# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 10:43:43*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549150.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_SRR1549150 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549150.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 10:43:43 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1549150.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 14,842,191 |
| Mapped reads | 12,859,967 / 86.64% |
| Unmapped reads | 1,982,224 / 13.36% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Read min/max/mean length | 40 / 40 / 40 |
| Duplicated reads (estimated) | 734,281 / 4.95% |
| Duplication rate | 4.44% |
| Clipped reads | 622,707 / 4.2% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 149,648,691 / 29.31% |
| Number/percentage of C's | 104,822,558 / 20.53% |
| Number/percentage of T's | 151,160,062 / 29.6% |
| Number/percentage of G's | 104,878,828 / 20.54% |
| Number/percentage of N's | 103,719 / 0.02% |
| GC Percentage | 41.07% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.165 |
| Standard Deviation | 1.1753 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.03 |

## 2.5. Mismatches and indels

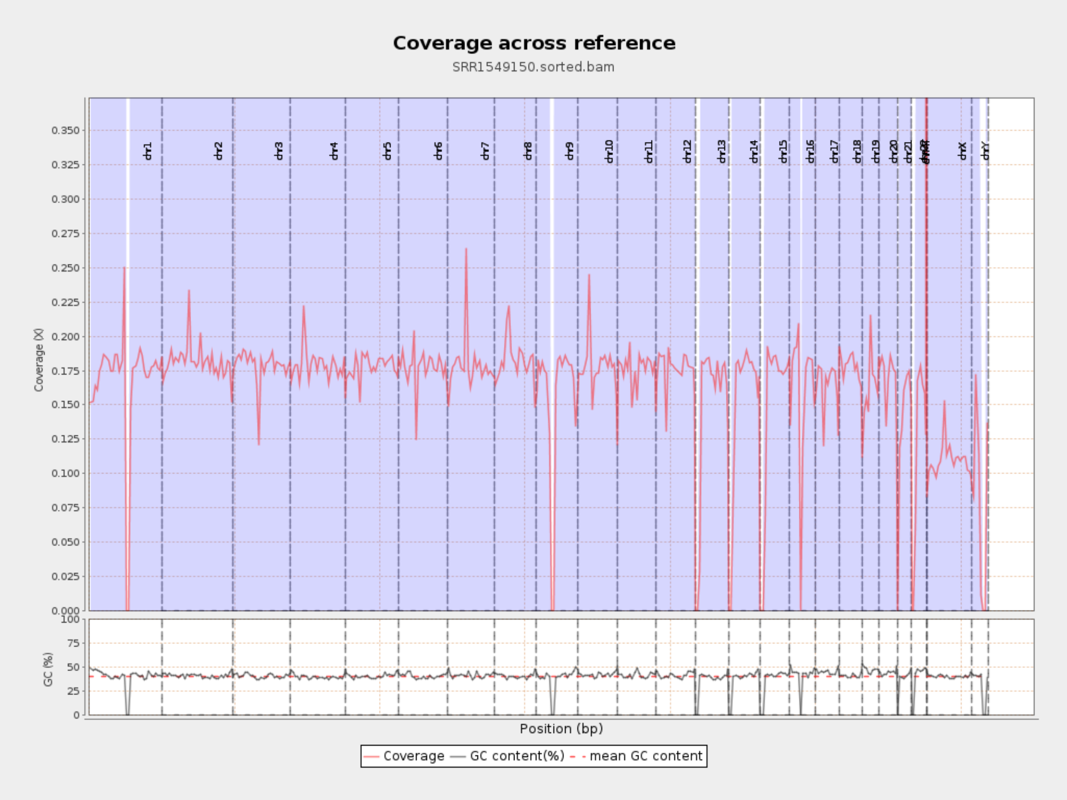
| | |
|---|---|
| General error rate | 0.32% |
| Mismatches | 1,624,866 |
| Insertions | 12,379 |
| Mapped reads with at least one insertion | 0.1% |
| Deletions | 44,869 |
| Mapped reads with at least one deletion | 0.35% |
| Homopolymer indels | 45.17% |

## 2.6. Chromosome stats

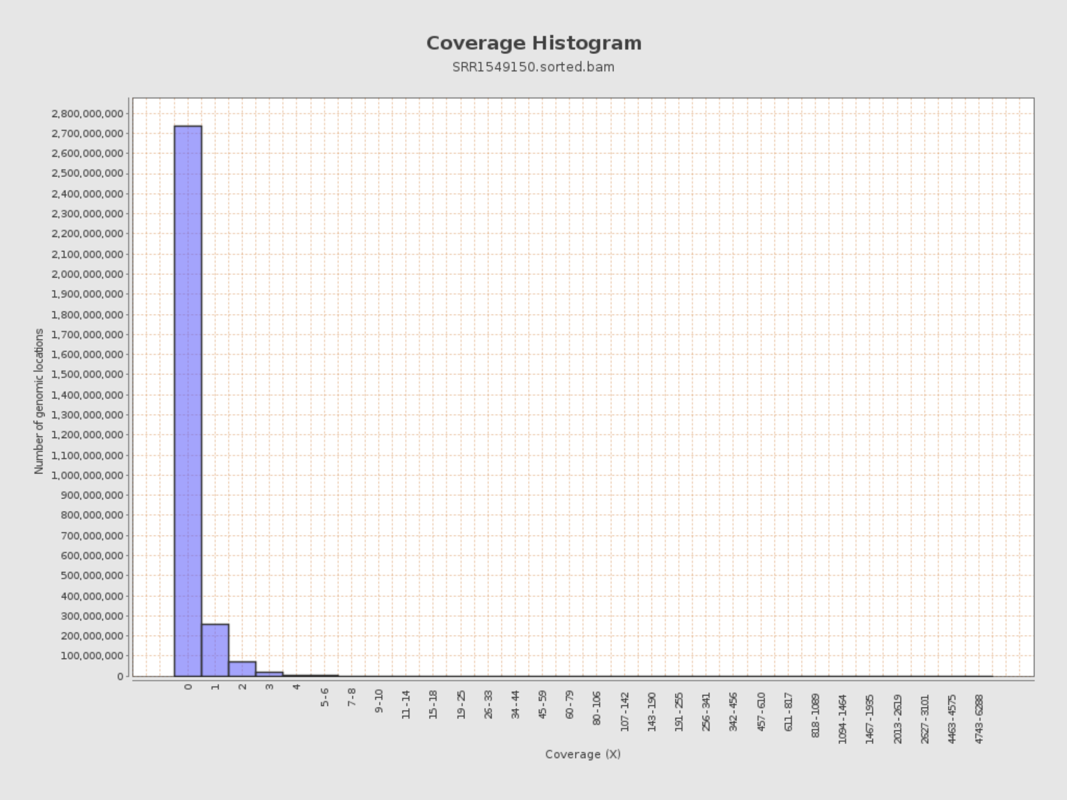
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 41623661 | 0.167 | 2.0445 |
| chr2 | 243199373 | 44255852 | 0.182 | 0.8794 |
| chr3 | 198022430 | 35367387 | 0.1786 | 0.5596 |
| chr4 | 191154276 | 34246001 | 0.1792 | 0.6493 |
| chr5 | 180915260 | 32224538 | 0.1781 | 0.5745 |
| chr6 | 171115067 | 30398609 | 0.1777 | 0.6458 |
| chr7 | 159138663 | 28586526 | 0.1796 | 1.3833 |
| chr8 | 146364022 | 26671001 | 0.1822 | 3.1413 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr9 | 141213431 | 21679804 | 0.1535 | 0.7989 |
| chr10 | 135534747 | 24334482 | 0.1795 | 0.9353 |
| chr11 | 135006516 | 23726878 | 0.1757 | 0.7997 |
| chr12 | 133851895 | 23666003 | 0.1768 | 0.5847 |
| chr13 | 115169878 | 16747492 | 0.1454 | 0.497 |
| chr14 | 107349540 | 15853006 | 0.1477 | 0.6802 |
| chr15 | 102531392 | 15036914 | 0.1467 | 0.5002 |
| chr16 | 90354753 | 14453763 | 0.16 | 0.6085 |
| chr17 | 81195210 | 13248569 | 0.1632 | 0.5892 |
| chr18 | 78077248 | 13971270 | 0.1789 | 1.6794 |
| chr19 | 59128983 | 9693597 | 0.1639 | 1.6125 |
| chr20 | 63025520 | 10726567 | 0.1702 | 0.6033 |
| chr21 | 48129895 | 6606808 | 0.1373 | 0.6266 |
| chr22 | 51304566 | 5889962 | 0.1148 | 0.4859 |
| chrMT | 16571 | 146397 | 8.8345 | 10.8458 |
| chrX | 155270560 | 17043561 | 0.1098 | 0.5815 |
| chrY | 59373566 | 4474001 | 0.0754 | 0.7365 |

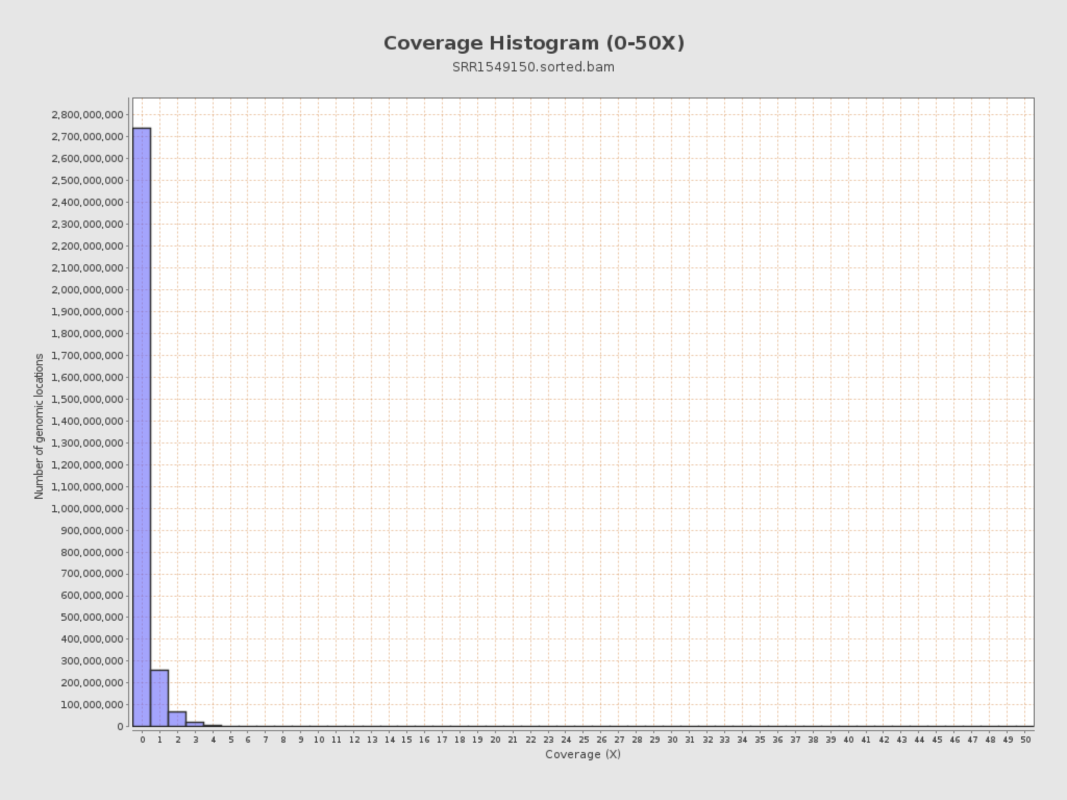
# 3. Results : Coverage across reference



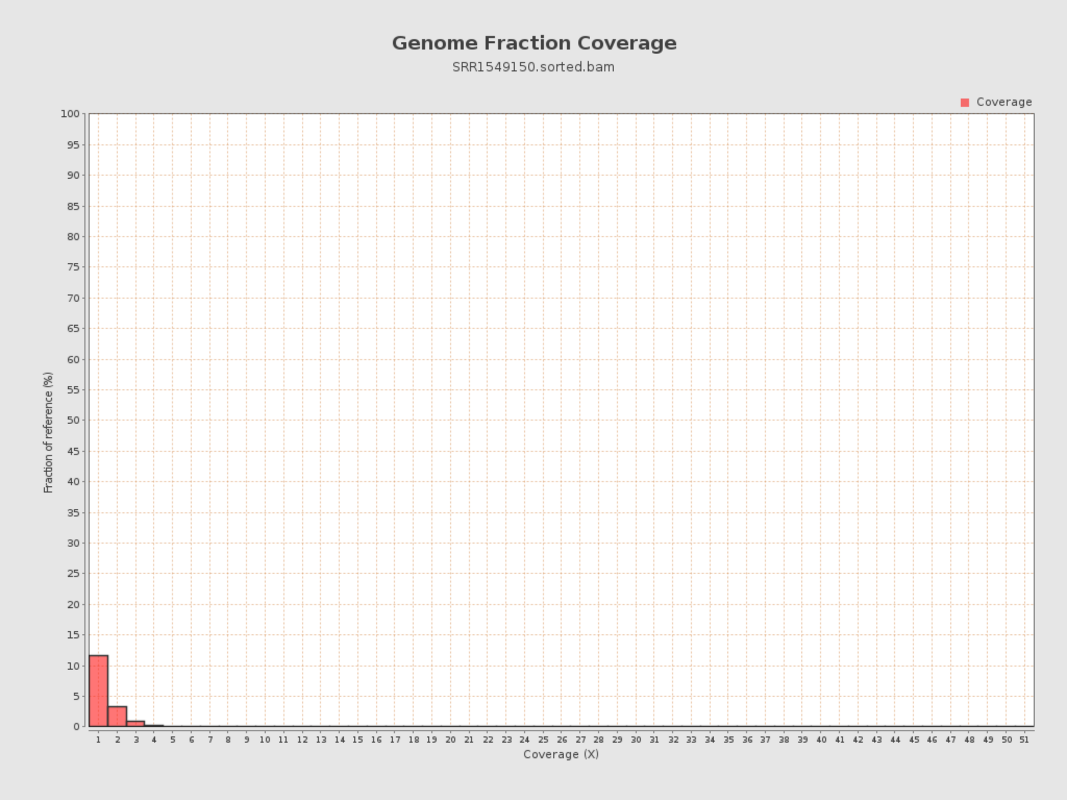
# 4. Results : Coverage Histogram



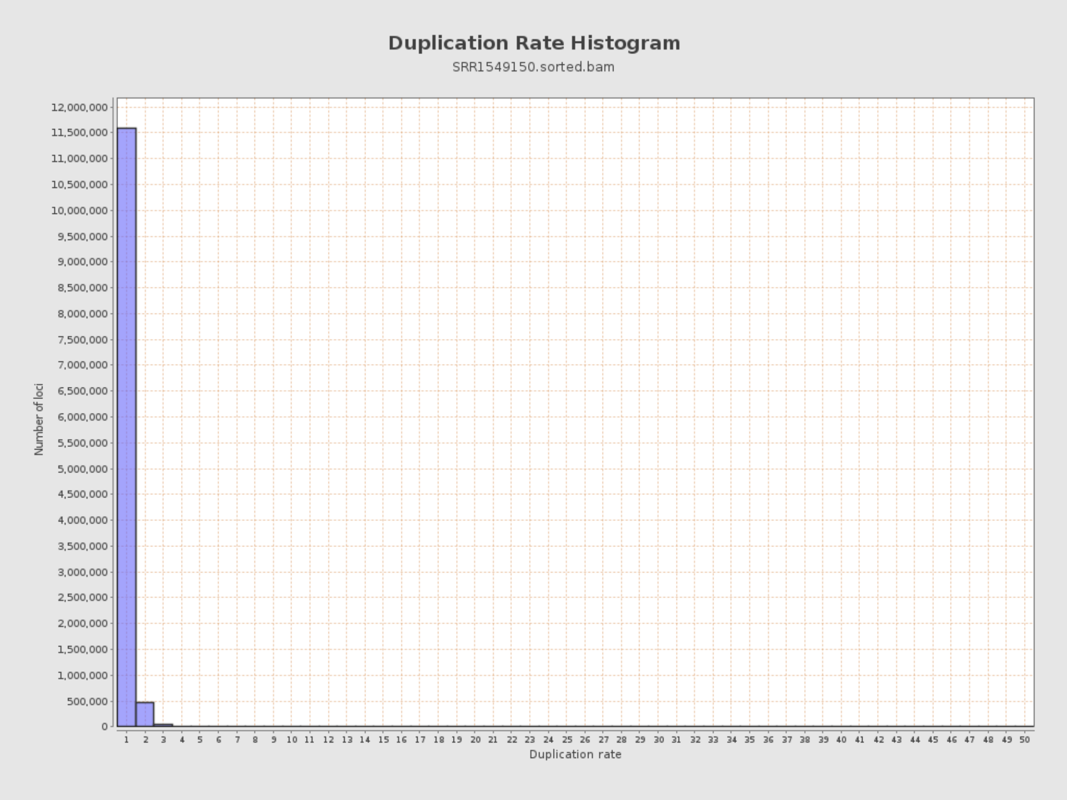
# 5. Results : Coverage Histogram (0-50X)



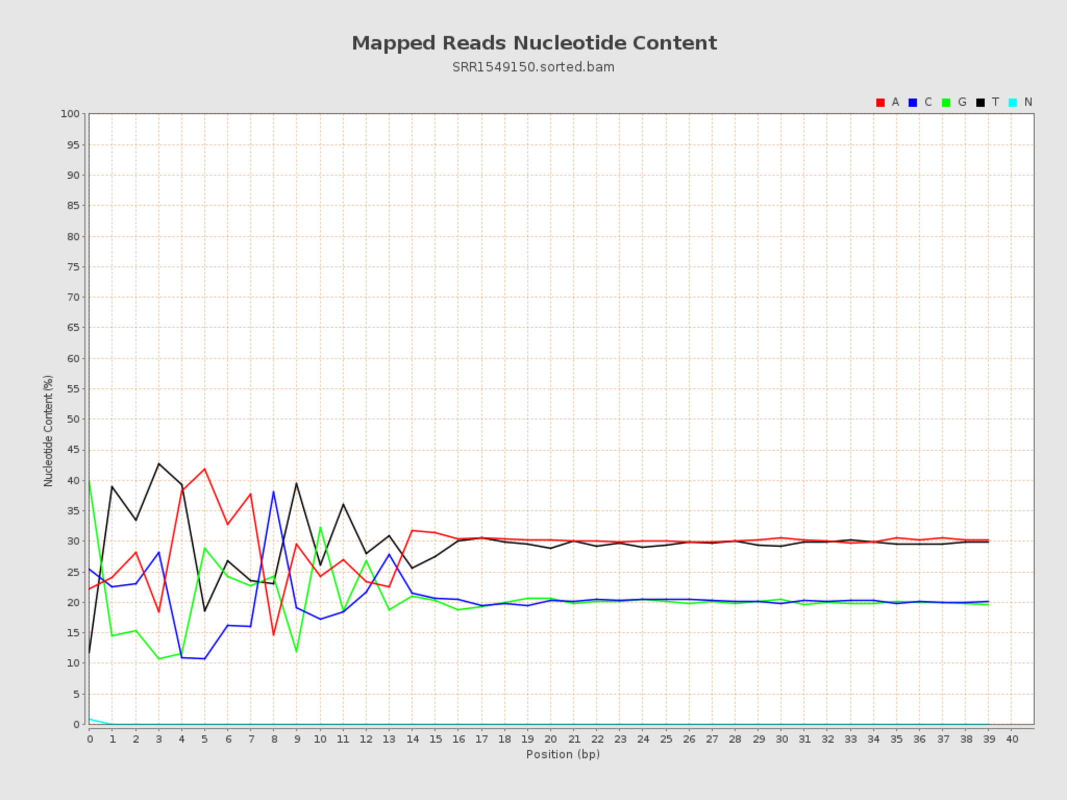
# 6. Results : Genome Fraction Coverage



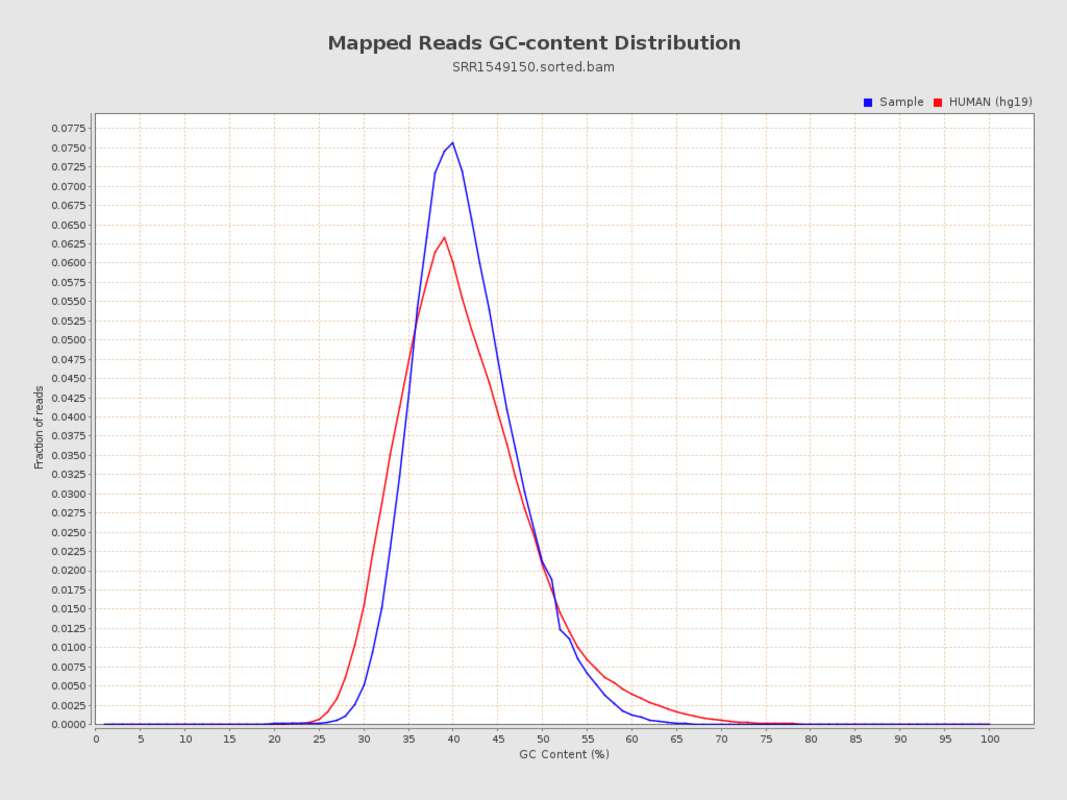
# 7. Results : Duplication Rate Histogram



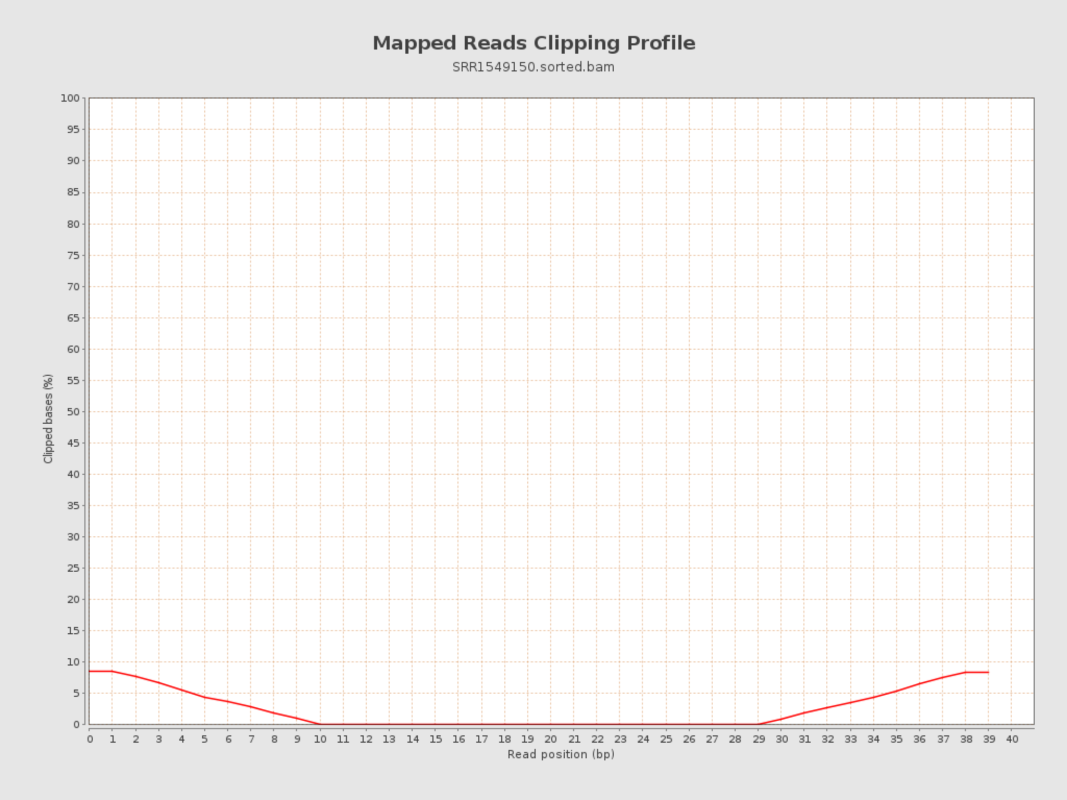
# 8. Results : Mapped Reads Nucleotide Content



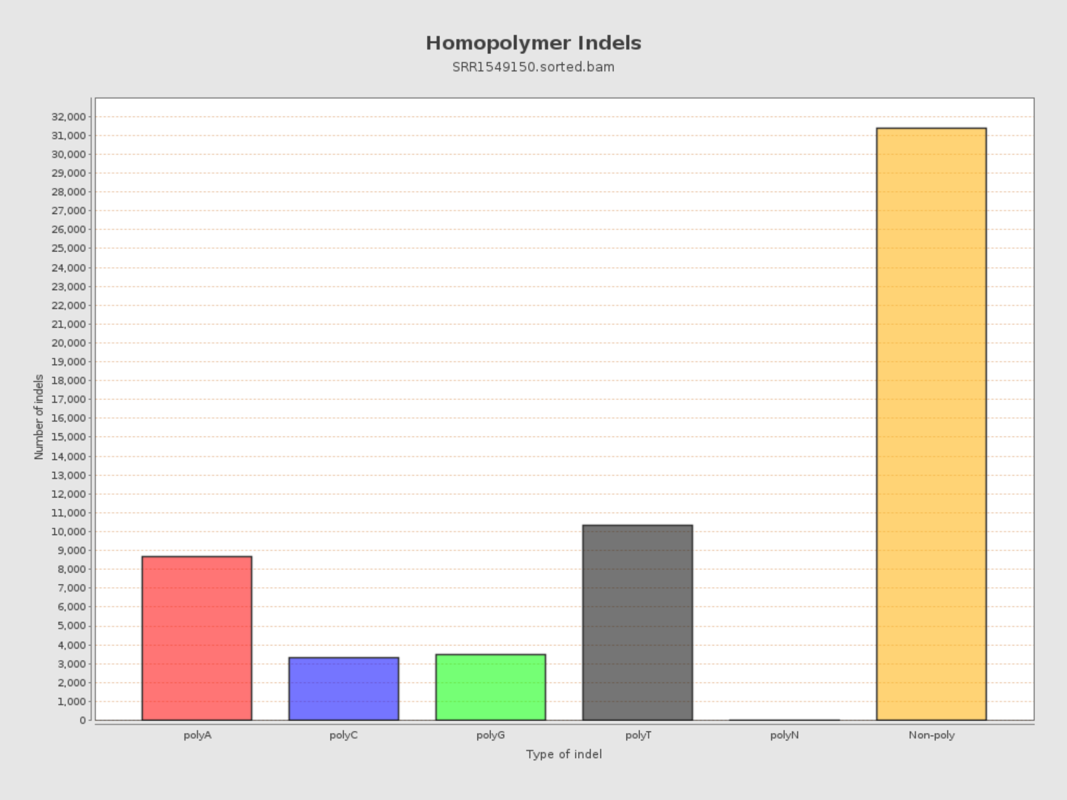
# 9. Results : Mapped Reads GC-content Distribution



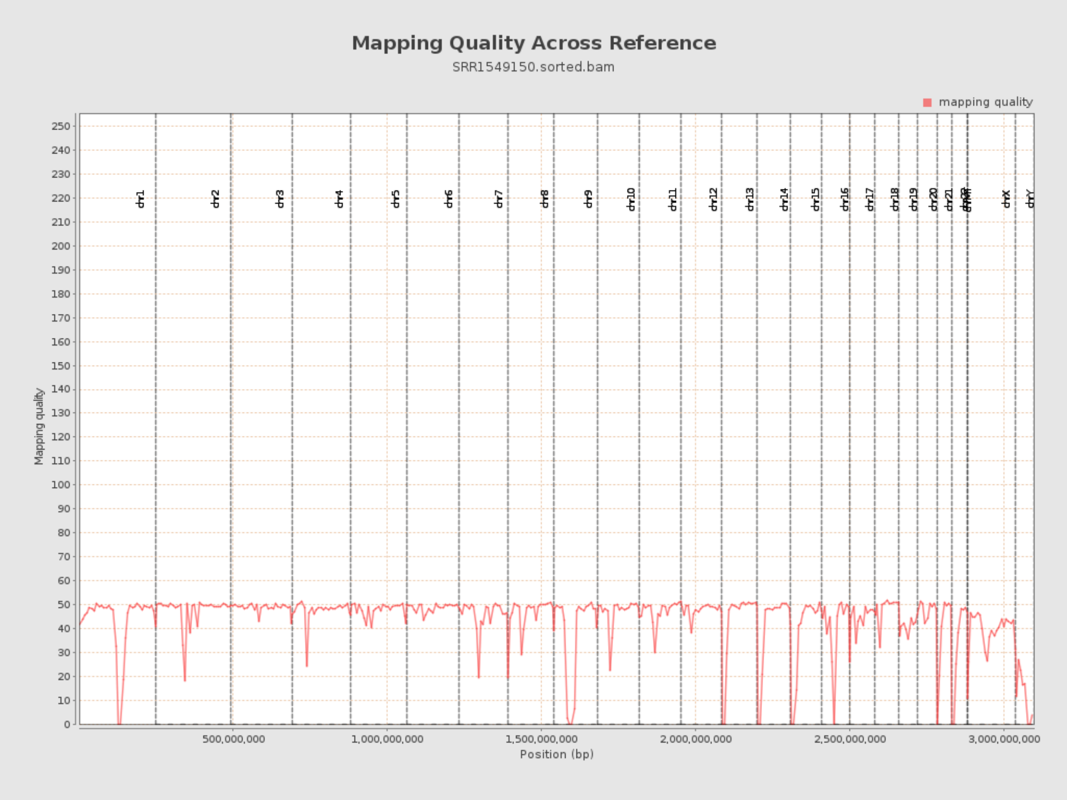
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram