# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/11 05:41:08*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514715.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_SRR5514715 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514715.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Apr 11 05:41:07 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR5514715.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 40,663,090 |
| Mapped reads | 40,358,864 / 99.25% |
| Unmapped reads | 304,226 / 0.75% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 2,579,057 / 6.34% |
| Read min/max/mean length | 30 / 100 / 100.33 |
| Duplicated reads (estimated) | 23,742,532 / 58.39% |
| Duplication rate | 33.28% |
| Clipped reads | 10,553,651 / 25.95% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,058,912,615 / 27.65% |
| Number/percentage of C's | 847,593,205 / 22.13% |
| Number/percentage of T's | 1,058,962,889 / 27.65% |
| Number/percentage of G's | 858,069,992 / 22.41% |
| Number/percentage of N's | 5,680,917 / 0.15% |
| GC Percentage | 44.54% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 1.2382 |
| | |

| | |
|---|---|
| Standard Deviation | 142.9043 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.94 |

## 2.5. Mismatches and indels

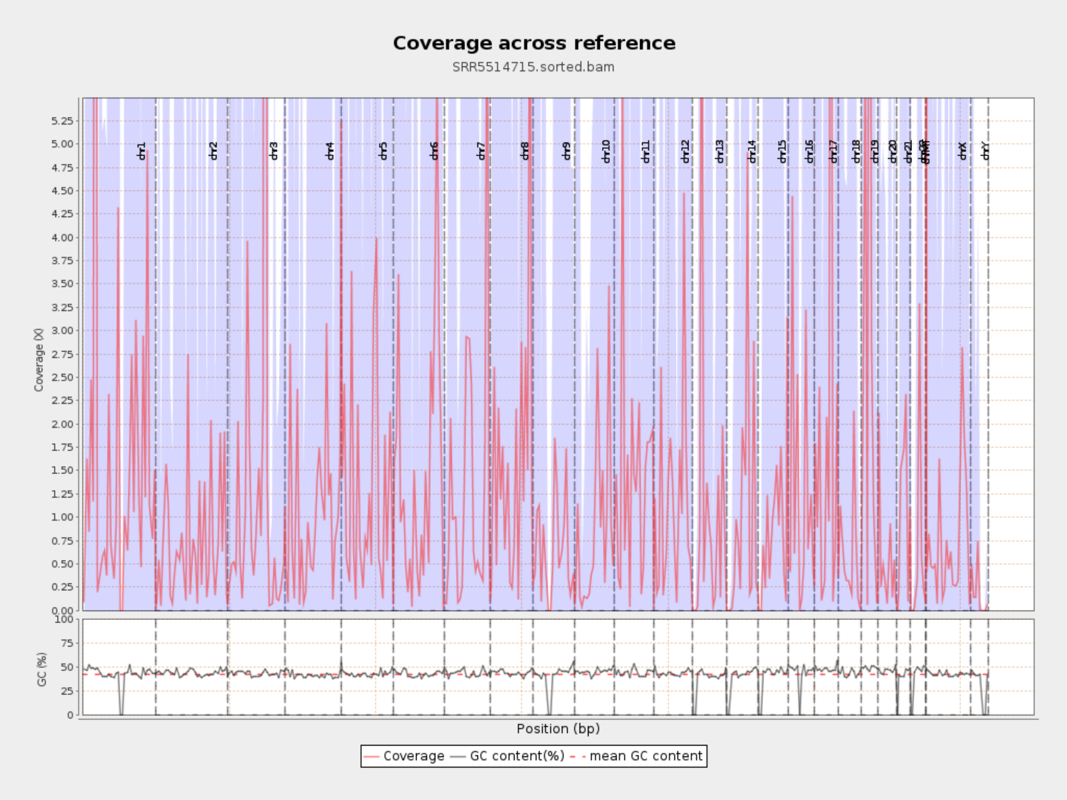
| | |
|---|---|
| General error rate | 0.78% |
| Mismatches | 27,074,901 |
| Insertions | 1,486,422 |
| Mapped reads with at least one insertion | 3.47% |
| Deletions | 1,681,886 |
| Mapped reads with at least one deletion | 3.86% |
| Homopolymer indels | 30.53% |

## 2.6. Chromosome stats

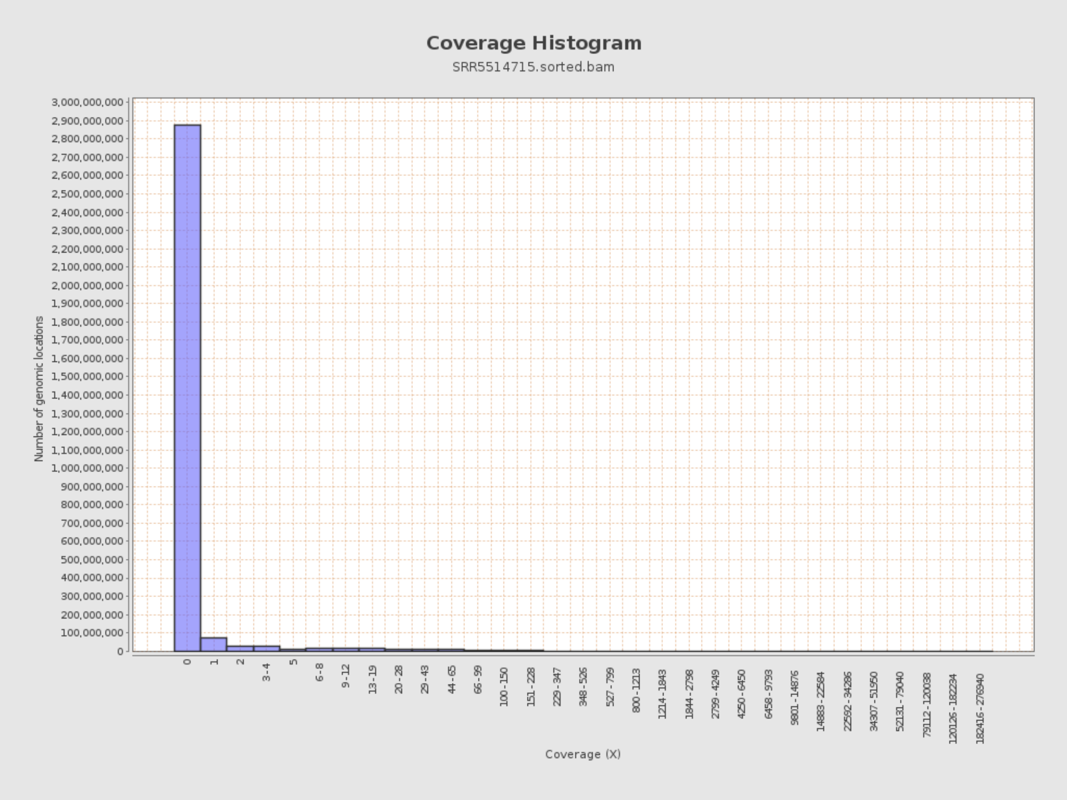
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 474340331 | 1.9031 | 265.168 |
| chr2 | 243199373 | 180371060 | 0.7417 | 14.4647 |
| chr3 | 198022430 | 380710824 | 1.9226 | 408.9235 |
| chr4 | 191154276 | 192545086 | 1.0073 | 14.2447 |
| chr5 | 180915260 | 229220015 | 1.267 | 13.0218 |
| chr6 | 171115067 | 258892164 | 1.513 | 12.4146 |
| chr7 | 159138663 | 208666820 | 1.3112 | 11.8797 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 241362052 | 1.6491 | 33.0944 |
| chr9 | 141213431 | 96914645 | 0.6863 | 14.0995 |
| chr10 | 135534747 | 119993856 | 0.8853 | 74.0122 |
| chr11 | 135006516 | 198196455 | 1.4681 | 15.8519 |
| chr12 | 133851895 | 159689064 | 1.193 | 14.3571 |
| chr13 | 115169878 | 130420906 | 1.1324 | 96.2181 |
| chr14 | 107349540 | 109983579 | 1.0245 | 11.4888 |
| chr15 | 102531392 | 82199750 | 0.8017 | 9.5976 |
| chr16 | 90354753 | 112186025 | 1.2416 | 21.9974 |
| chr17 | 81195210 | 169909317 | 2.0926 | 23.9577 |
| chr18 | 78077248 | 49281412 | 0.6312 | 10.0149 |
| chr19 | 59128983 | 190800073 | 3.2268 | 415.0669 |
| chr20 | 63025520 | 33760807 | 0.5357 | 8.2125 |
| chr21 | 48129895 | 50554034 | 1.0504 | 18.0616 |
| chr22 | 51304566 | 34551362 | 0.6735 | 9.7654 |
| chrMT | 16571 | 1859418 | 112.2092 | 62.7931 |
| chrX | 155270560 | 115729272 | 0.7453 | 9.6804 |
| chrY | 59373566 | 11057792 | 0.1862 | 7.6411 |

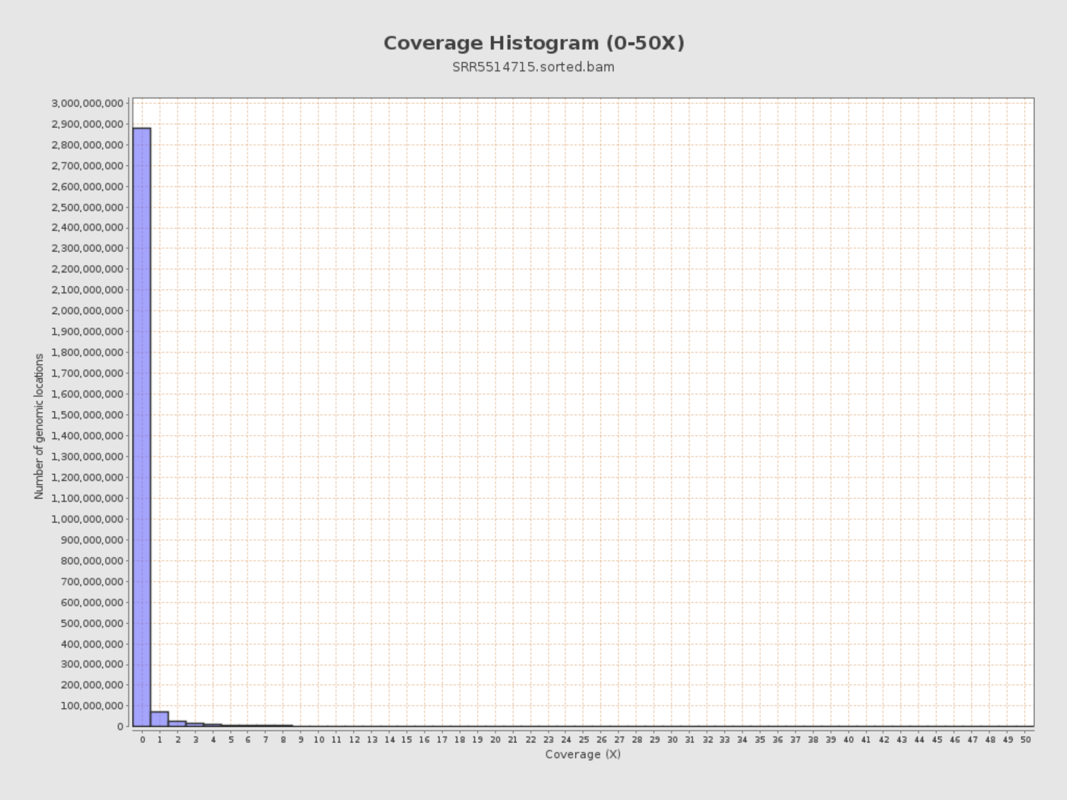
# 3. Results : Coverage across reference



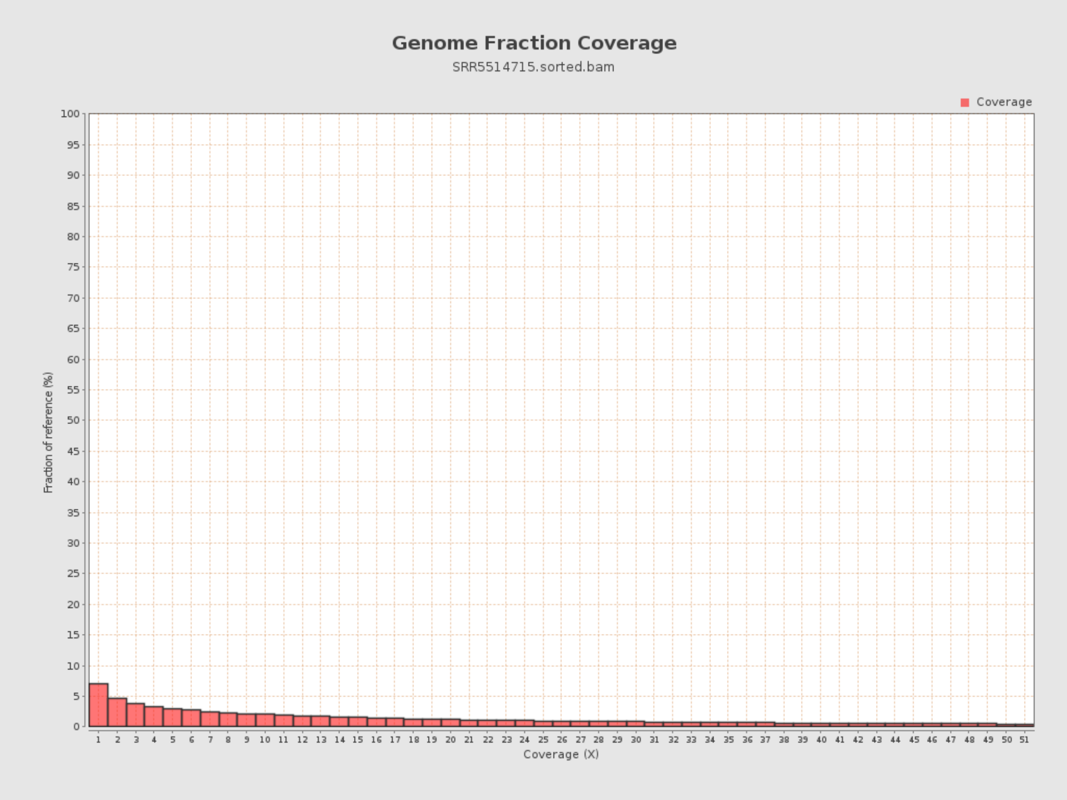
# 4. Results : Coverage Histogram



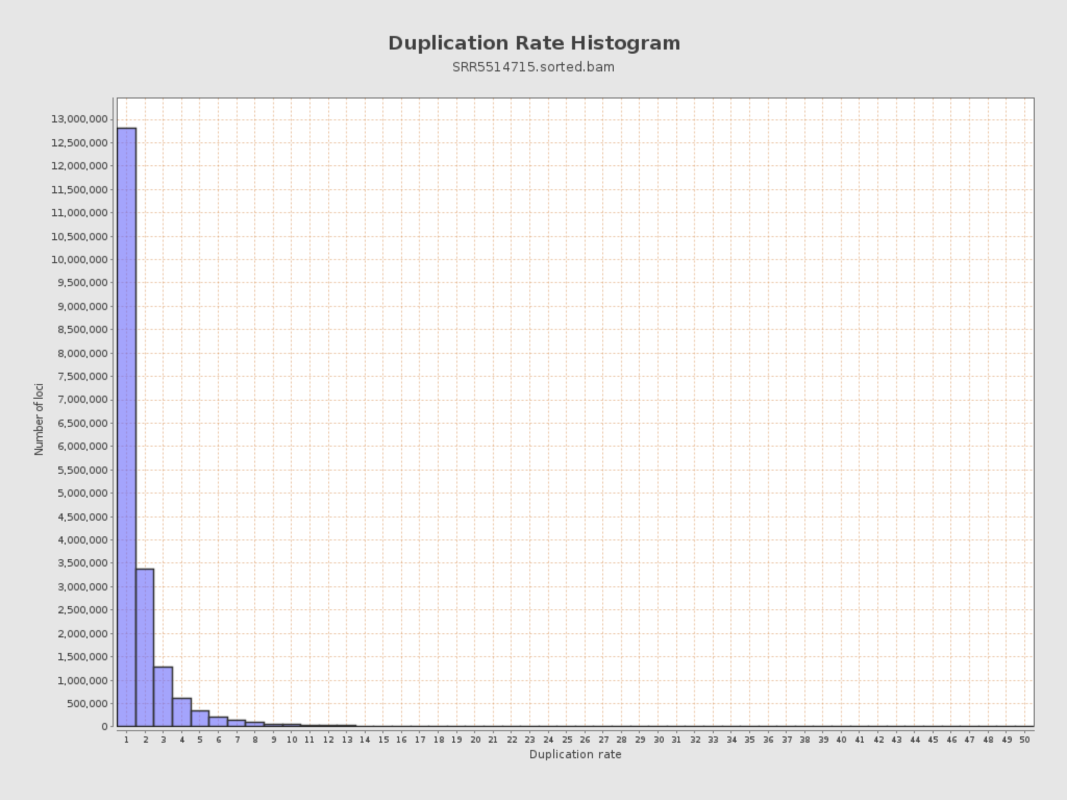
# 5. Results : Coverage Histogram (0-50X)



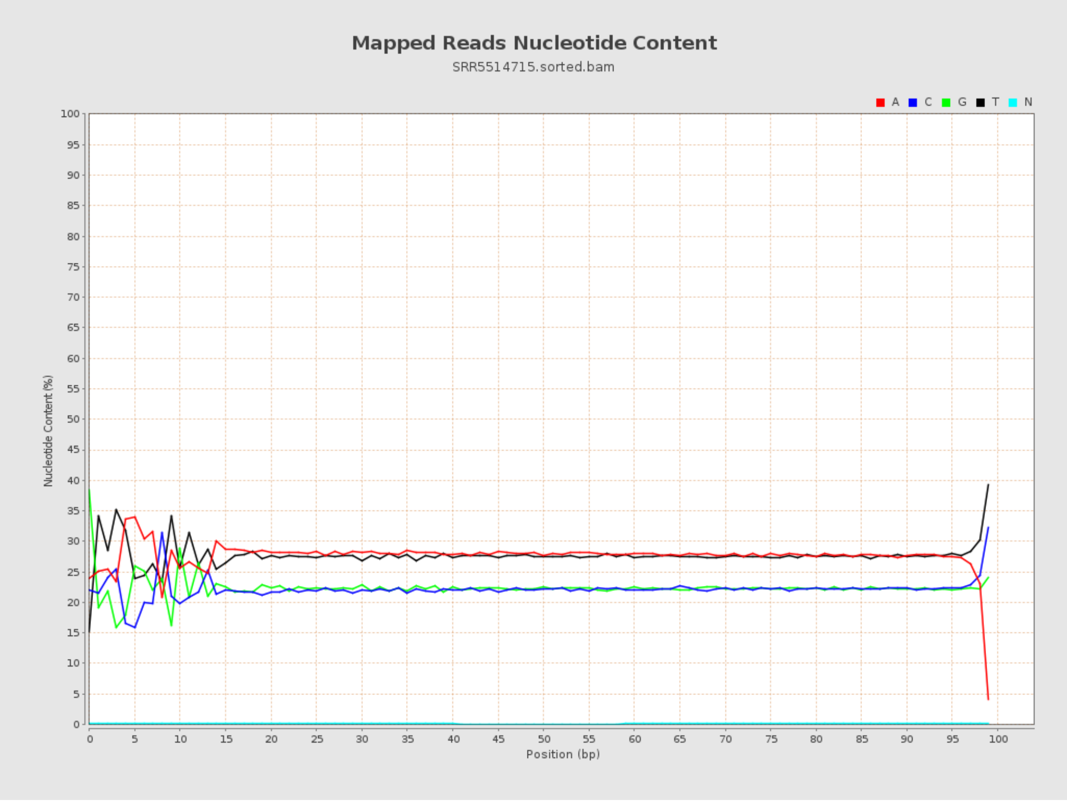
# 6. Results : Genome Fraction Coverage



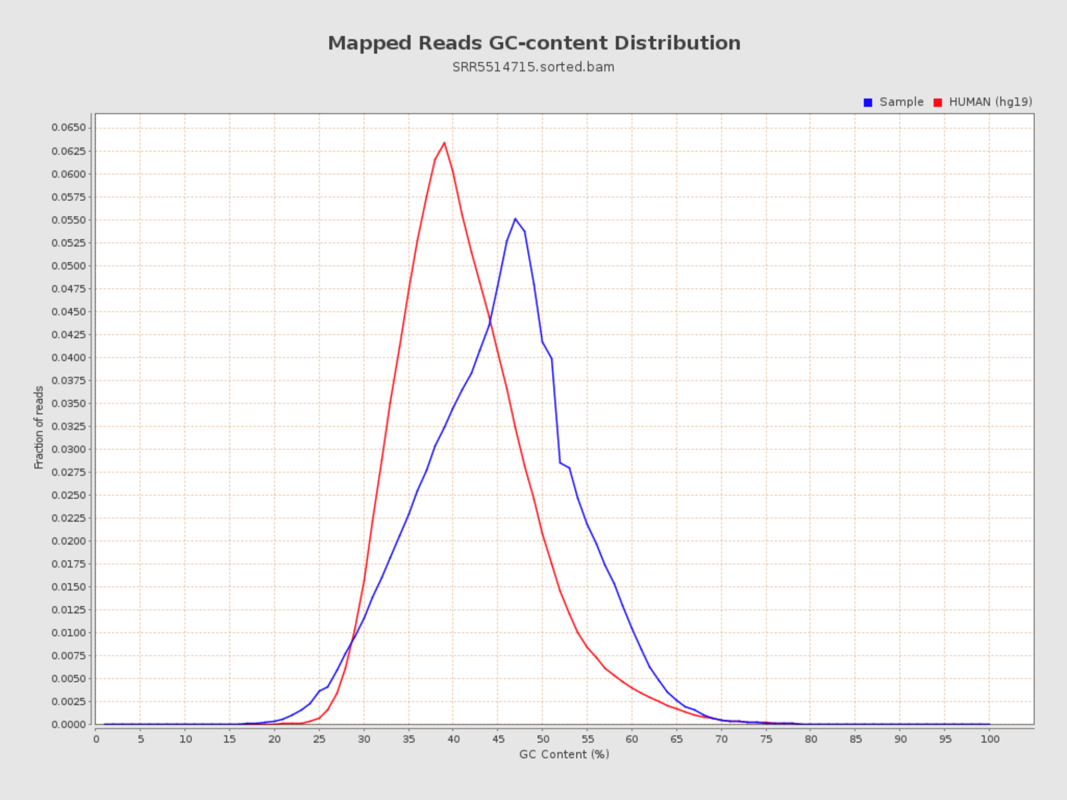
# 7. Results : Duplication Rate Histogram



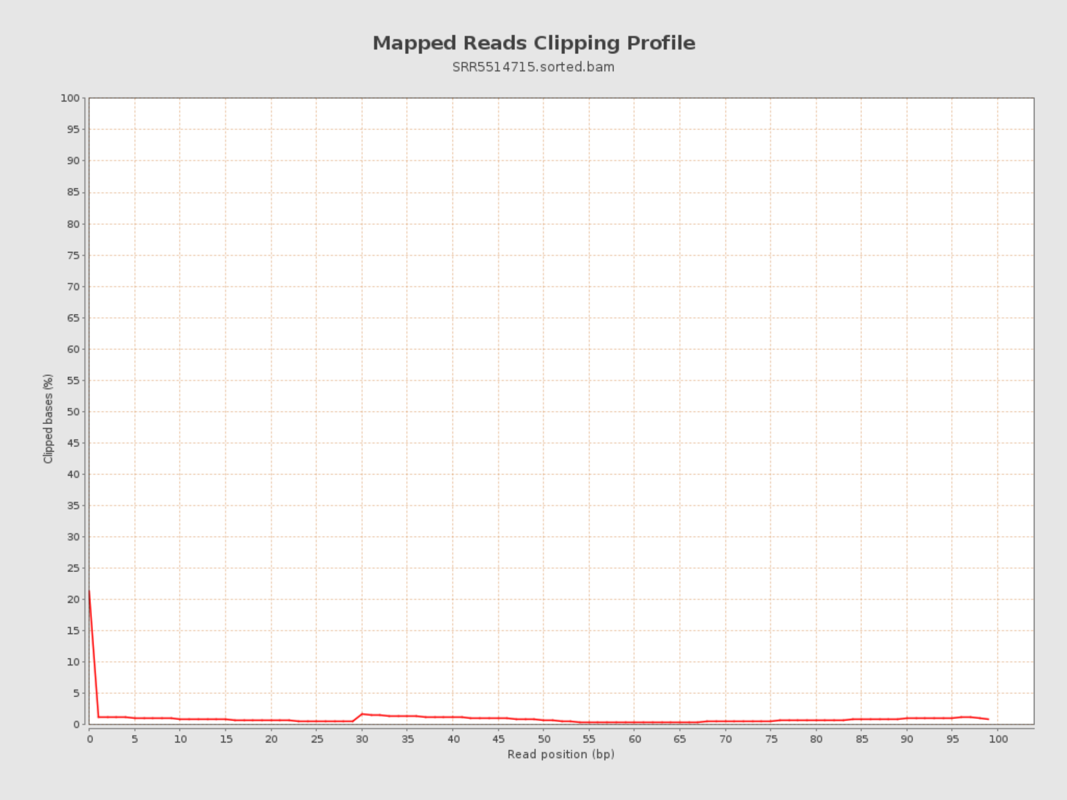
# 8. Results : Mapped Reads Nucleotide Content



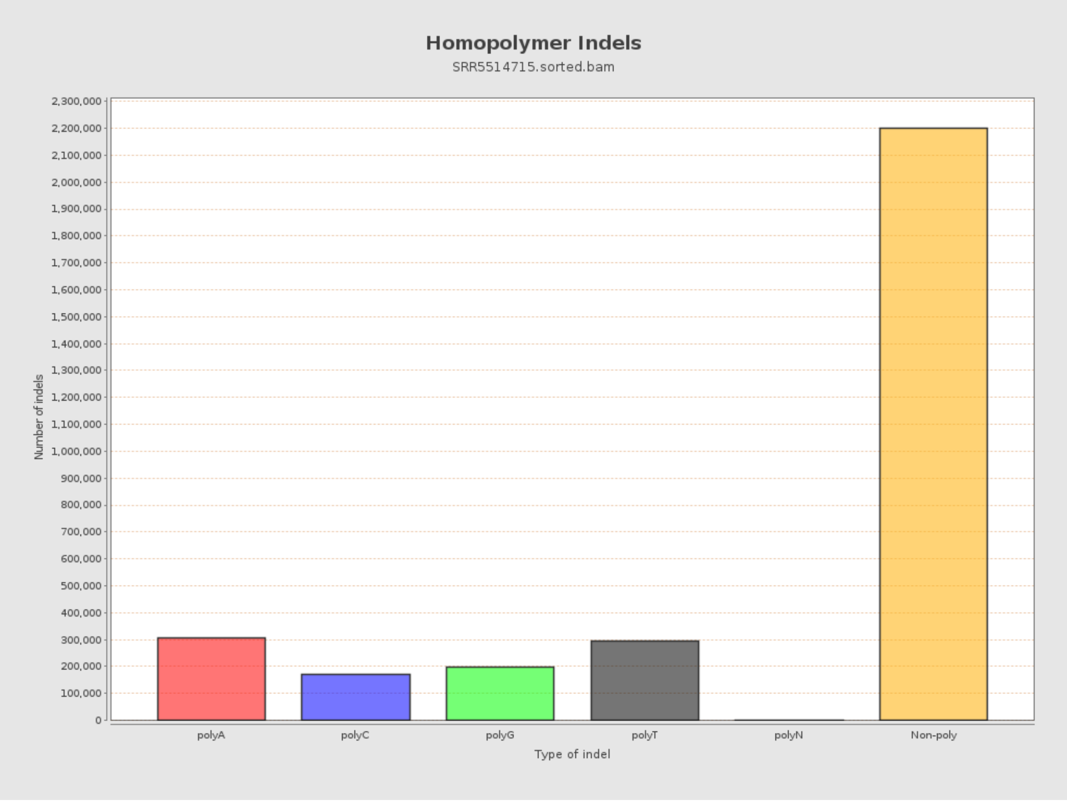
# 9. Results : Mapped Reads GC-content Distribution



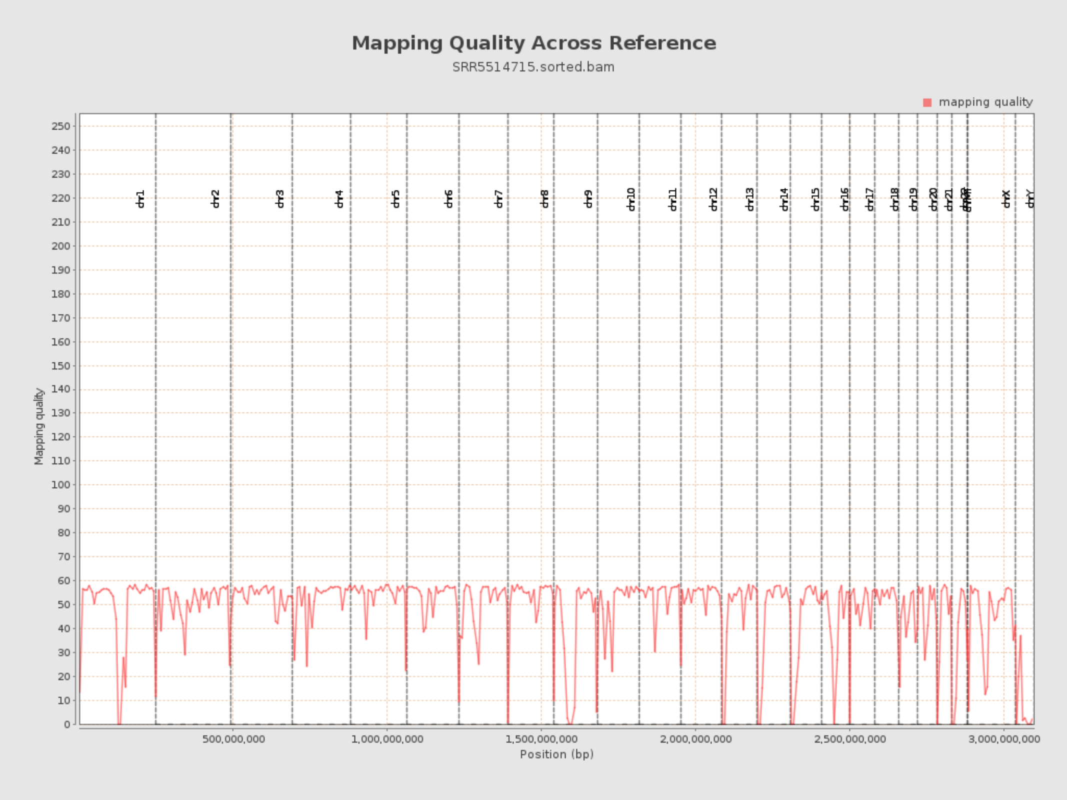
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram