# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/19 14:42:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR089589.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_SRR089589 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089589.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Apr 19 14:42:52 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR089589.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 11,105,952 |
| Mapped reads | 9,449,083 / 85.08% |
| Unmapped reads | 1,656,869 / 14.92% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 391 / 0% |
| Read min/max/mean length | 30 / 48 / 48 |
| Duplicated reads (estimated) | 2,545,945 / 22.92% |
| Duplication rate | 19.42% |
| Clipped reads | 987,342 / 8.89% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 140,713,385 / 31.65% |
| Number/percentage of C's | 84,264,695 / 18.95% |
| Number/percentage of T's | 121,362,426 / 27.3% |
| Number/percentage of G's | 98,218,776 / 22.09% |
| Number/percentage of N's | 18,693 / 0% |
| GC Percentage | 41.05% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1436 |
| | |

| | |
|---|---|
| Standard Deviation | 1.1044 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.49 |

## 2.5. Mismatches and indels

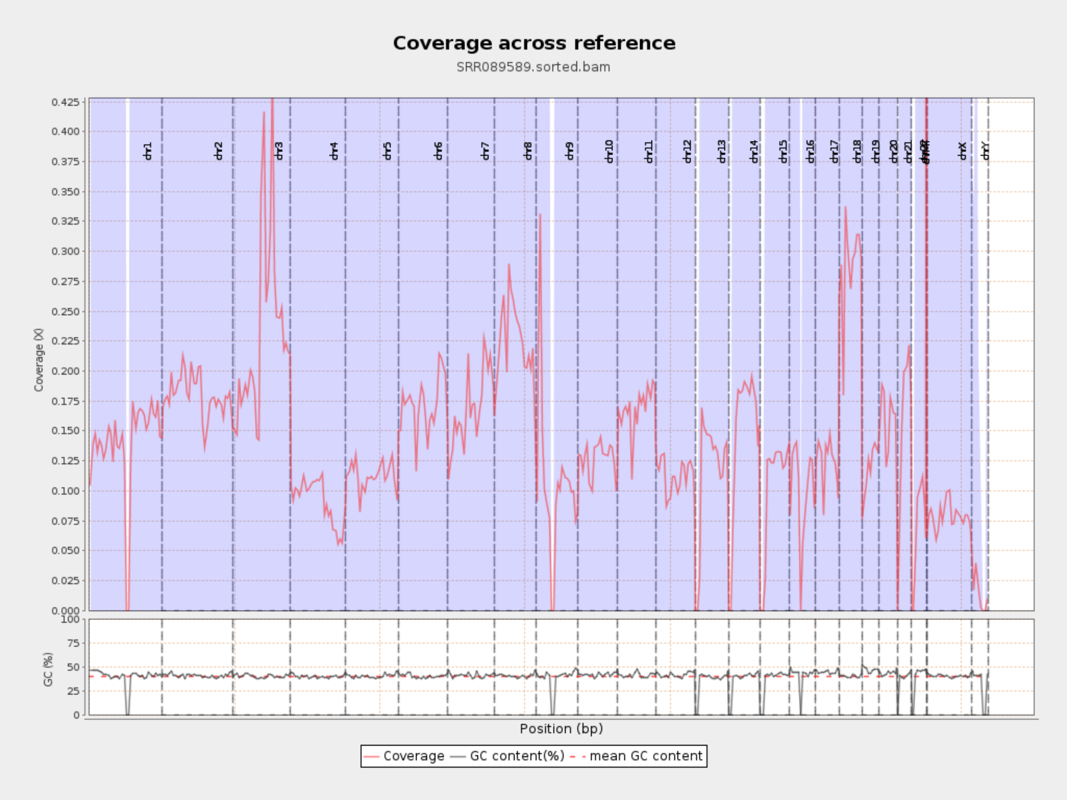
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 2,273,353 |
| Insertions | 18,771 |
| Mapped reads with at least one insertion | 0.2% |
| Deletions | 58,559 |
| Mapped reads with at least one deletion | 0.62% |
| Homopolymer indels | 46.59% |

## 2.6. Chromosome stats

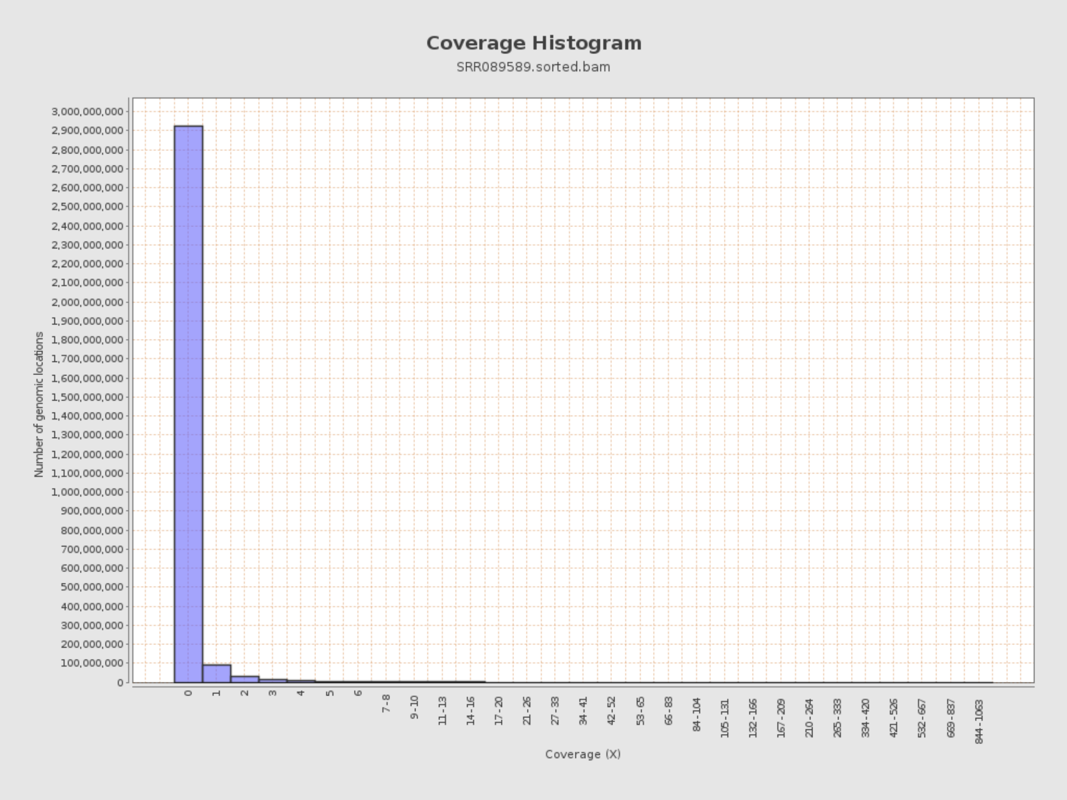
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 34612878 | 0.1389 | 1.0536 |
| chr2 | 243199373 | 43931988 | 0.1806 | 1.4332 |
| chr3 | 198022430 | 45886261 | 0.2317 | 1.4529 |
| chr4 | 191154276 | 17406973 | 0.0911 | 0.7794 |
| chr5 | 180915260 | 20339961 | 0.1124 | 0.873 |
| chr6 | 171115067 | 29440747 | 0.1721 | 1.1638 |
| chr7 | 159138663 | 27076836 | 0.1701 | 1.2686 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 32921163 | 0.2249 | 1.5664 |
| chr9 | 141213431 | 15464722 | 0.1095 | 0.9349 |
| chr10 | 135534747 | 17370793 | 0.1282 | 0.9645 |
| chr11 | 135006516 | 22716547 | 0.1683 | 1.1488 |
| chr12 | 133851895 | 14999312 | 0.1121 | 0.8635 |
| chr13 | 115169878 | 13316010 | 0.1156 | 0.9048 |
| chr14 | 107349540 | 15923499 | 0.1483 | 1.0894 |
| chr15 | 102531392 | 10433133 | 0.1018 | 0.8151 |
| chr16 | 90354753 | 9072828 | 0.1004 | 0.815 |
| chr17 | 81195210 | 10090456 | 0.1243 | 0.9166 |
| chr18 | 78077248 | 22504057 | 0.2882 | 1.6454 |
| chr19 | 59128983 | 7078624 | 0.1197 | 1.0628 |
| chr20 | 63025520 | 9985212 | 0.1584 | 1.0758 |
| chr21 | 48129895 | 7471730 | 0.1552 | 1.1633 |
| chr22 | 51304566 | 3513867 | 0.0685 | 0.6166 |
| chrMT | 16571 | 54128 | 3.2664 | 9.0888 |
| chrX | 155270560 | 12208204 | 0.0786 | 0.7364 |
| chrY | 59373566 | 846746 | 0.0143 | 0.3004 |

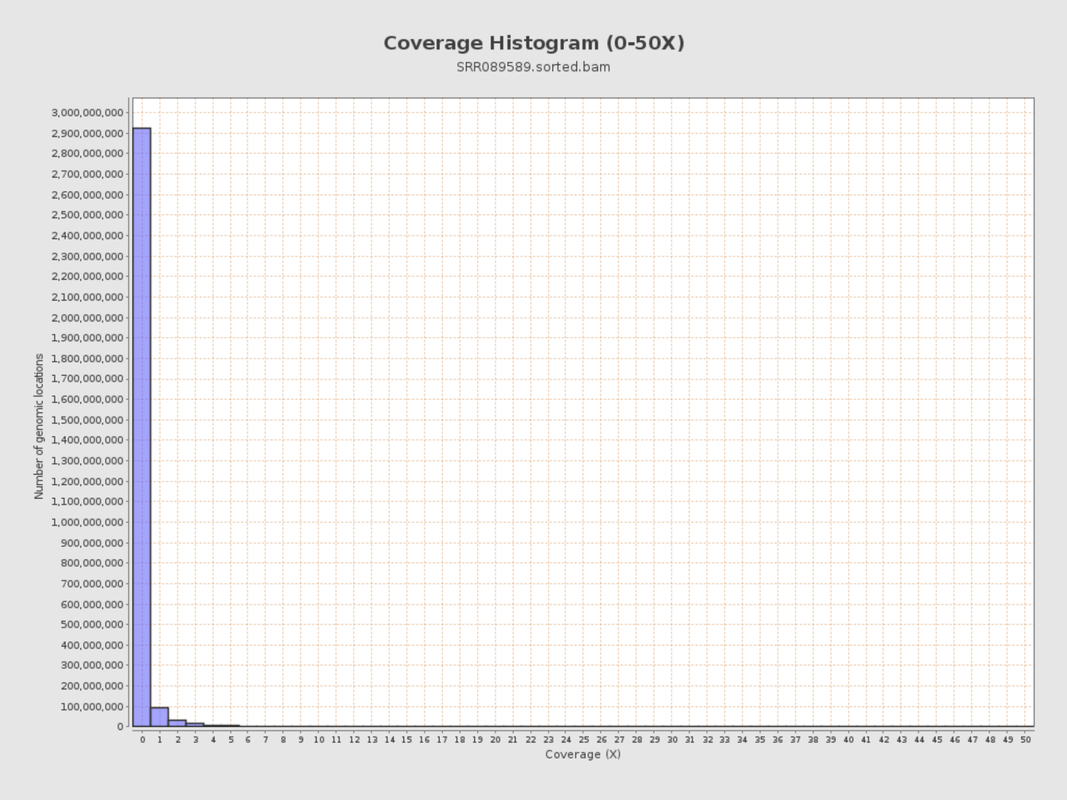
# 3. Results : Coverage across reference



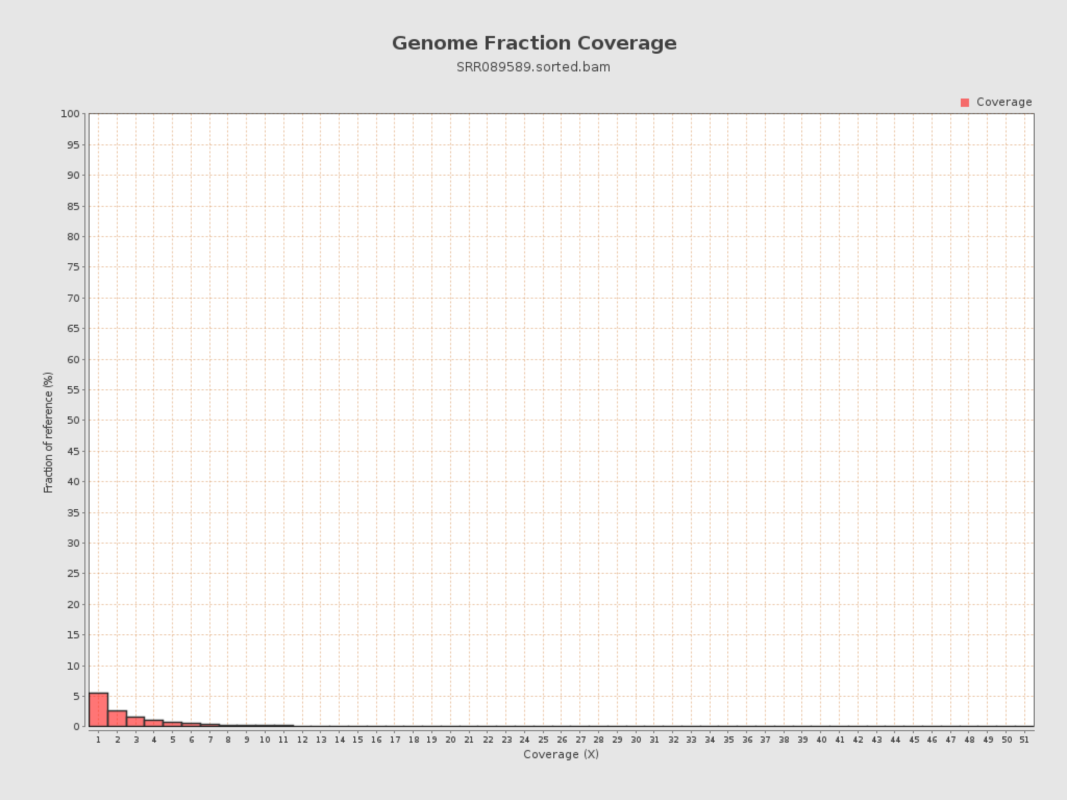
# 4. Results : Coverage Histogram



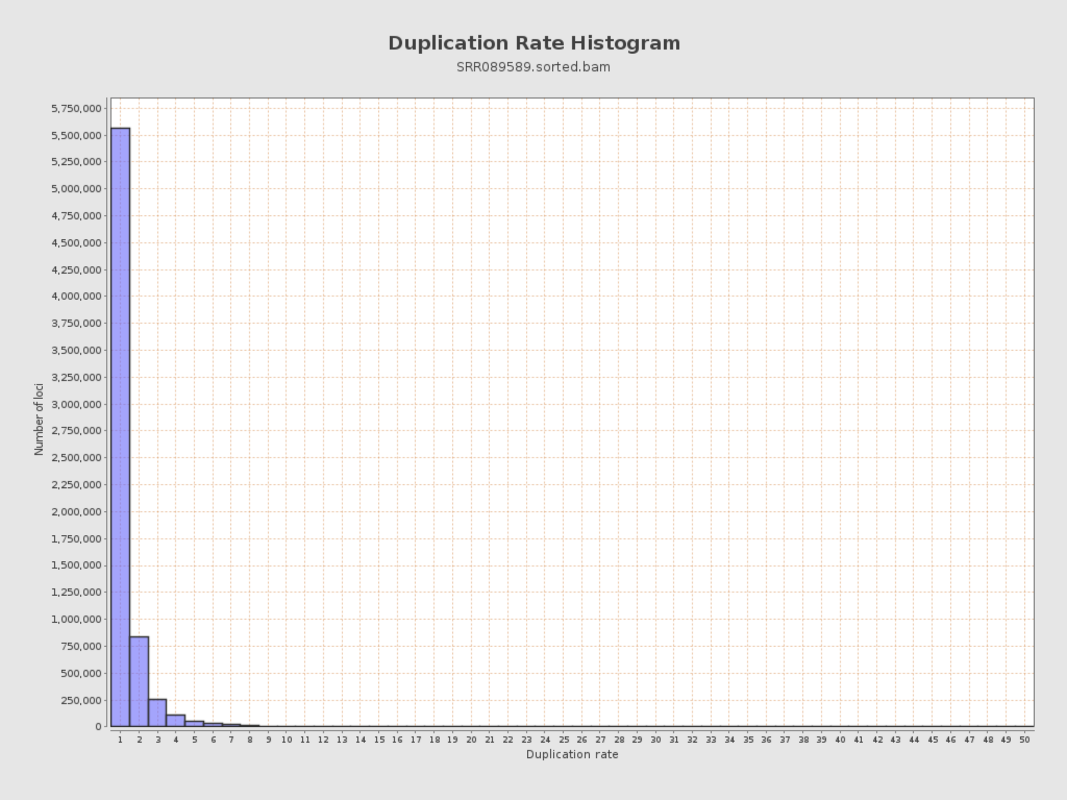
# 5. Results : Coverage Histogram (0-50X)



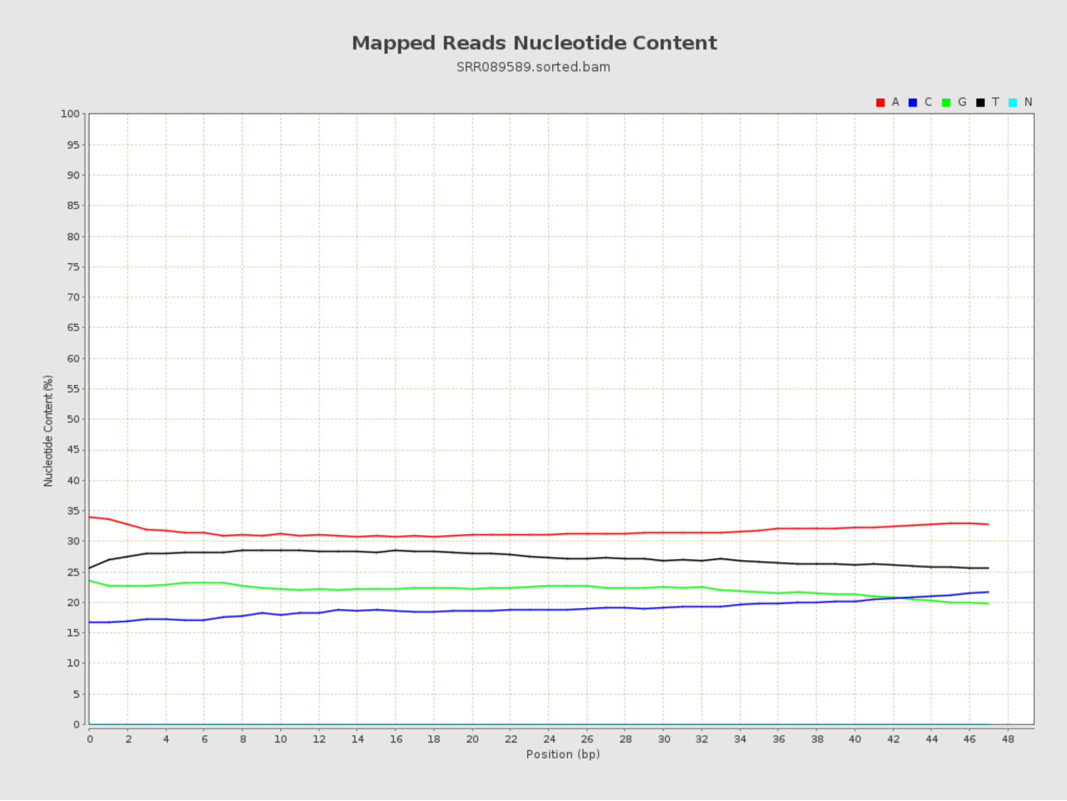
# 6. Results : Genome Fraction Coverage



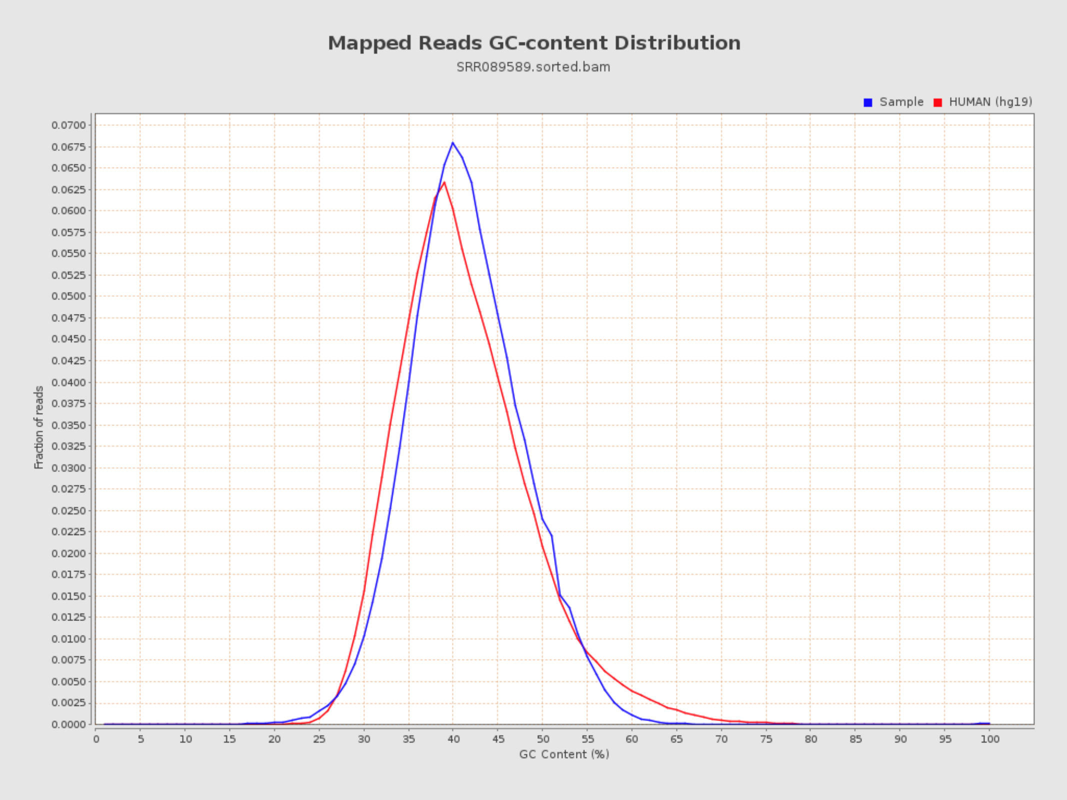
# 7. Results : Duplication Rate Histogram



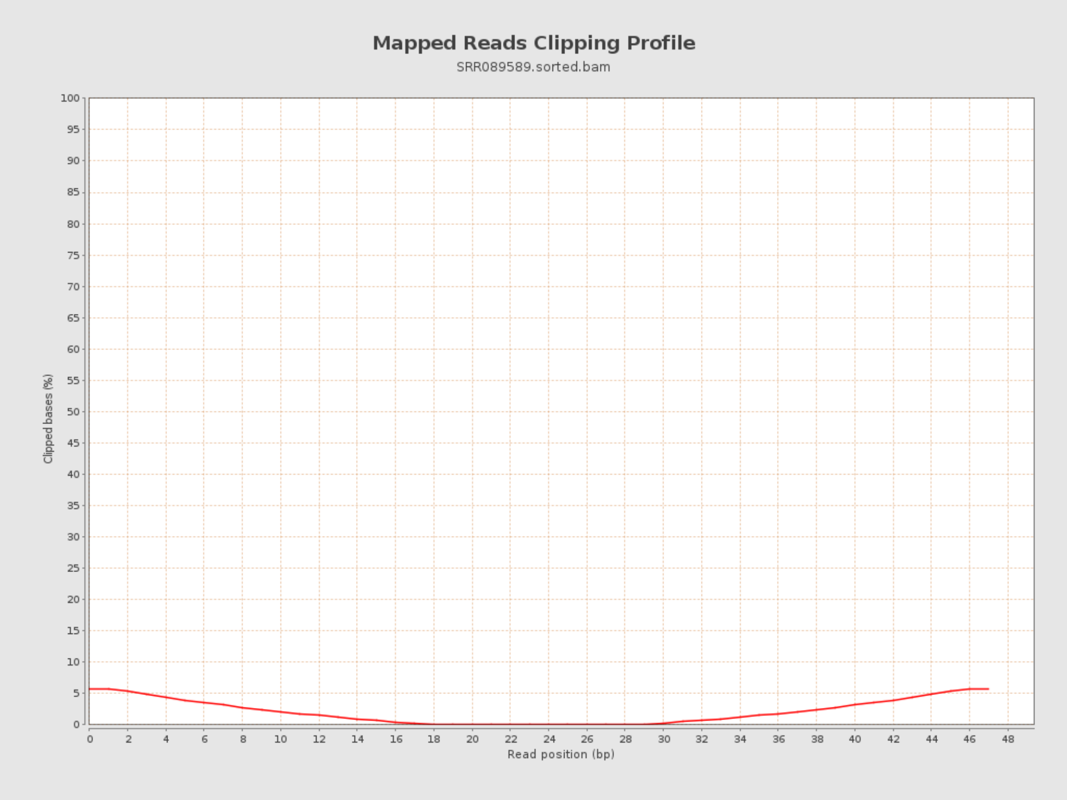
# 8. Results : Mapped Reads Nucleotide Content



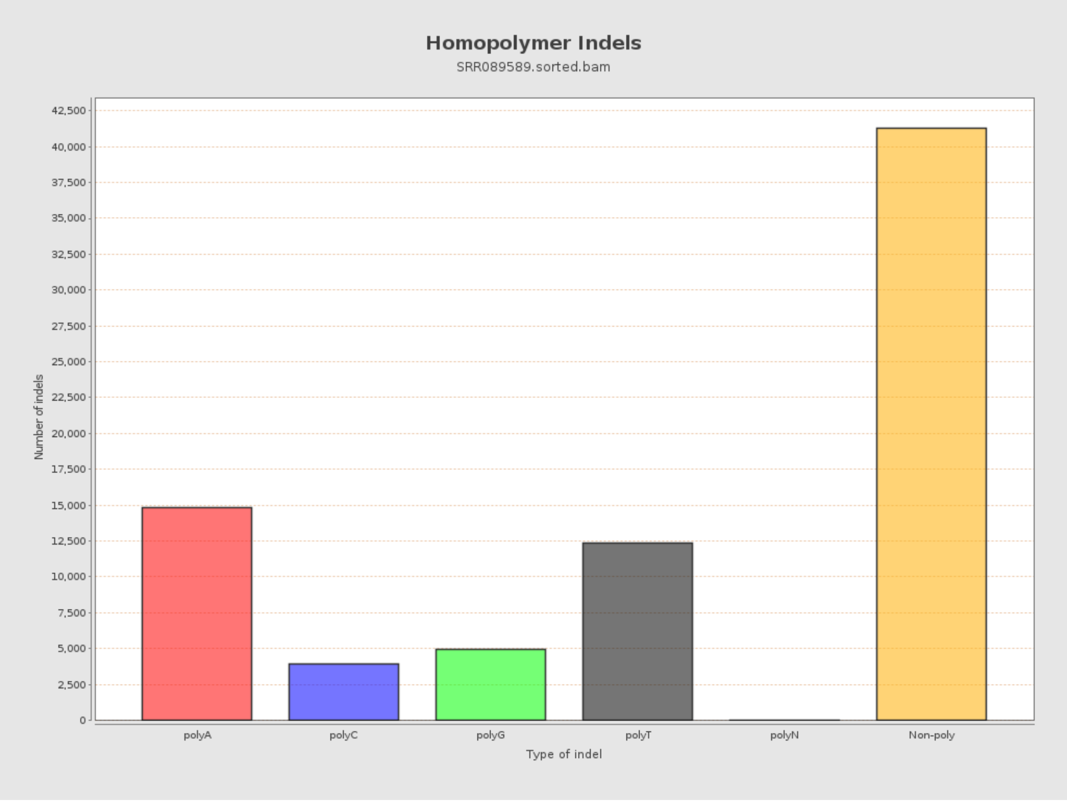
# 9. Results : Mapped Reads GC-content Distribution



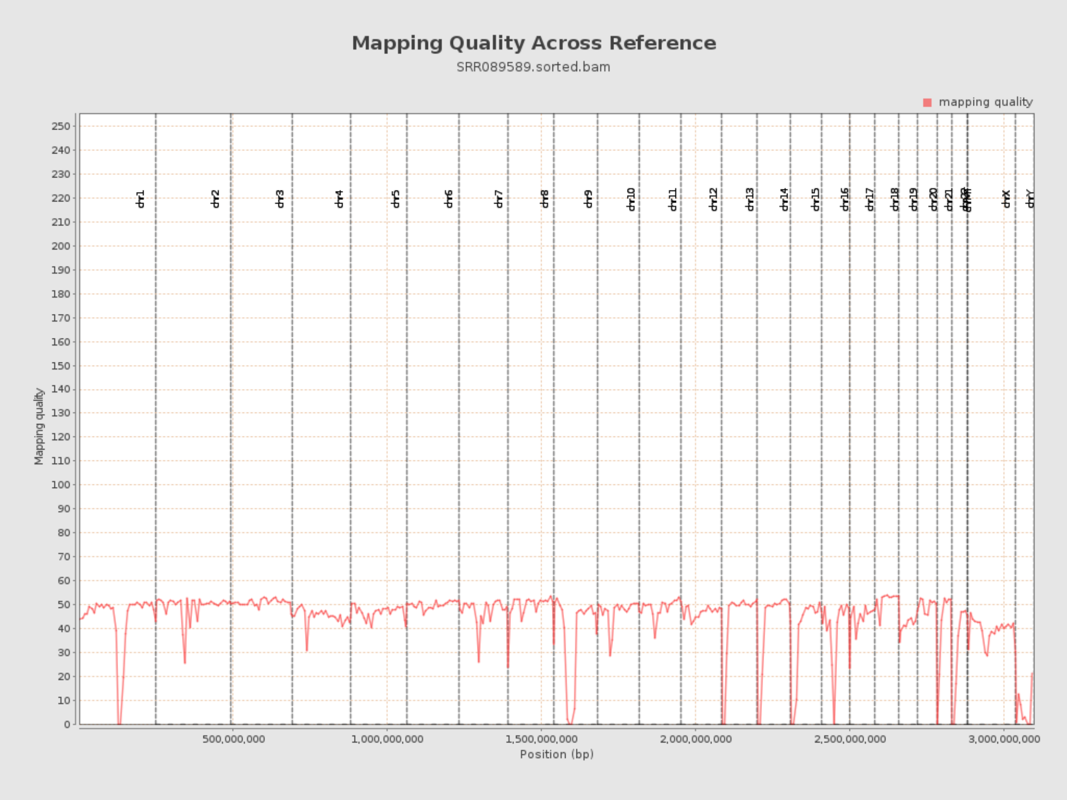
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram