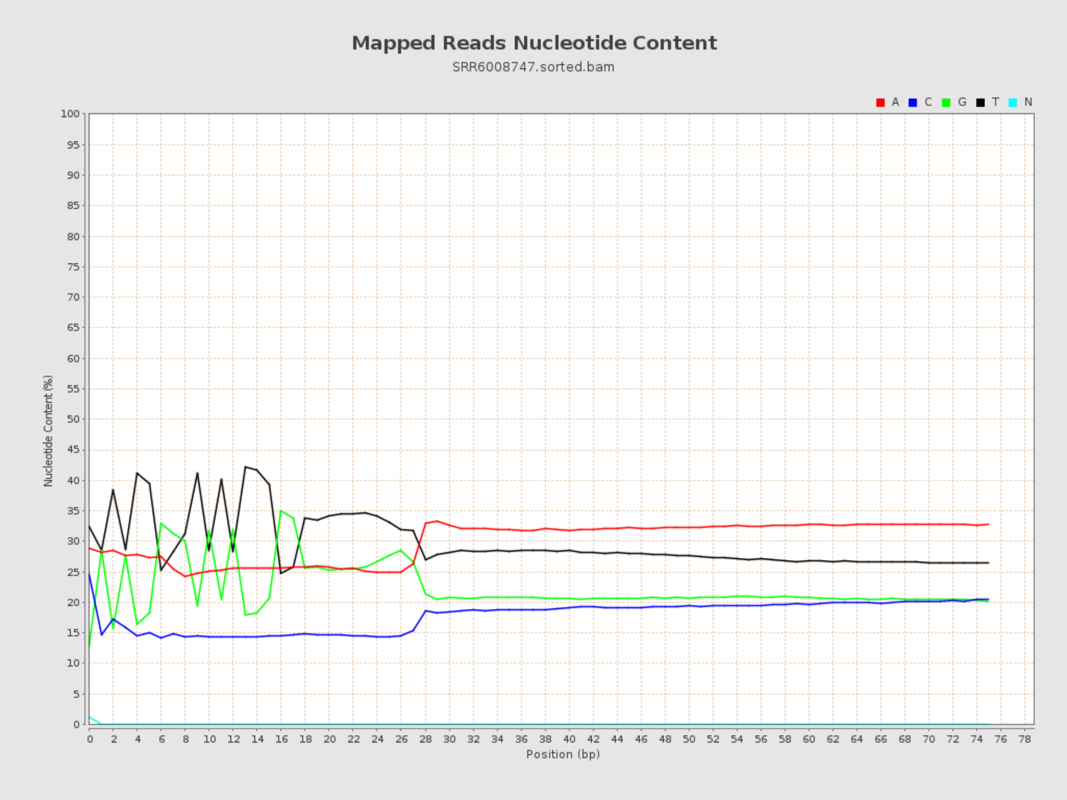
# 6. Results : Genome Fraction Coverage



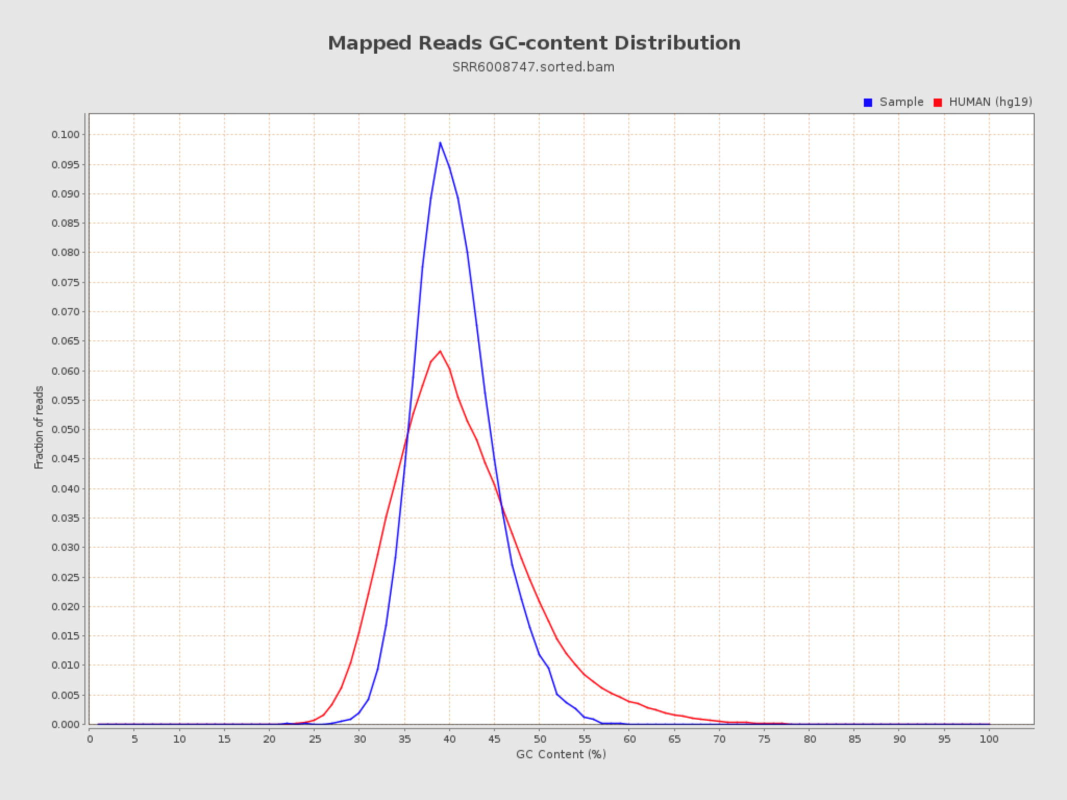
# 7. Results : Duplication Rate Histogram



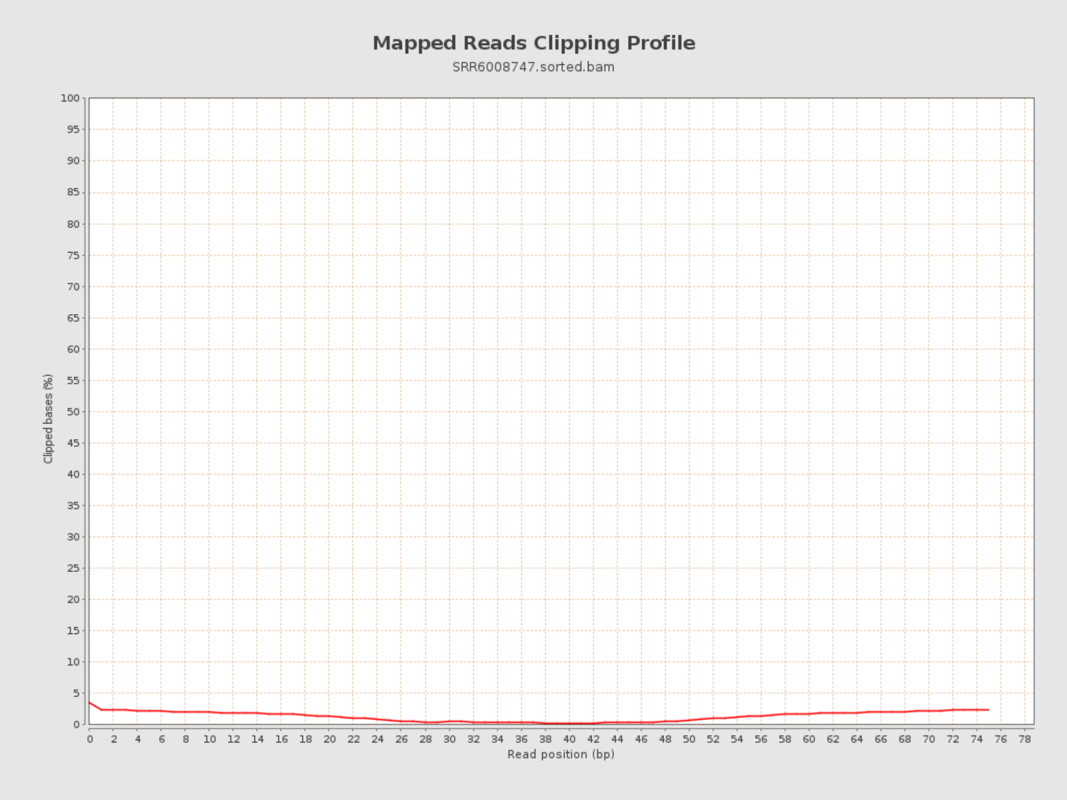
# 8. Results : Mapped Reads Nucleotide Content



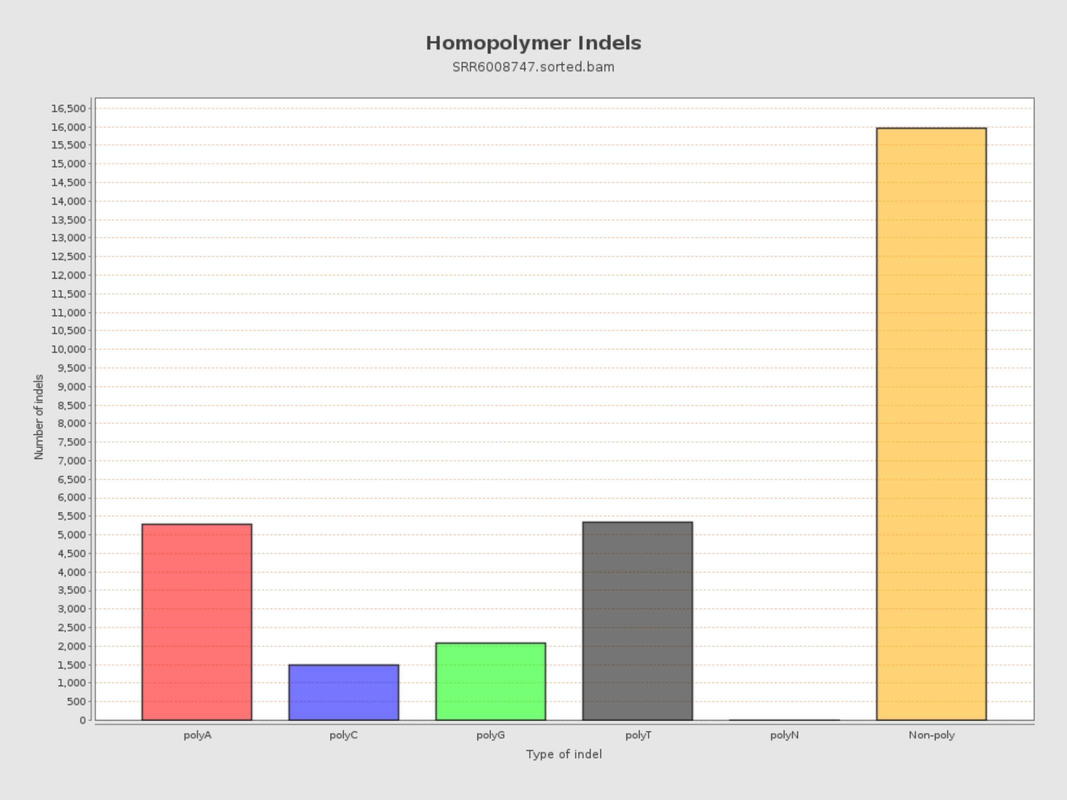
# 9. Results : Mapped Reads GC-content Distribution



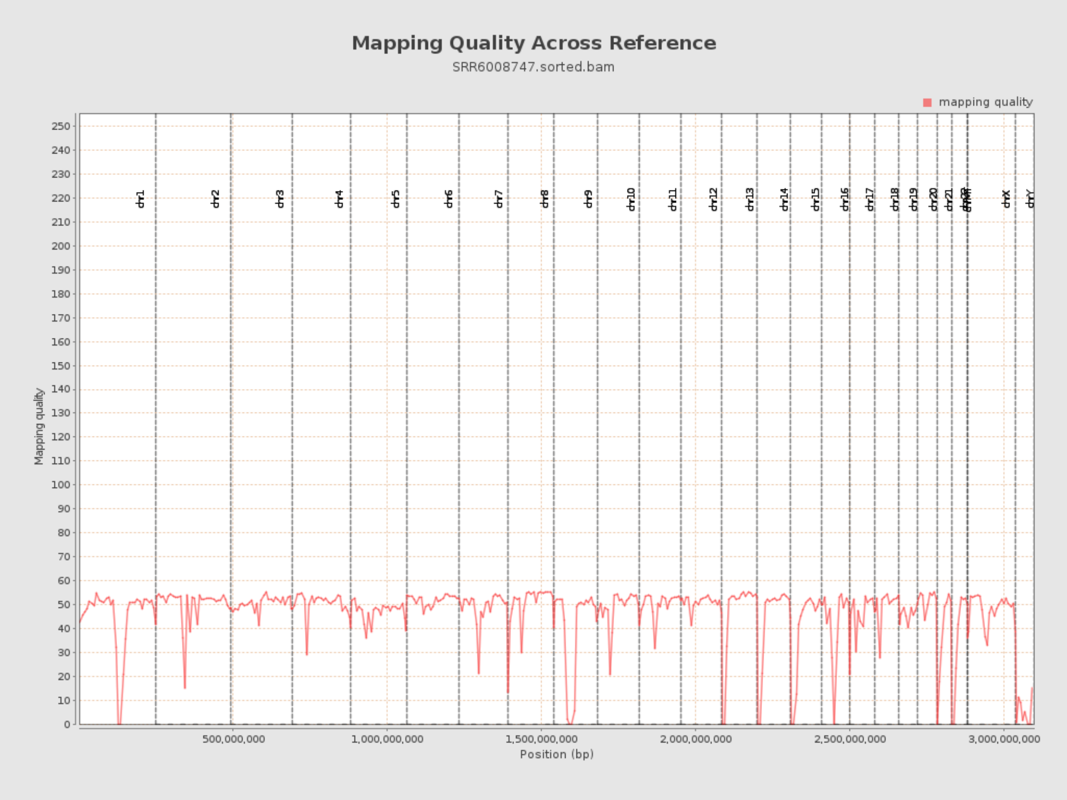
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram