# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/20 01:31:33*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506315.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_SRR1506315 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506315.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Dec 20 01:31:33 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1506315.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 9,889,590 |
| Mapped reads | 7,237,427 / 73.18% |
| Unmapped reads | 2,652,163 / 26.82% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 116,627 / 1.18% |
| Read min/max/mean length | 30 / 94 / 94.42 |
| Duplicated reads (estimated) | 1,462,154 / 14.78% |
| Duplication rate | 14.97% |
| Clipped reads | 4,380,889 / 44.3% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 166,536,237 / 28.95% |
| Number/percentage of C's | 102,423,192 / 17.81% |
| Number/percentage of T's | 161,127,666 / 28.01% |
| Number/percentage of G's | 144,976,871 / 25.21% |
| Number/percentage of N's | 96,070 / 0.02% |
| GC Percentage | 43.01% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1859 |
| | |

| | |
|---|---|
| Standard Deviation | 1.2386 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.51 |

## 2.5. Mismatches and indels

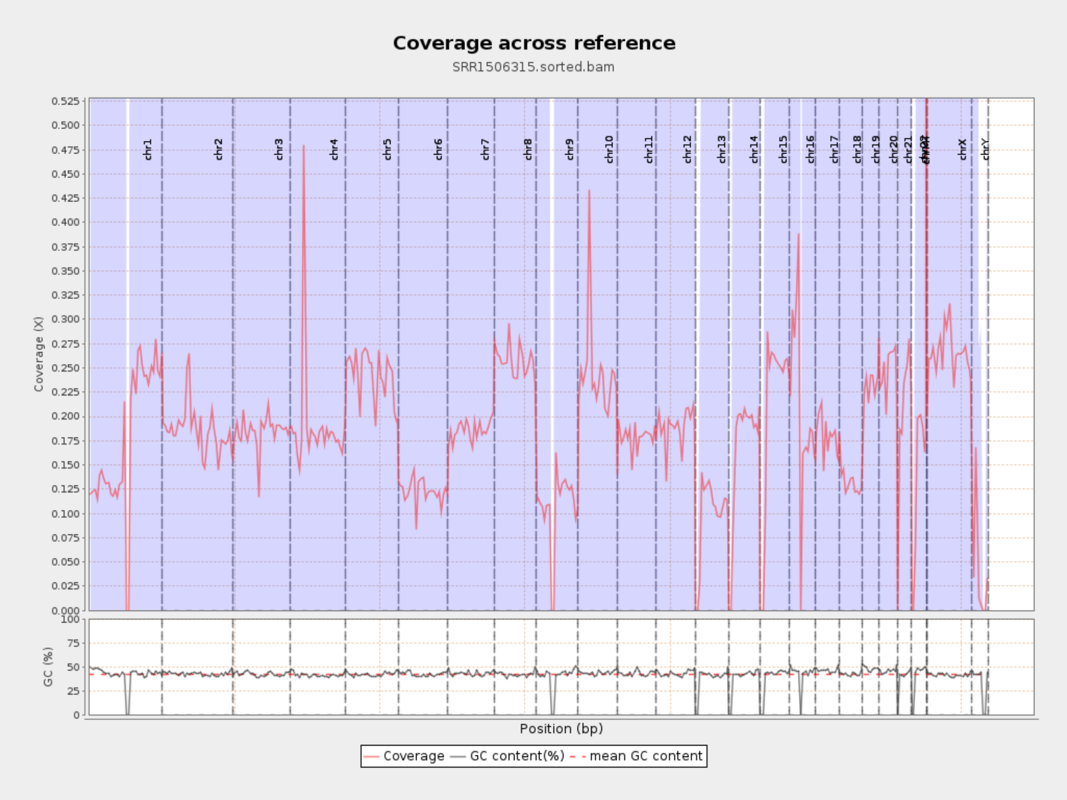
| | |
|---|---|
| General error rate | 0.88% |
| Mismatches | 4,929,041 |
| Insertions | 53,003 |
| Mapped reads with at least one insertion | 0.71% |
| Deletions | 128,439 |
| Mapped reads with at least one deletion | 1.74% |
| Homopolymer indels | 43.19% |

## 2.6. Chromosome stats

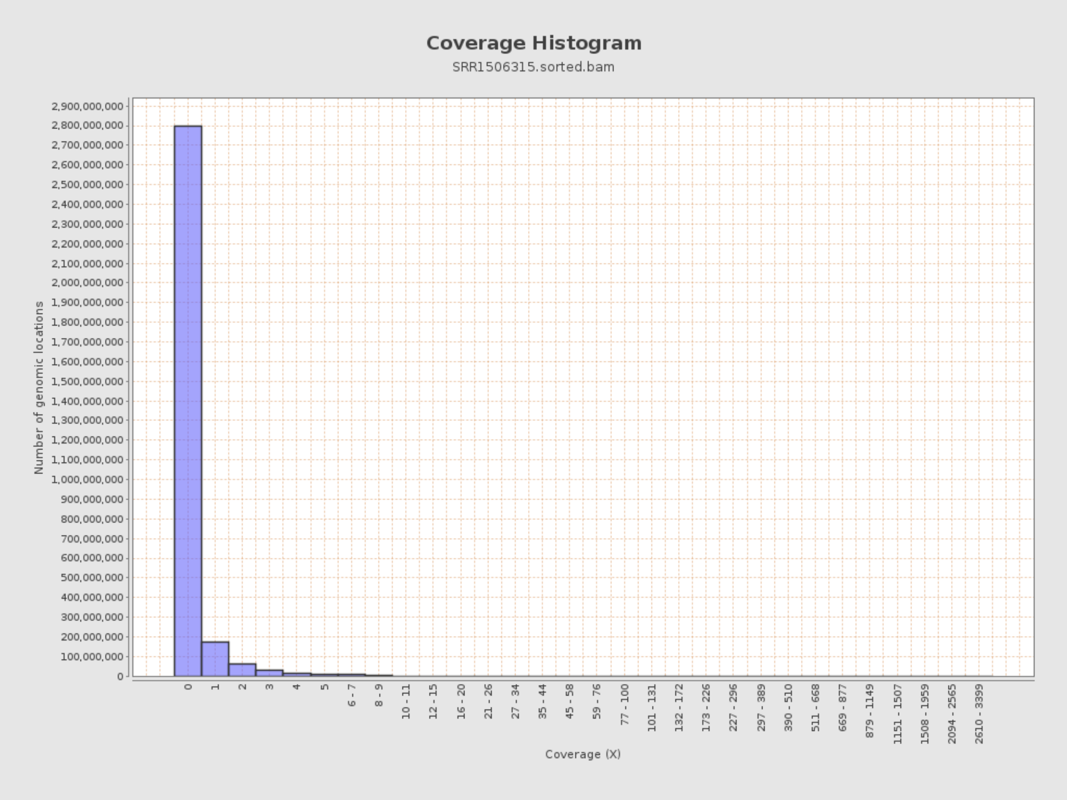
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 43663608 | 0.1752 | 1.8242 |
| chr2 | 243199373 | 45438844 | 0.1868 | 1.2374 |
| chr3 | 198022430 | 36494210 | 0.1843 | 0.7469 |
| chr4 | 191154276 | 36174067 | 0.1892 | 1.313 |
| chr5 | 180915260 | 43731786 | 0.2417 | 0.8844 |
| chr6 | 171115067 | 21098546 | 0.1233 | 0.6533 |
| chr7 | 159138663 | 29549290 | 0.1857 | 1.1341 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 37640445 | 0.2572 | 2.4371 |
| chr9 | 141213431 | 15016991 | 0.1063 | 0.9528 |
| chr10 | 135534747 | 33223569 | 0.2451 | 1.6208 |
| chr11 | 135006516 | 24127597 | 0.1787 | 1.0784 |
| chr12 | 133851895 | 25338832 | 0.1893 | 0.7835 |
| chr13 | 115169878 | 11236715 | 0.0976 | 0.5366 |
| chr14 | 107349540 | 17594746 | 0.1639 | 0.7716 |
| chr15 | 102531392 | 21525408 | 0.2099 | 0.8214 |
| chr16 | 90354753 | 19181816 | 0.2123 | 1.1239 |
| chr17 | 81195210 | 14578387 | 0.1795 | 0.869 |
| chr18 | 78077248 | 10320908 | 0.1322 | 1.5805 |
| chr19 | 59128983 | 13629604 | 0.2305 | 1.4601 |
| chr20 | 63025520 | 15636112 | 0.2481 | 0.9793 |
| chr21 | 48129895 | 9932421 | 0.2064 | 1.0896 |
| chr22 | 51304566 | 6702643 | 0.1306 | 0.6536 |
| chrMT | 16571 | 55034 | 3.3211 | 3.9846 |
| chrX | 155270560 | 41098064 | 0.2647 | 0.9975 |
| chrY | 59373566 | 2435061 | 0.041 | 1.4861 |

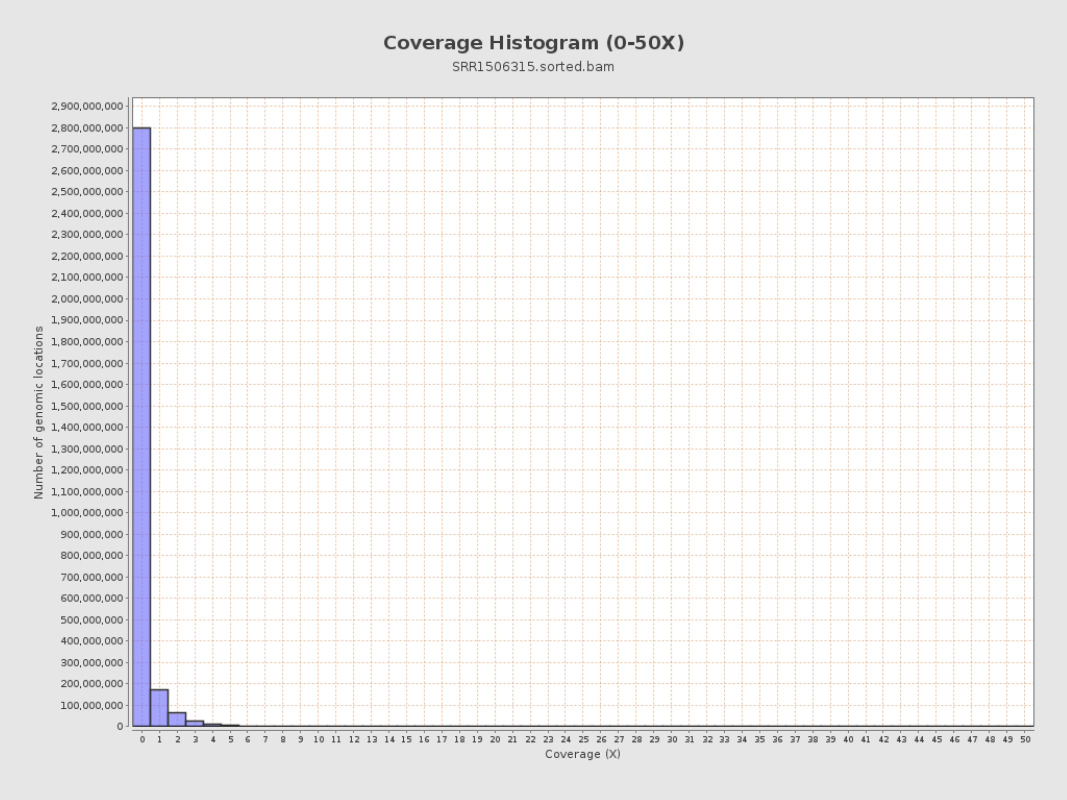
# 3. Results : Coverage across reference



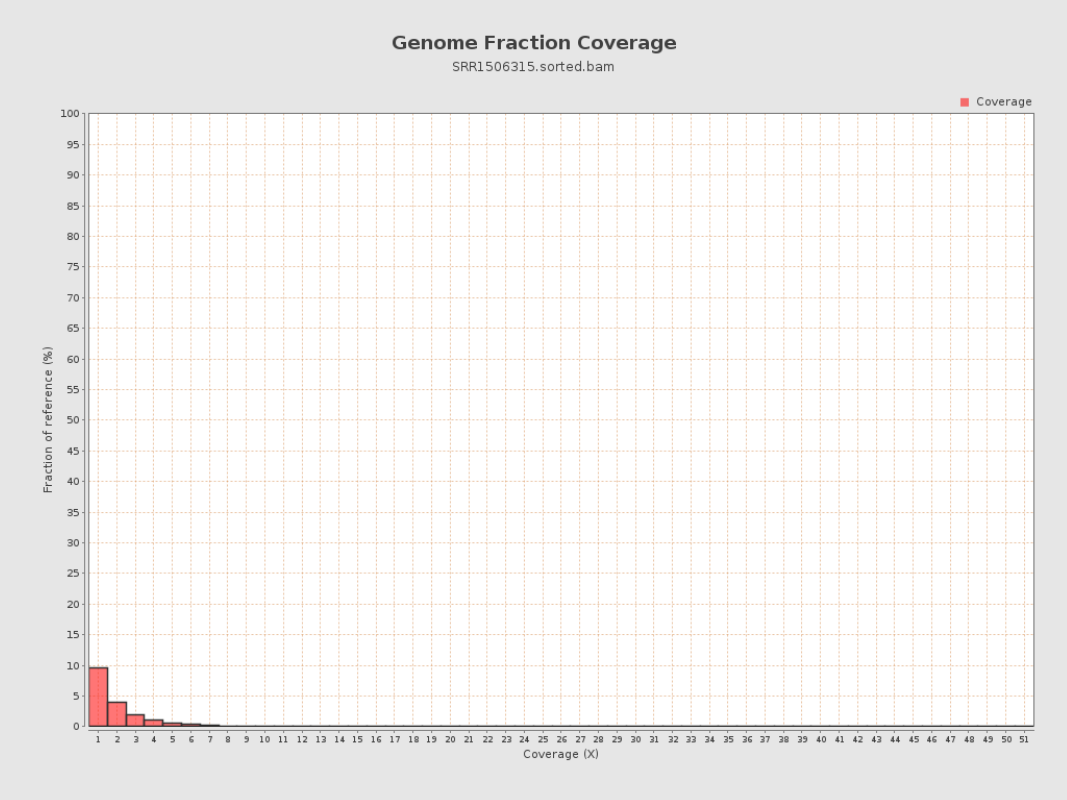
# 4. Results : Coverage Histogram



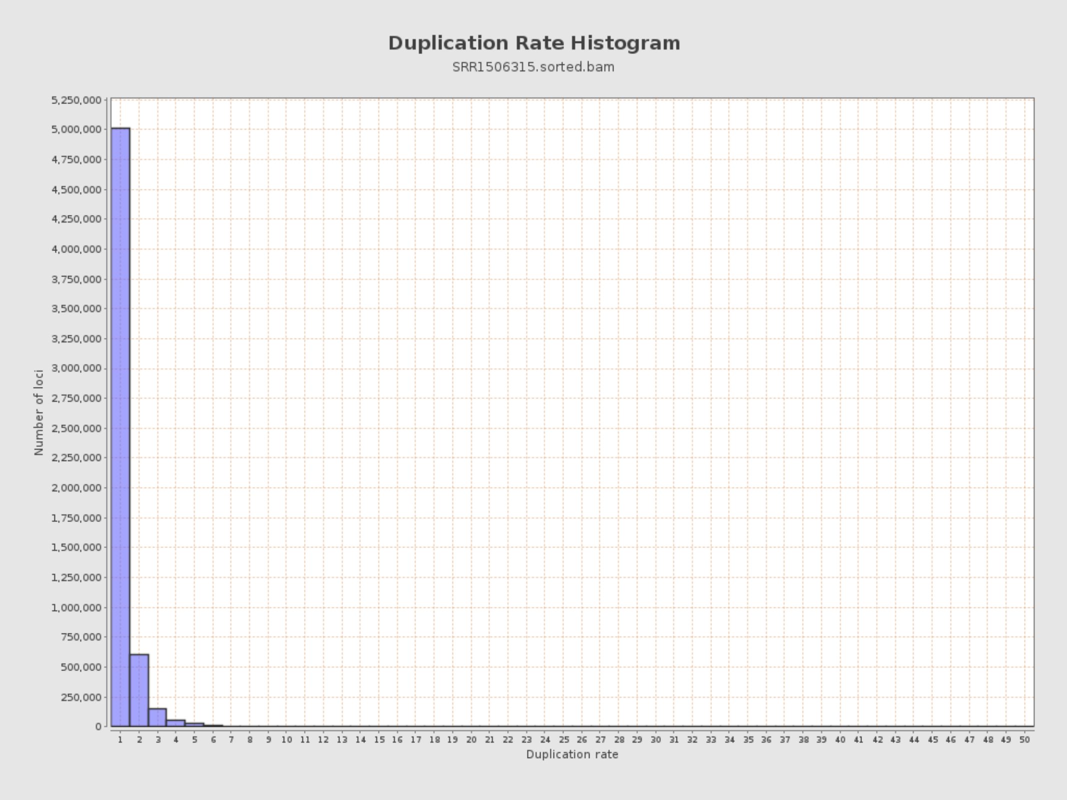
# 5. Results : Coverage Histogram (0-50X)



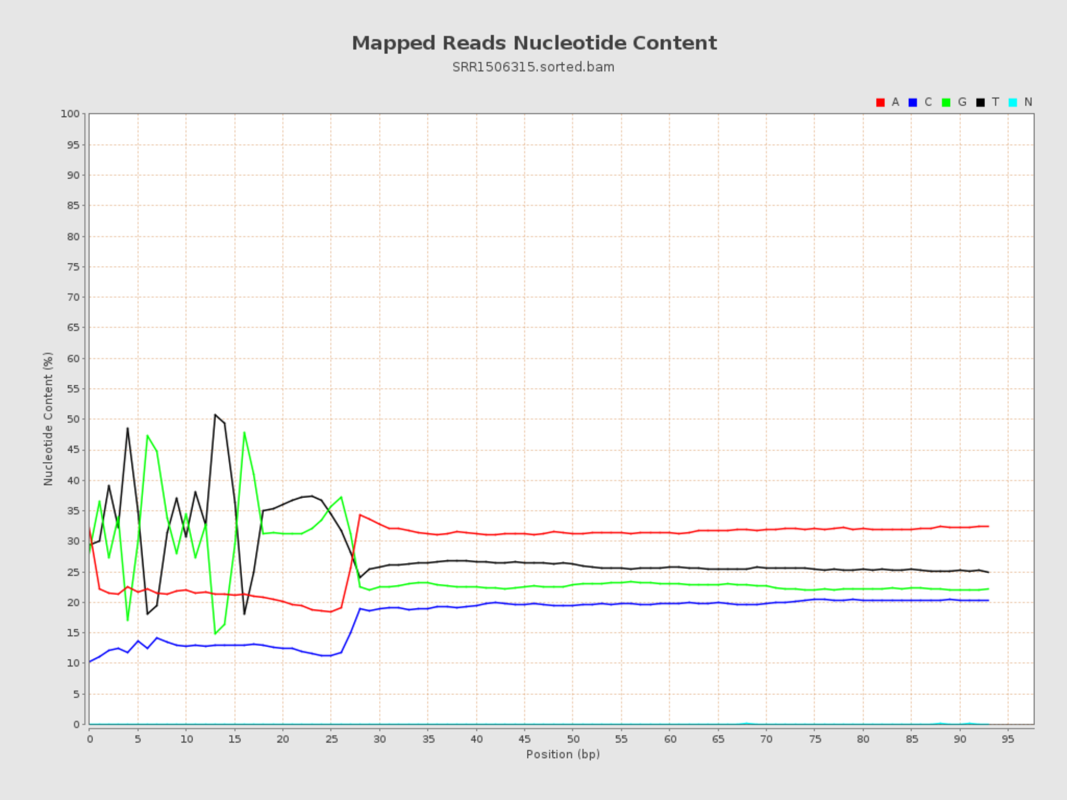
# 6. Results : Genome Fraction Coverage



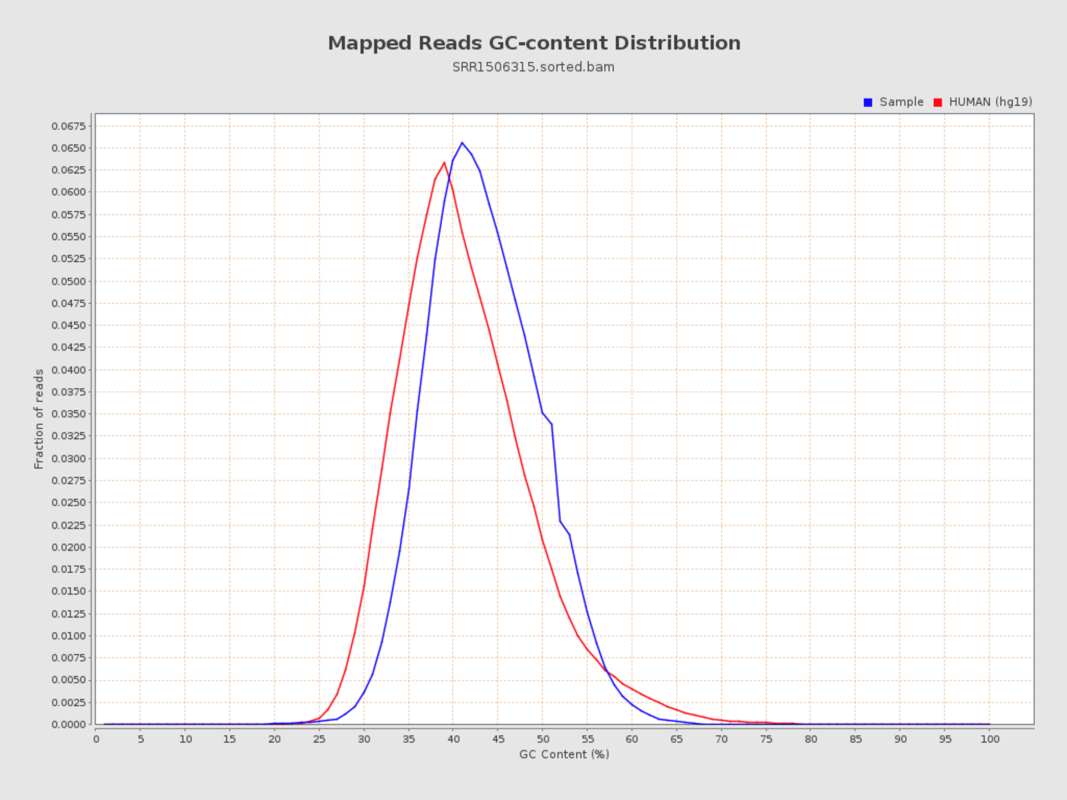
# 7. Results : Duplication Rate Histogram



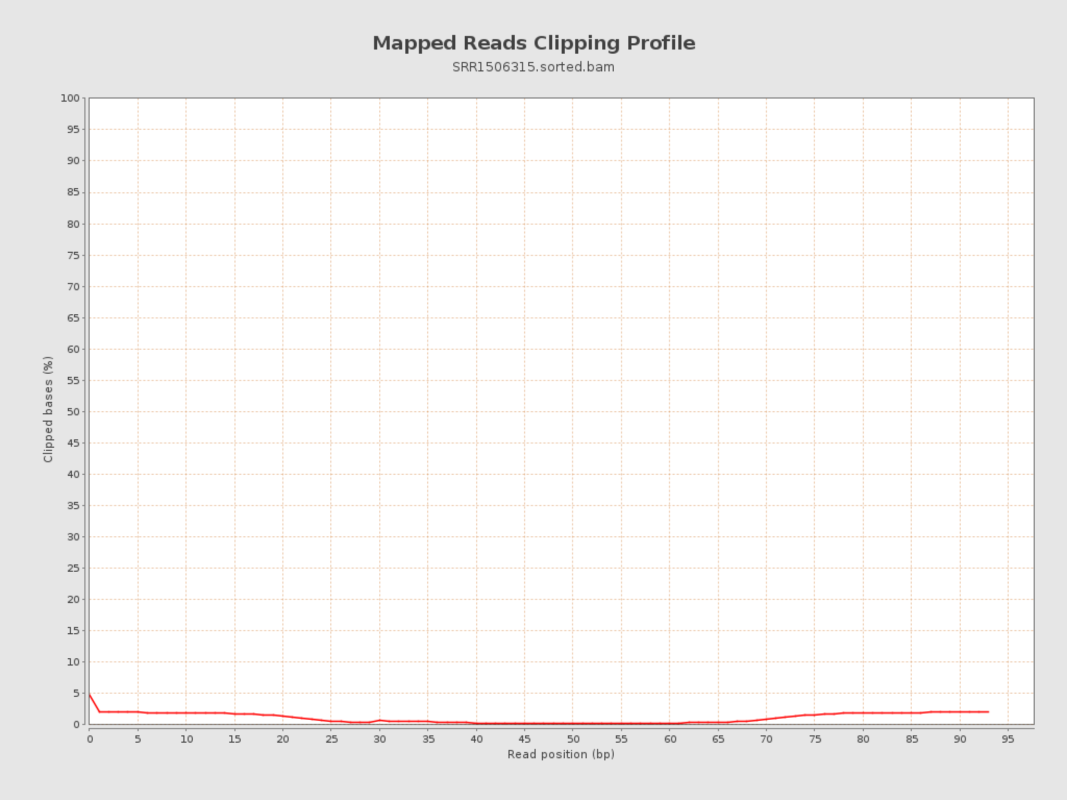
# 8. Results : Mapped Reads Nucleotide Content



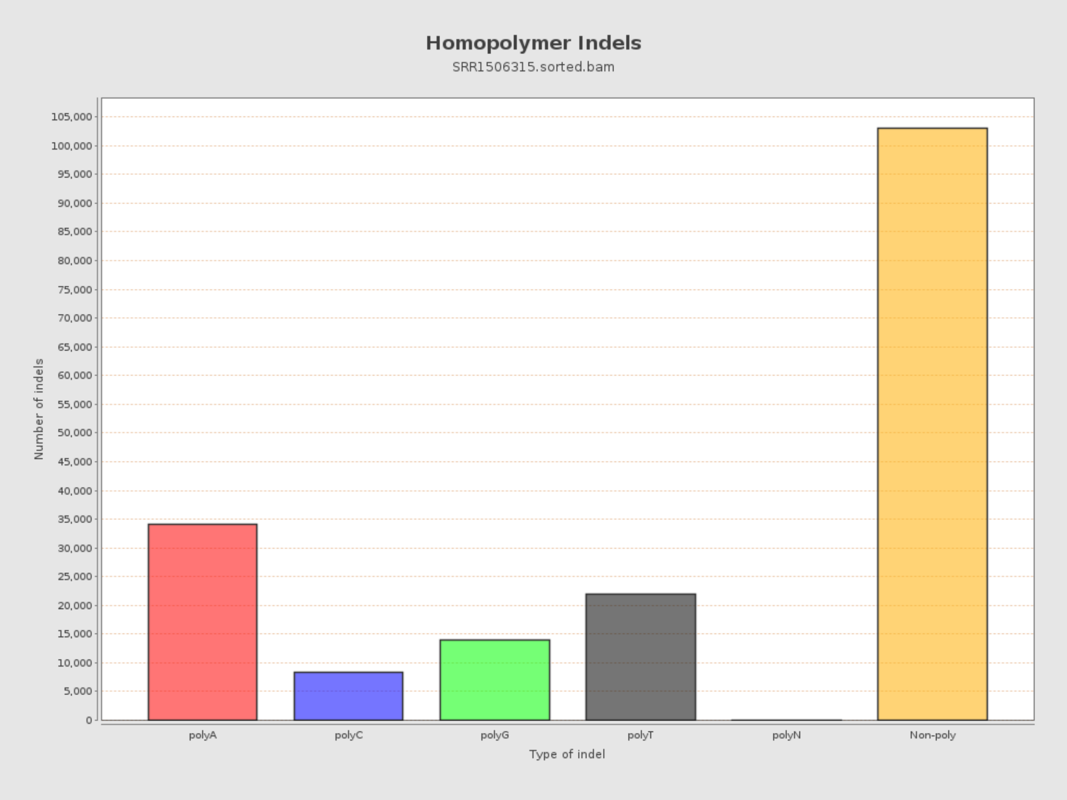
# 9. Results : Mapped Reads GC-content Distribution



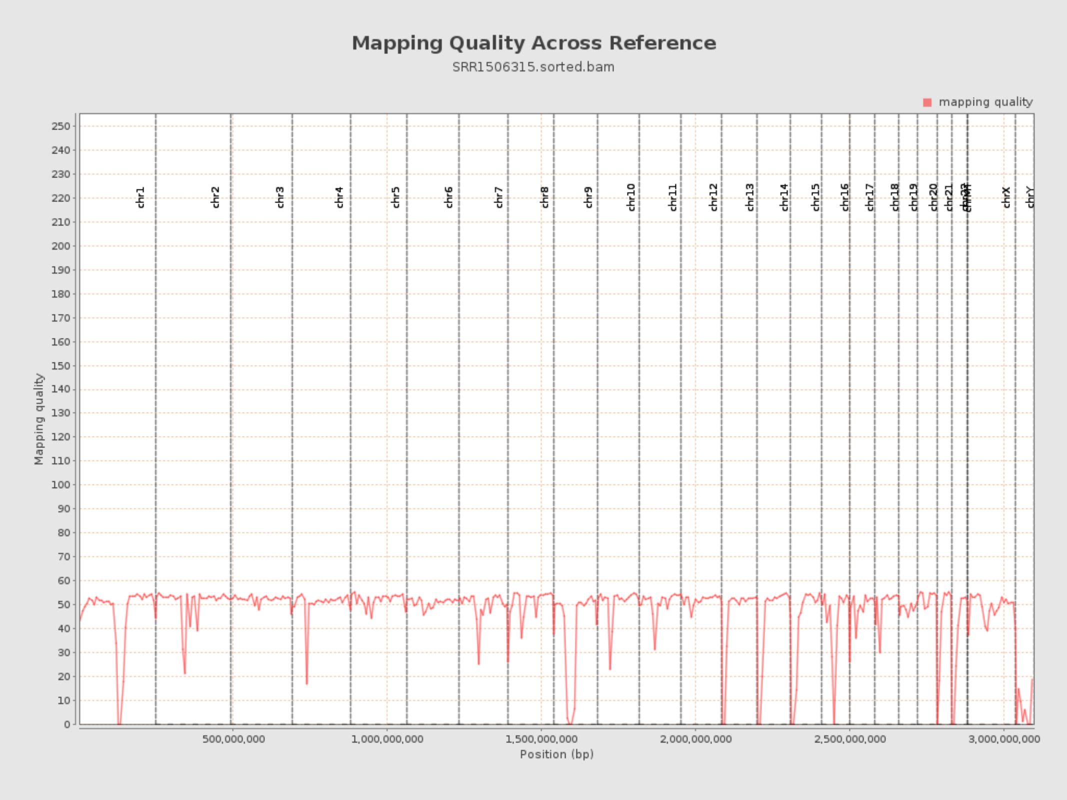
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram