# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 03:56:34*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548977.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_SRR1548977 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548977.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 03:56:32 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1548977.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 10,332,845 |
| Mapped reads | 4,563,820 / 44.17% |
| Unmapped reads | 5,769,025 / 55.83% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Read min/max/mean length | 40 / 40 / 40 |
| Duplicated reads (estimated) | 137,502 / 1.33% |
| Duplication rate | 2.15% |
| Clipped reads | 397,666 / 3.85% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 56,007,621 / 31.04% |
| Number/percentage of C's | 33,542,274 / 18.59% |
| Number/percentage of T's | 56,703,406 / 31.43% |
| Number/percentage of G's | 34,163,438 / 18.93% |
| Number/percentage of N's | 9,832 / 0.01% |
| GC Percentage | 37.53% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0583 |
| Standard Deviation | 0.4192 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.11 |

## 2.5. Mismatches and indels

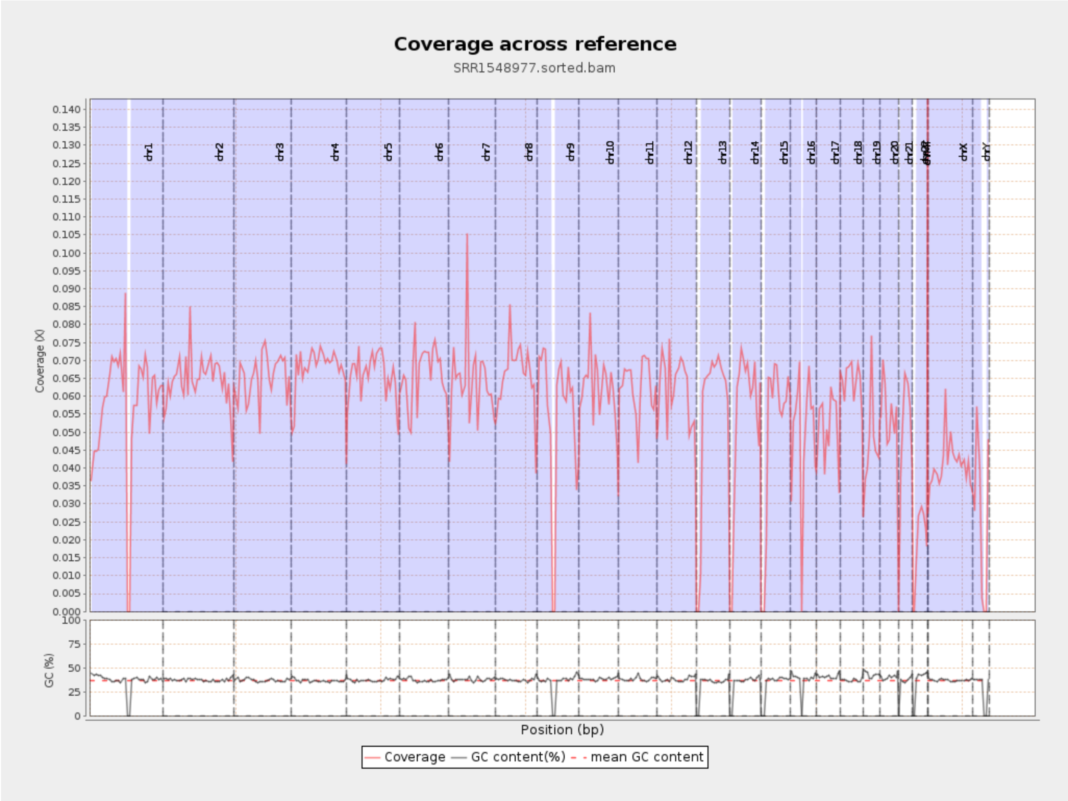
| | |
|---|---|
| General error rate | 0.31% |
| Mismatches | 555,842 |
| Insertions | 6,952 |
| Mapped reads with at least one insertion | 0.15% |
| Deletions | 18,848 |
| Mapped reads with at least one deletion | 0.41% |
| Homopolymer indels | 45.03% |

## 2.6. Chromosome stats

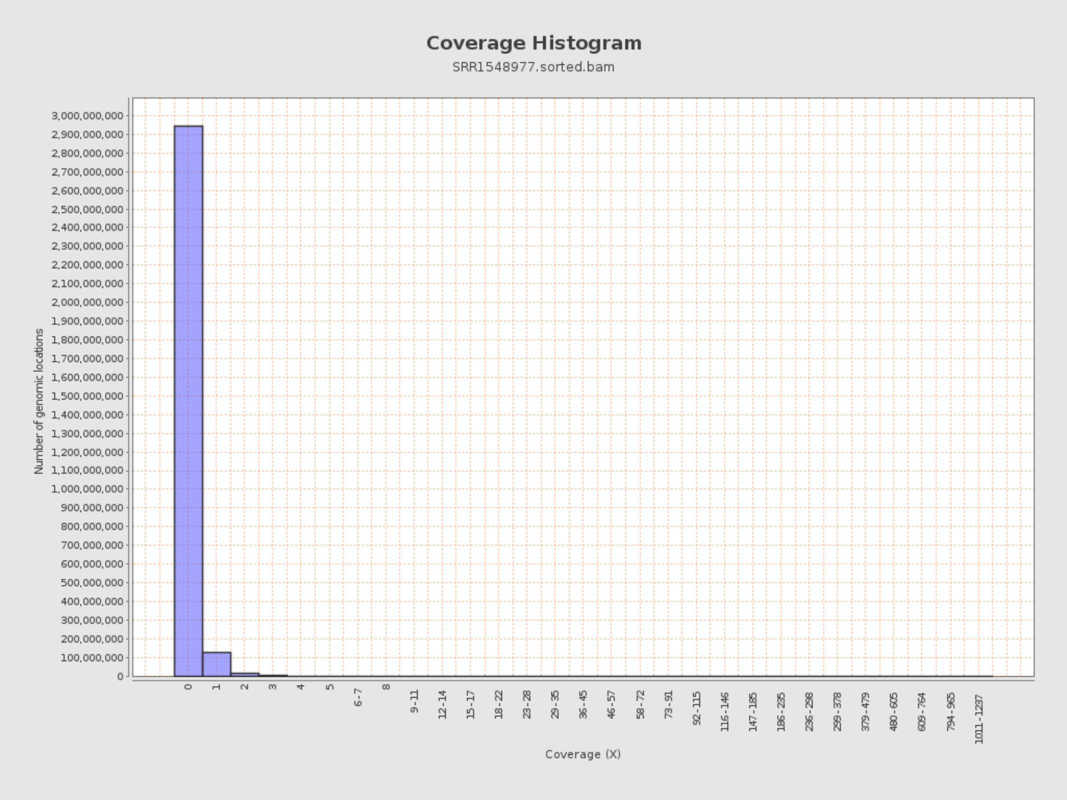
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 14306010 | 0.0574 | 0.7356 |
| chr2 | 243199373 | 15719464 | 0.0646 | 0.3789 |
| chr3 | 198022430 | 12941485 | 0.0654 | 0.2969 |
| chr4 | 191154276 | 13033769 | 0.0682 | 0.3094 |
| chr5 | 180915260 | 11948278 | 0.066 | 0.304 |
| chr6 | 171115067 | 11303080 | 0.0661 | 0.3552 |
| chr7 | 159138663 | 10304776 | 0.0648 | 0.6353 |
| chr8 | 146364022 | 9670873 | 0.0661 | 0.521 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr9 | 141213431 | 7755418 | 0.0549 | 0.3648 |
| chr10 | 135534747 | 8516528 | 0.0628 | 0.3683 |
| chr11 | 135006516 | 8406939 | 0.0623 | 0.3854 |
| chr12 | 133851895 | 8296014 | 0.062 | 0.3012 |
| chr13 | 115169878 | 6293194 | 0.0546 | 0.2696 |
| chr14 | 107349540 | 5706567 | 0.0532 | 0.3284 |
| chr15 | 102531392 | 5118512 | 0.0499 | 0.2569 |
| chr16 | 90354753 | 4523961 | 0.0501 | 0.273 |
| chr17 | 81195210 | 4114414 | 0.0507 | 0.2793 |
| chr18 | 78077248 | 5036015 | 0.0645 | 0.6003 |
| chr19 | 59128983 | 2808611 | 0.0475 | 0.7256 |
| chr20 | 63025520 | 3438610 | 0.0546 | 0.2801 |
| chr21 | 48129895 | 2352468 | 0.0489 | 0.2835 |
| chr22 | 51304566 | 969047 | 0.0189 | 0.1784 |
| chrMT | 16571 | 2789 | 0.1683 | 0.4686 |
| chrX | 155270560 | 6354586 | 0.0409 | 0.281 |
| chrY | 59373566 | 1528847 | 0.0257 | 0.2824 |

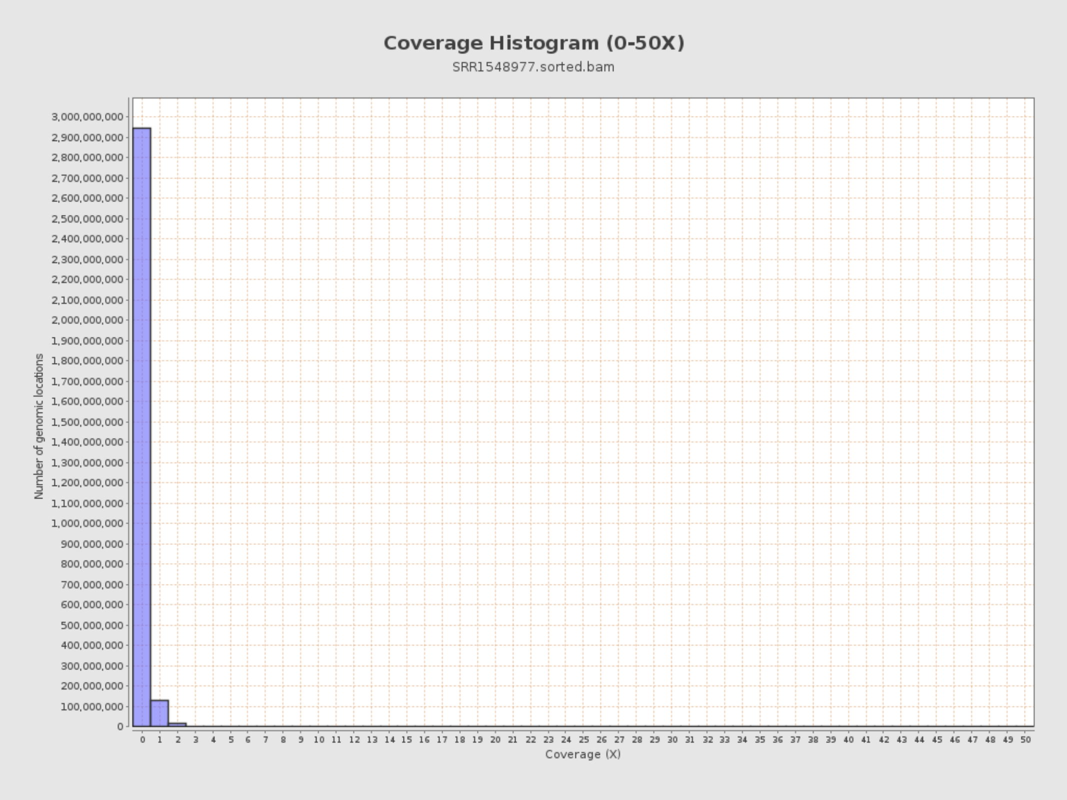
# 3. Results : Coverage across reference



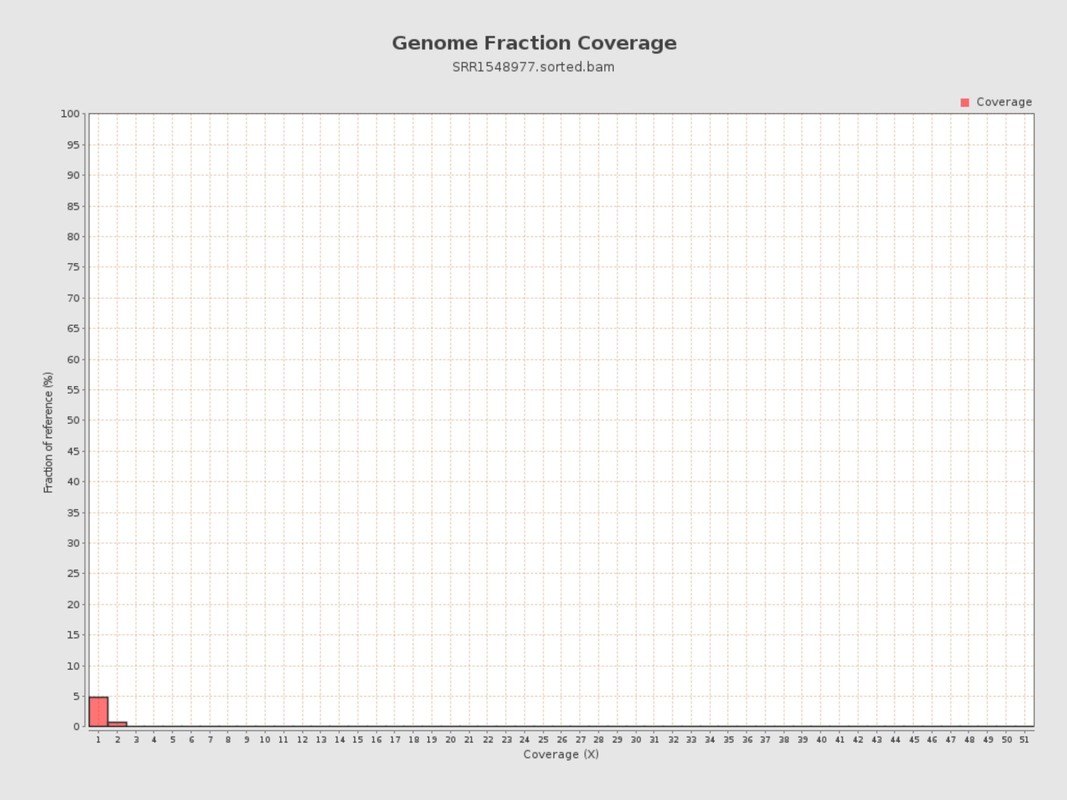
# 4. Results : Coverage Histogram



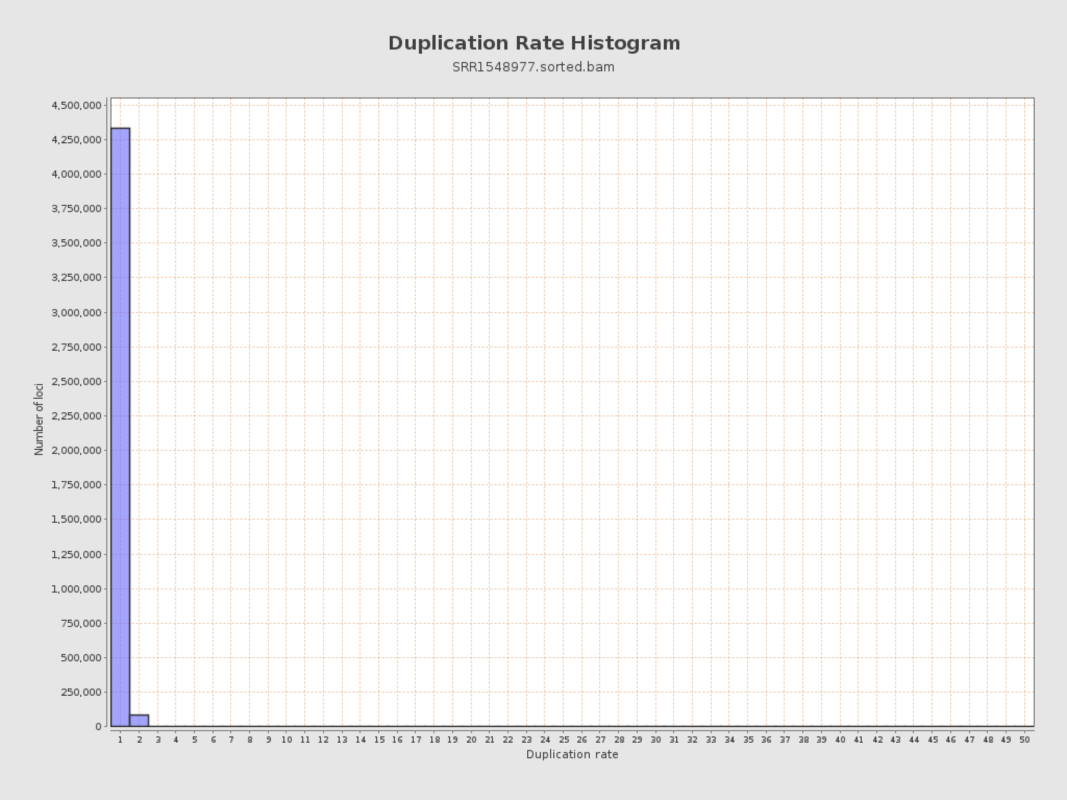
# 5. Results : Coverage Histogram (0-50X)



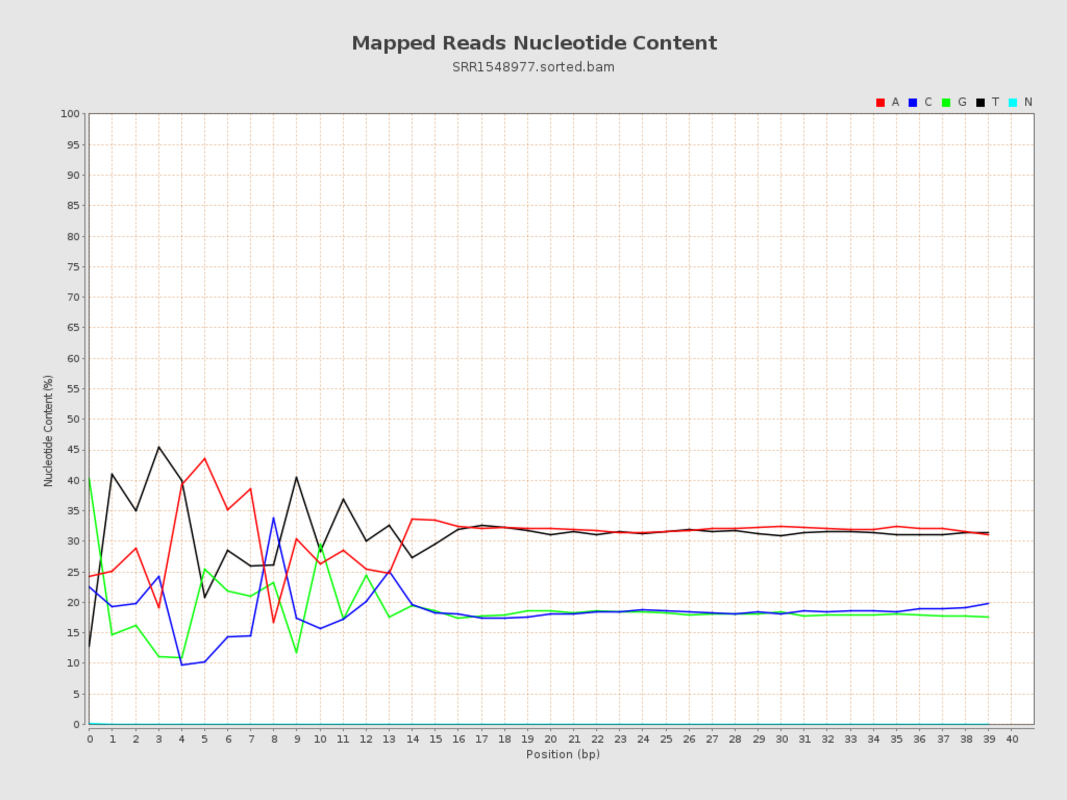
# 6. Results : Genome Fraction Coverage



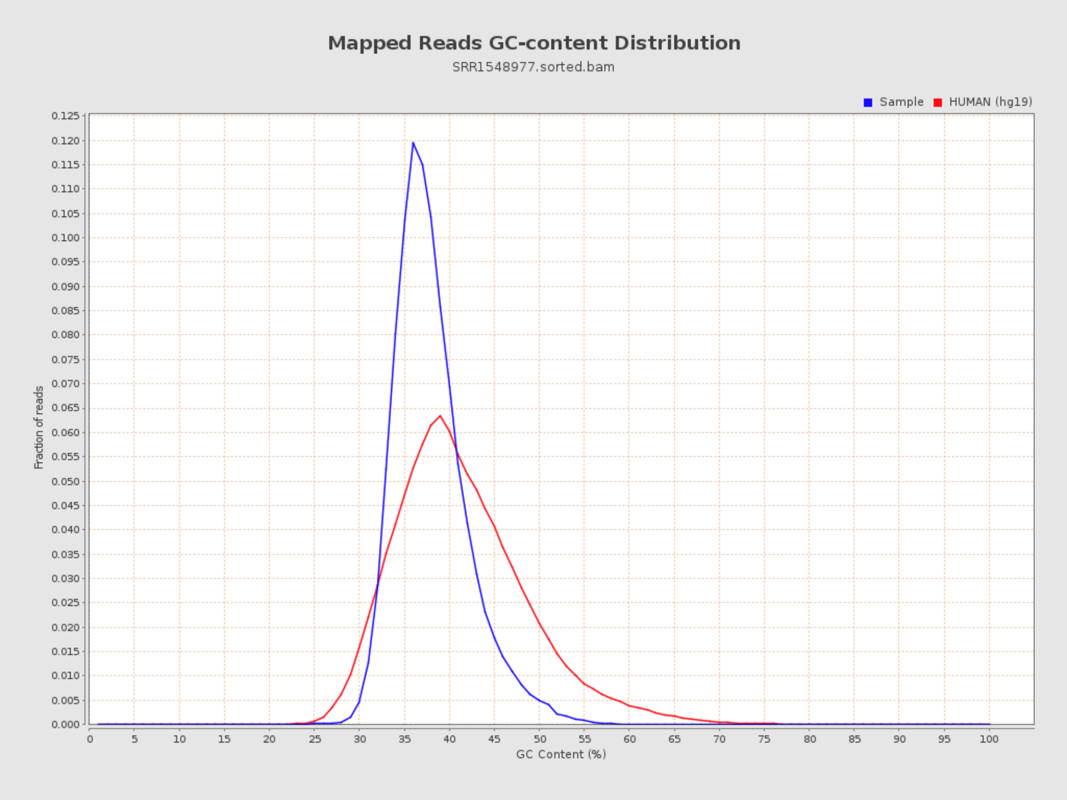
# 7. Results : Duplication Rate Histogram



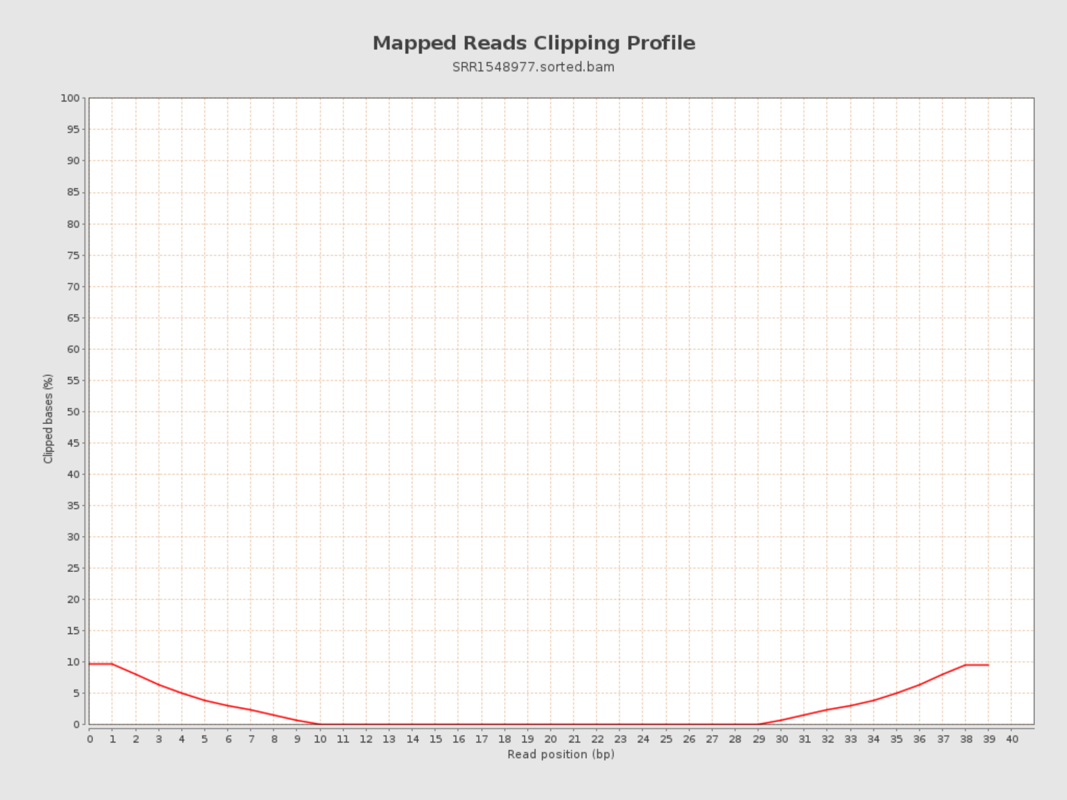
# 8. Results : Mapped Reads Nucleotide Content



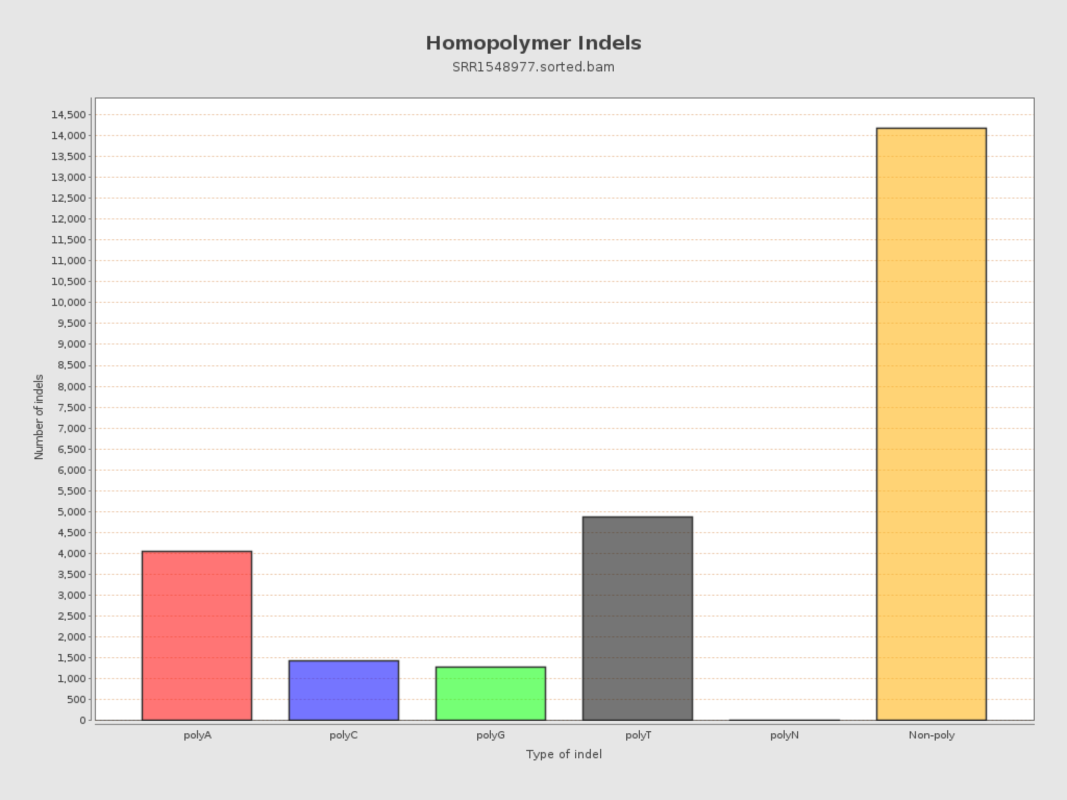
# 9. Results : Mapped Reads GC-content Distribution



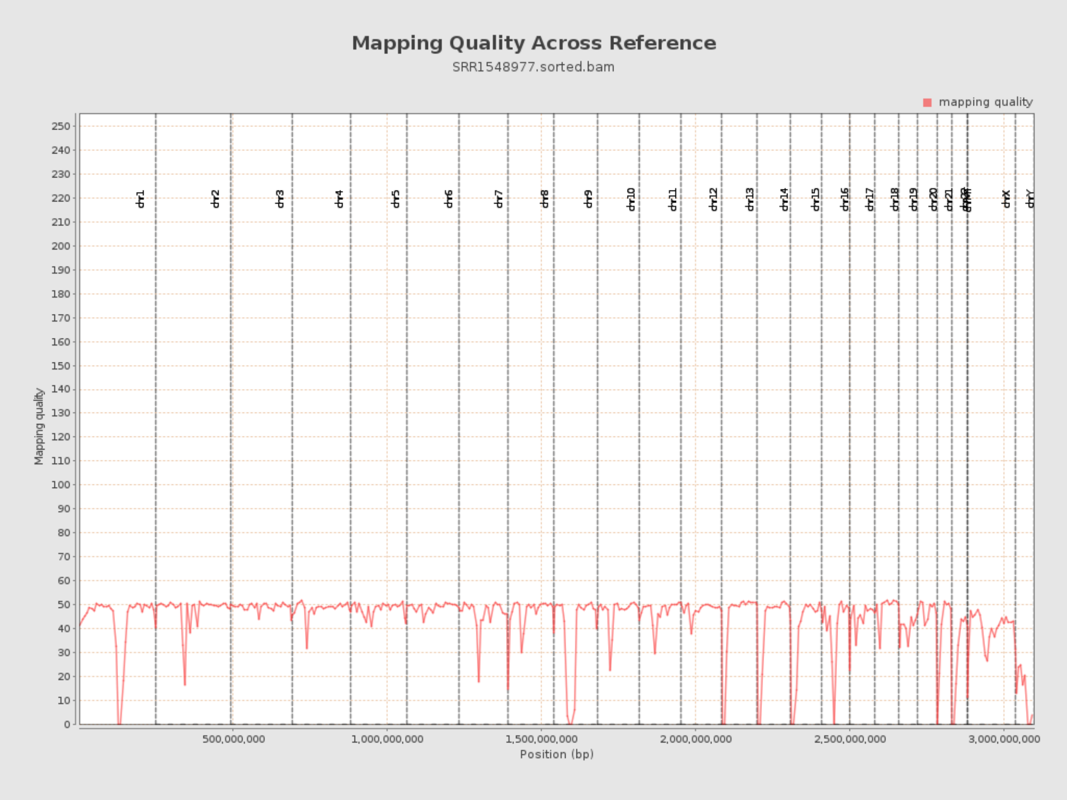
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram