# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/03/18 23:44:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR536759.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_SRR536759 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536759.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Mar 18 23:44:23 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR536759.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 23,342,018 |
| Mapped reads | 22,806,735 / 97.71% |
| Unmapped reads | 535,283 / 2.29% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 613 / 0% |
| Read min/max/mean length | 30 / 50 / 50 |
| Duplicated reads (estimated) | 255,194 / 1.09% |
| Duplication rate | 1.11% |
| Clipped reads | 278,378 / 1.19% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 353,468,762 / 31.07% |
| Number/percentage of C's | 213,797,466 / 18.79% |
| Number/percentage of T's | 353,126,027 / 31.04% |
| Number/percentage of G's | 217,180,680 / 19.09% |
| Number/percentage of N's | 39,439 / 0% |
| GC Percentage | 37.88% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.3675 |
| | |

| | |
|---|---|
| Standard Deviation | 0.7071 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.66 |

## 2.5. Mismatches and indels

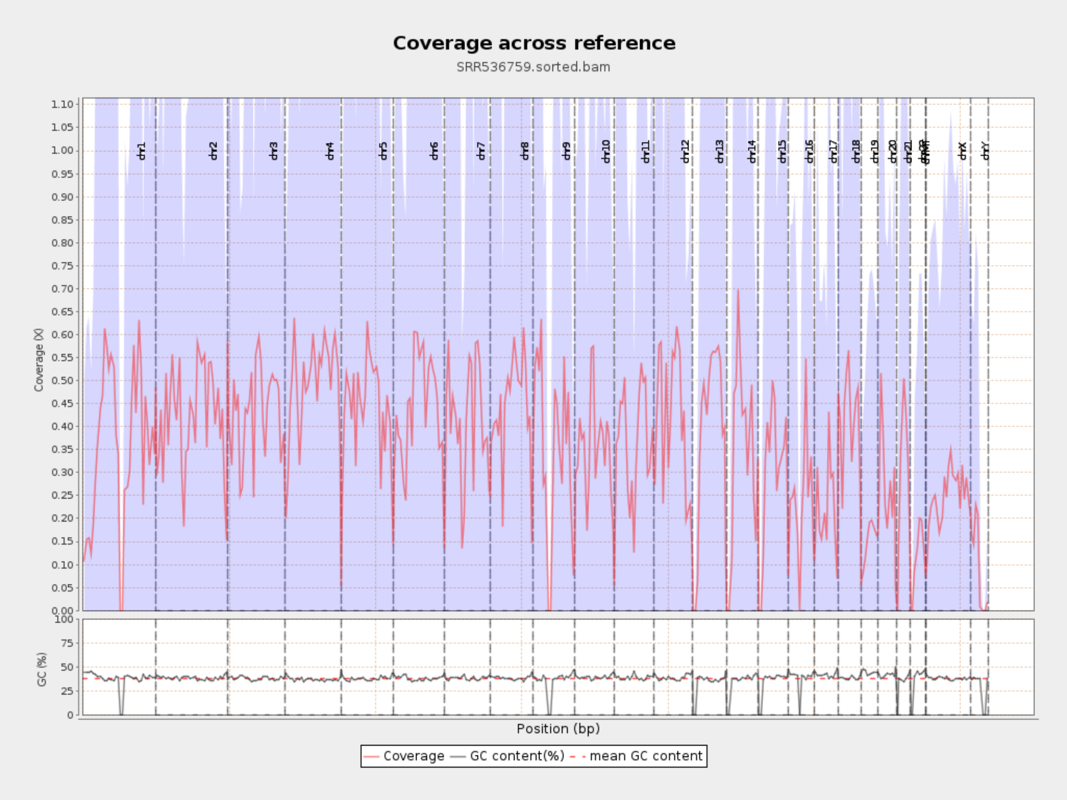
| | |
|---|---|
| General error rate | 0.2% |
| Mismatches | 2,139,731 |
| Insertions | 67,516 |
| Mapped reads with at least one insertion | 0.3% |
| Deletions | 61,453 |
| Mapped reads with at least one deletion | 0.27% |
| Homopolymer indels | 49.29% |

## 2.6. Chromosome stats

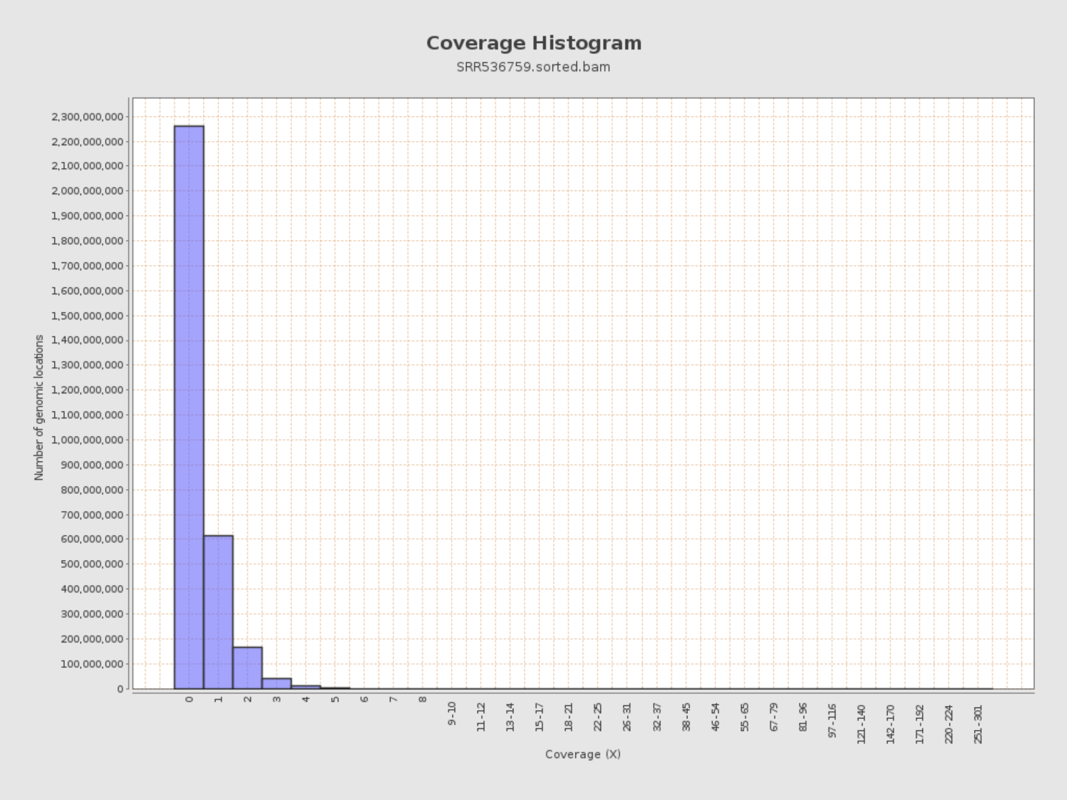
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 89217299 | 0.3579 | 0.7125 |
| chr2 | 243199373 | 102676321 | 0.4222 | 0.7472 |
| chr3 | 198022430 | 85894248 | 0.4338 | 0.7487 |
| chr4 | 191154276 | 94353171 | 0.4936 | 0.8004 |
| chr5 | 180915260 | 79216556 | 0.4379 | 0.7538 |
| chr6 | 171115067 | 76602688 | 0.4477 | 0.7674 |
| chr7 | 159138663 | 64617752 | 0.406 | 0.741 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 65309698 | 0.4462 | 0.7624 |
| chr9 | 141213431 | 49701761 | 0.352 | 0.7006 |
| chr10 | 135534747 | 48630976 | 0.3588 | 0.686 |
| chr11 | 135006516 | 49514376 | 0.3668 | 0.7103 |
| chr12 | 133851895 | 55171541 | 0.4122 | 0.7494 |
| chr13 | 115169878 | 45478462 | 0.3949 | 0.7308 |
| chr14 | 107349540 | 37152897 | 0.3461 | 0.6972 |
| chr15 | 102531392 | 30466078 | 0.2971 | 0.6509 |
| chr16 | 90354753 | 21394780 | 0.2368 | 0.5642 |
| chr17 | 81195210 | 18374191 | 0.2263 | 0.5559 |
| chr18 | 78077248 | 32766884 | 0.4197 | 0.742 |
| chr19 | 59128983 | 8961263 | 0.1516 | 0.4393 |
| chr20 | 63025520 | 17775362 | 0.282 | 0.6241 |
| chr21 | 48129895 | 14135497 | 0.2937 | 0.6554 |
| chr22 | 51304566 | 6024512 | 0.1174 | 0.3907 |
| chrMT | 16571 | 1339 | 0.0808 | 0.2819 |
| chrX | 155270560 | 38684332 | 0.2491 | 0.5566 |
| chrY | 59373566 | 5592940 | 0.0942 | 0.3603 |

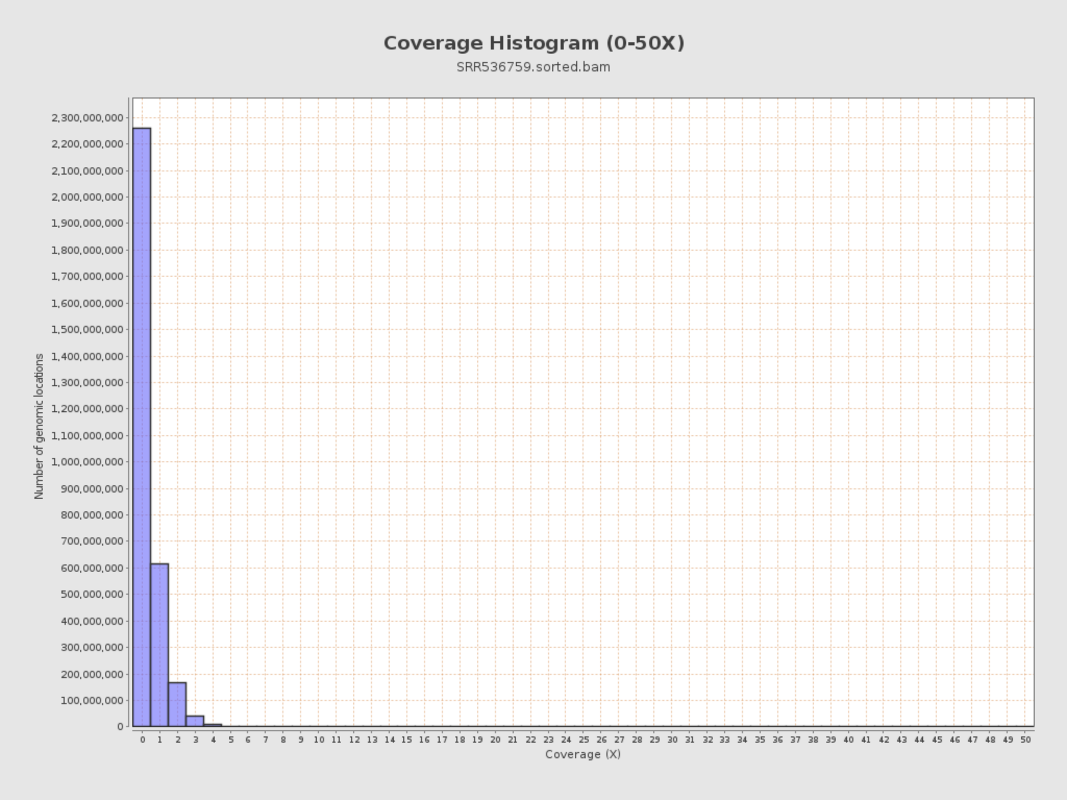
# 3. Results : Coverage across reference



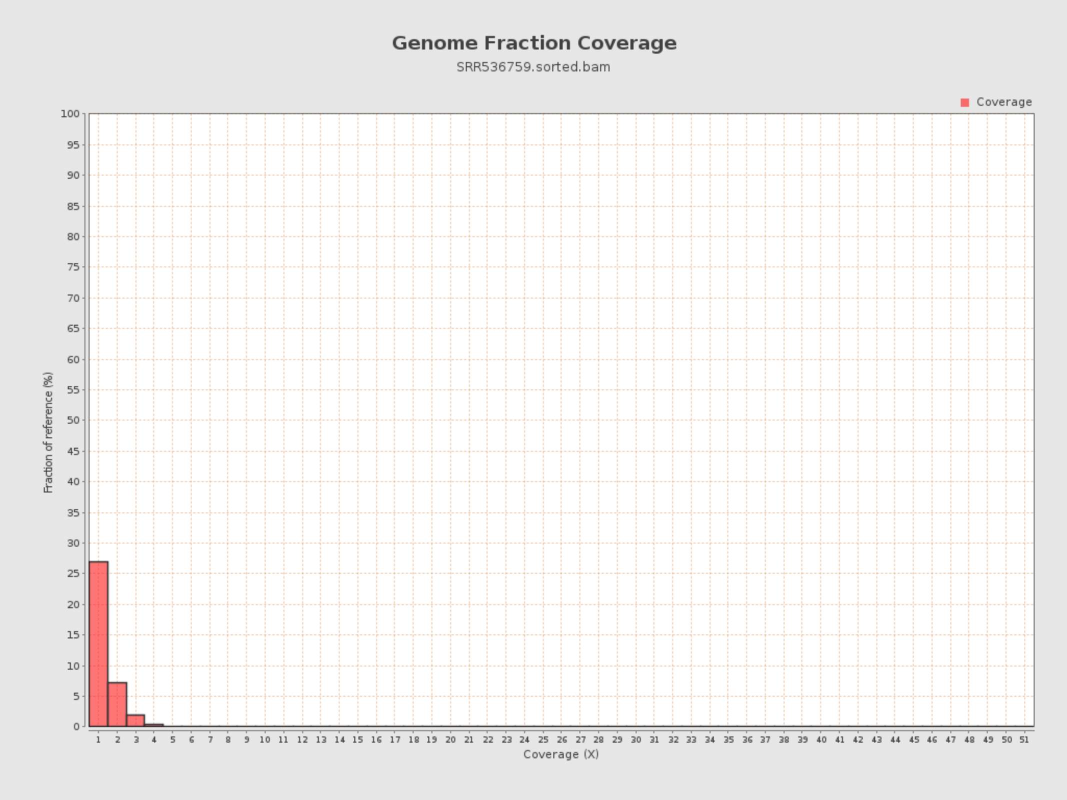
# 4. Results : Coverage Histogram



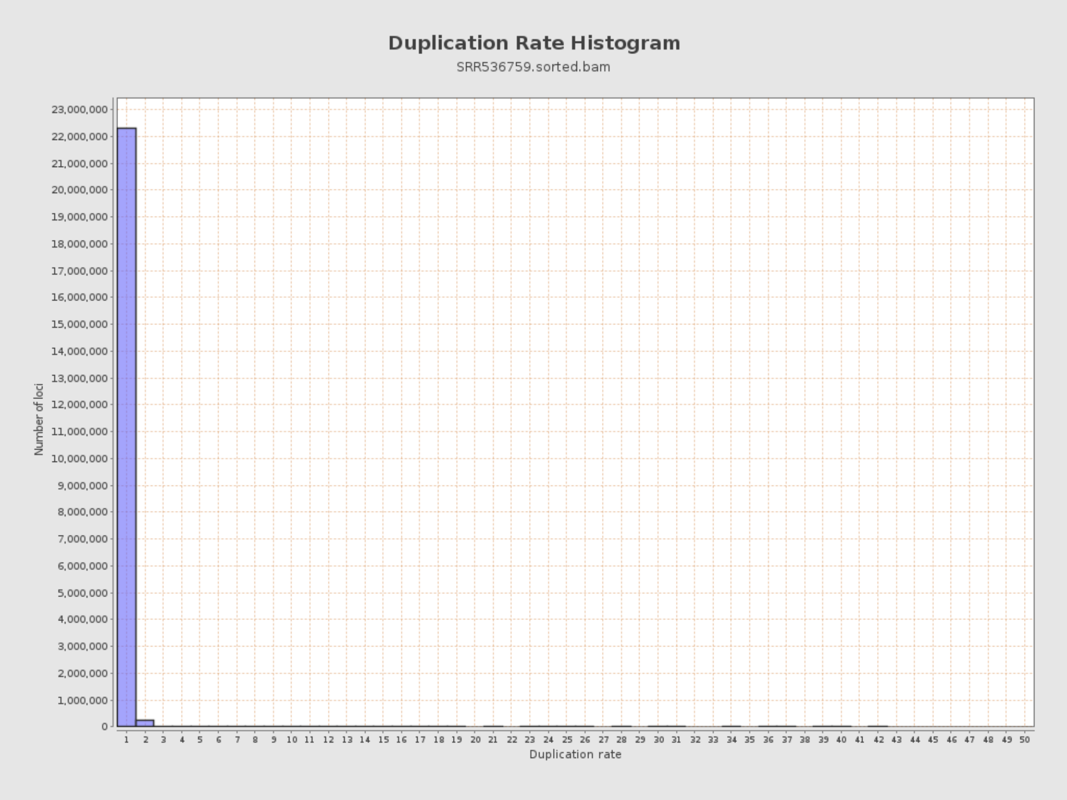
# 5. Results : Coverage Histogram (0-50X)



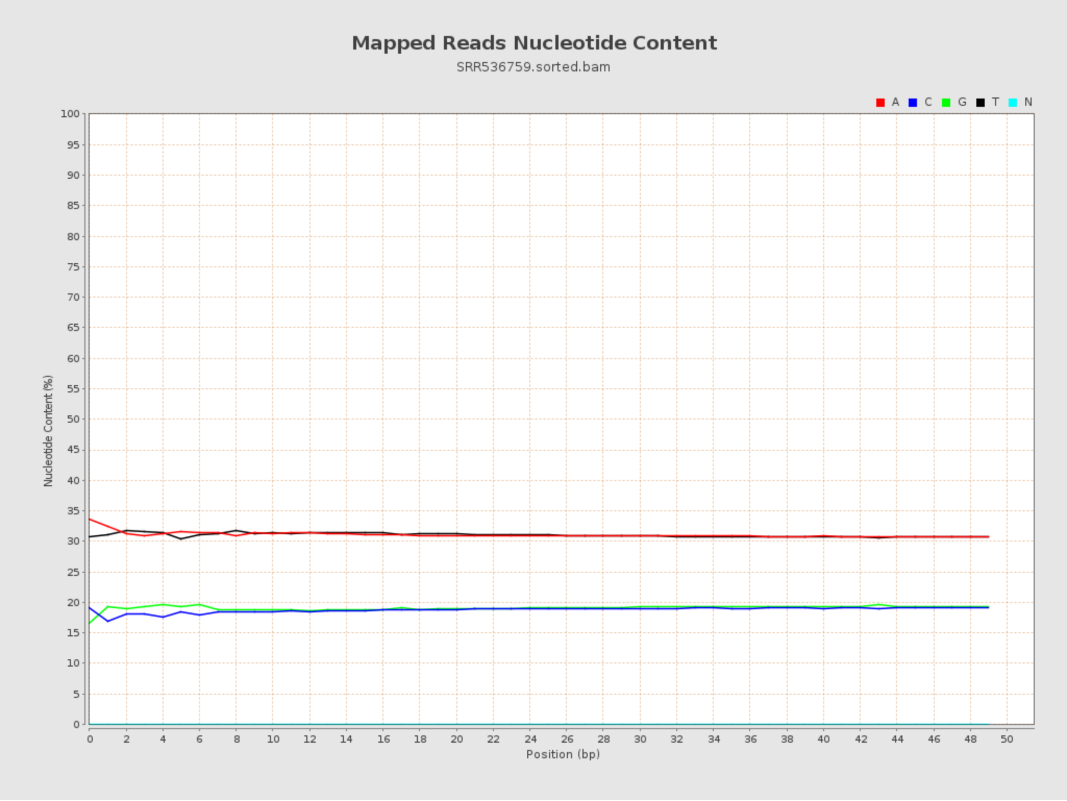
# 6. Results : Genome Fraction Coverage



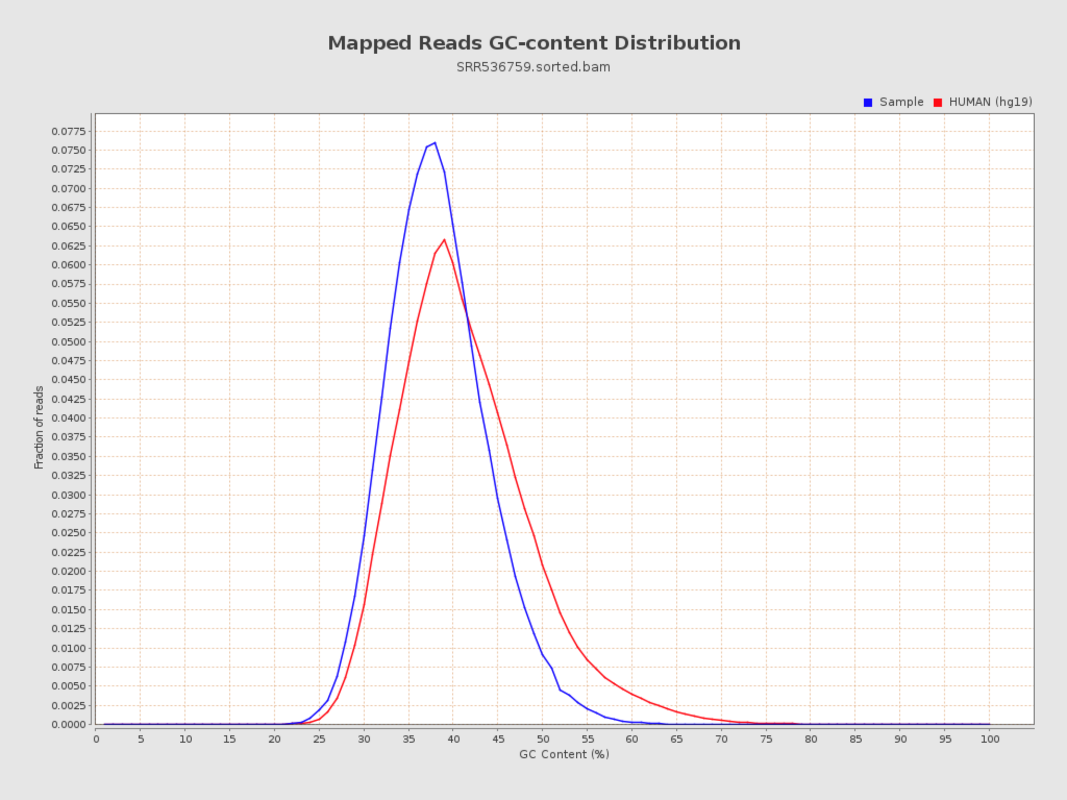
# 7. Results : Duplication Rate Histogram



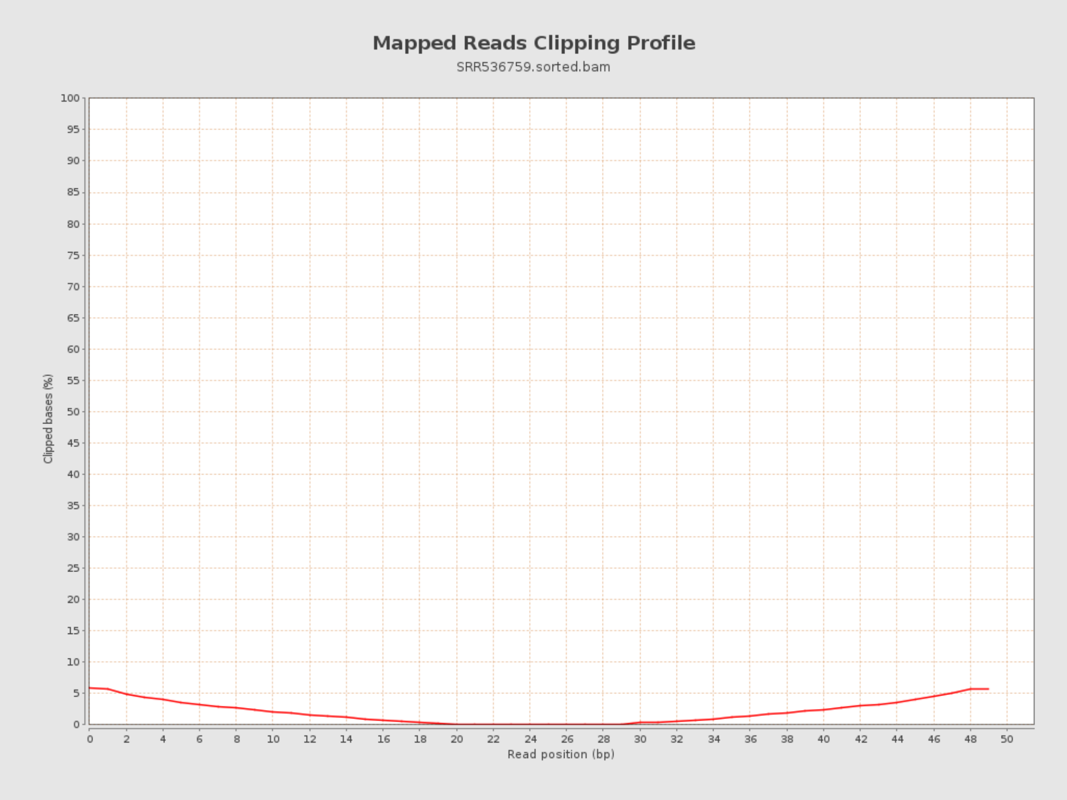
# 8. Results : Mapped Reads Nucleotide Content



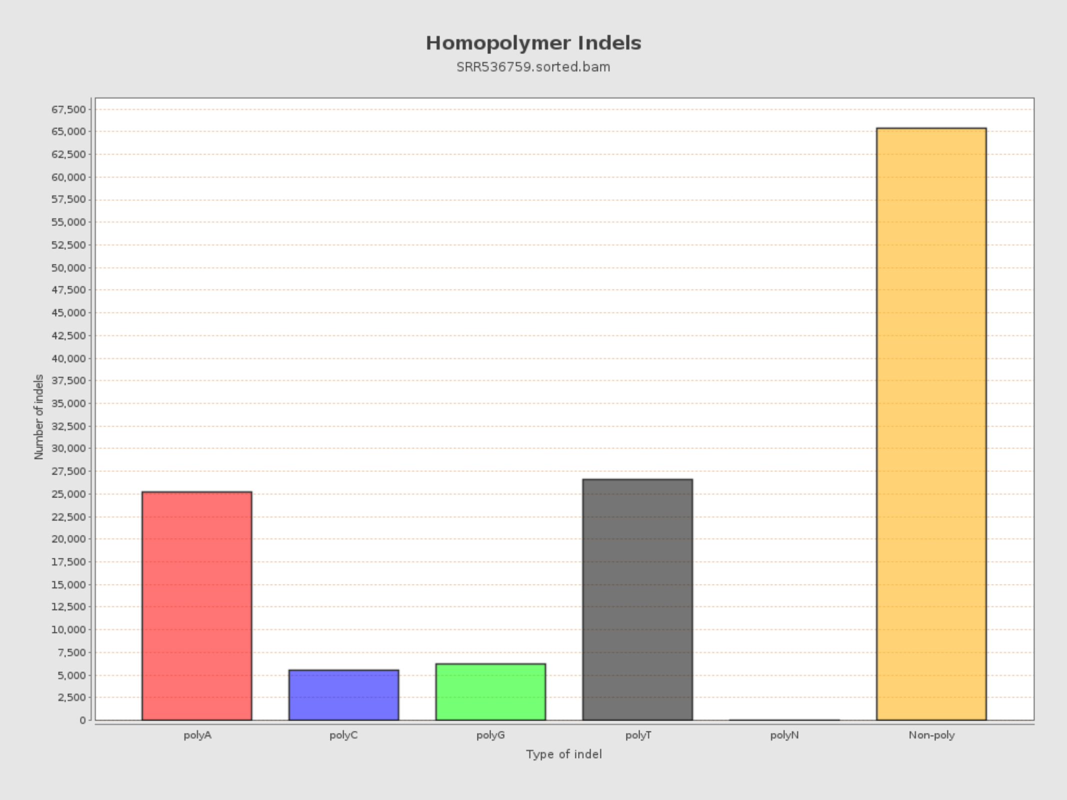
# 9. Results : Mapped Reads GC-content Distribution



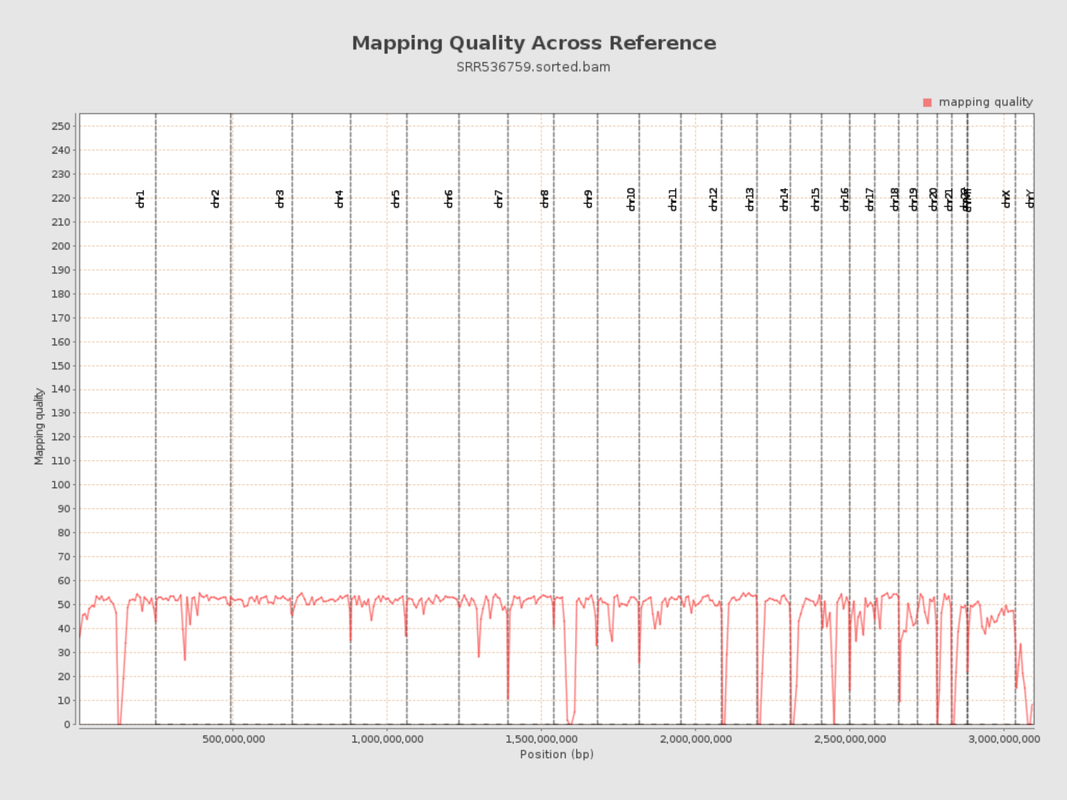
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram