# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:31:49*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/720.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/720.nodup.bam |
| Program: | bwa (0.7.17-r1188) |
| Analyze overlapping paired-end reads: | no |
| Command line: | bwa mem -M -t 8 -R @RG\tID:$unit\tPL:Illumina\tLB:LibA\tSM:$sample /proj/uppstore2018210/Aalpina/data/reference/GCA_900128785.1_MPIPZ.v5_genomic.fa /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_227/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_227_S308_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_227/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_227_S308_L003_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|---|---|
| Analysis date: | Mon May 29 21:31:48 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 74,633,731 |
| Mapped reads | 67,365,241 / 90.26% |
| Unmapped reads | 7,268,490 / 9.74% |
| Mapped paired reads | 67,365,241 / 90.26% |
| Mapped reads, first in pair | 33,762,245 / 45.24% |
| Mapped reads,  second in pair | 33,602,996 / 45.02% |
| Mapped reads, both in pair | 65,039,215 / 87.14% |
| Mapped reads, singletons | 2,326,026 / 3.12% |
| Read min/max/mean length | 30 / 151 / 148.01 |
| Duplicated reads (flagged) | 12,591,574 / 16.87% |
| Clipped reads | 17,032,906 / 22.82% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 2,828,295,767 / 30.89% |
| Number/percentage of C's | 1,748,912,470 / 19.1% |
| Number/percentage of T's | 2,829,752,336 / 30.91% |
| Number/percentage of G's | 1,747,995,067 / 19.09% |
| Number/percentage of N's | 33,547 / 0% |
| GC Percentage | 38.2% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 29.4531 |
| Standard Deviation | 322.6285 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.1 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 260,481.91 |
| Standard Deviation | 2,451,796.17 |
| P25/Median/P75 | 311 / 410 / 535 |

## 2.6. Mismatches and indels

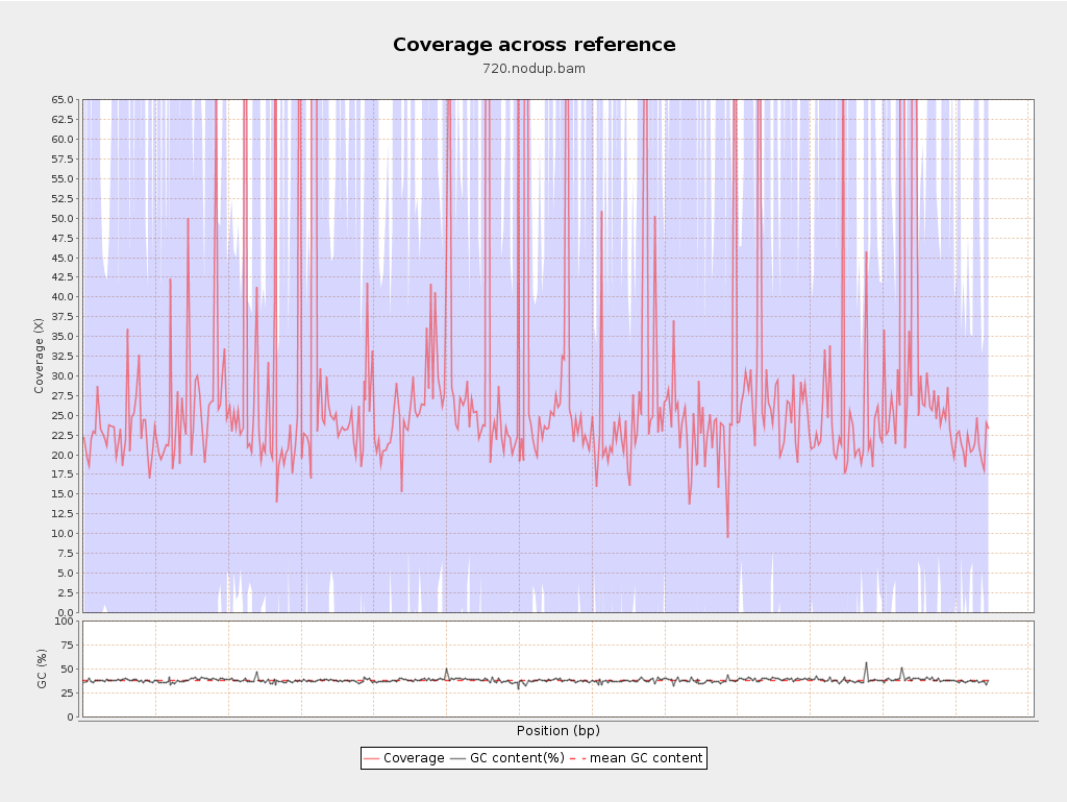
| | |
|---|---|
| General error rate | 2.43% |
| Mismatches | 203,857,319 |
| Insertions | 6,898,134 |
| Mapped reads with at least one insertion | 9.1% |
| Deletions | 6,469,260 |
| Mapped reads with at least one deletion | 8.52% |
| Homopolymer indels | 57.48% |

## 2.7. Chromosome stats

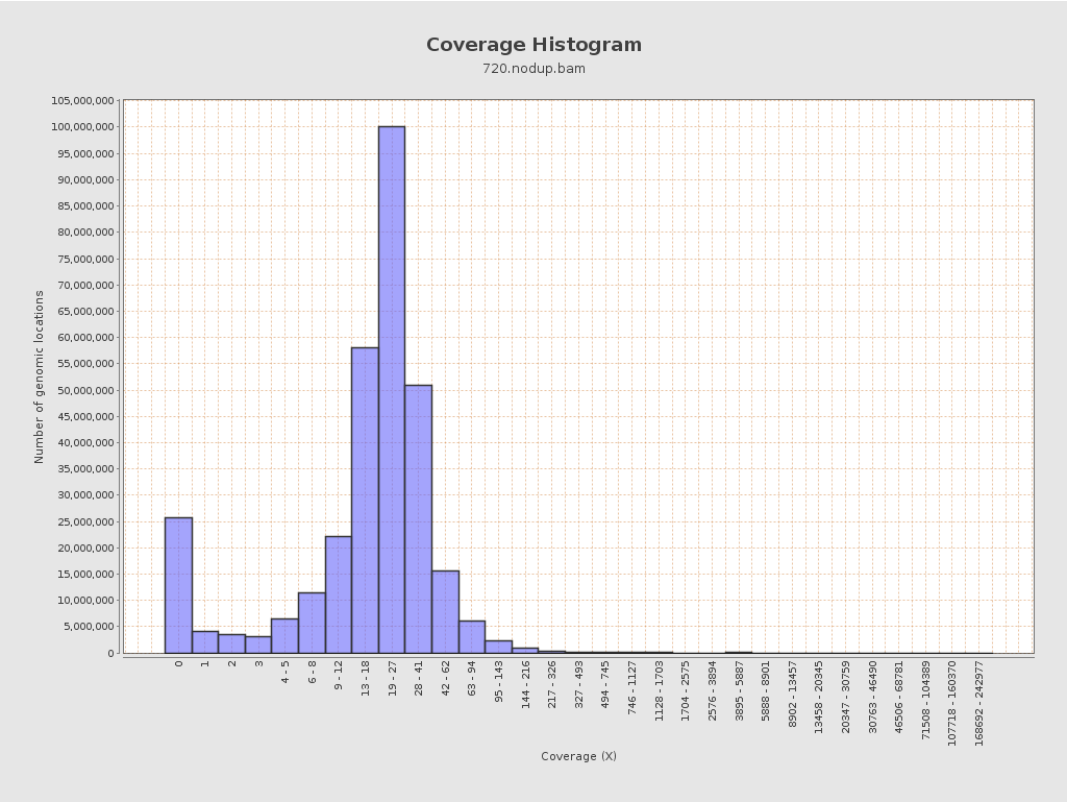
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 676479439 | 22.7584 | 122.9502 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 1076665461 | 29.4186 | 321.1414 |
| LT669790.1 | 30422129 | 1129068428 | 37.1134 | 477.3116 |
| LT669791.1 | 52758100 | 1545725150 | 29.2983 | 341.1262 |
| LT669792.1 | 28376109 | 844970513 | 29.7775 | 337.0271 |
| LT669793.1 | 33388210 | 885831929 | 26.5313 | 198.6963 |
| LT669794.1 | 50579949 | 1393471233 | 27.5499 | 261.7888 |
| LT669795.1 | 49795044 | 1626623616 | 32.6664 | 378.4713 |

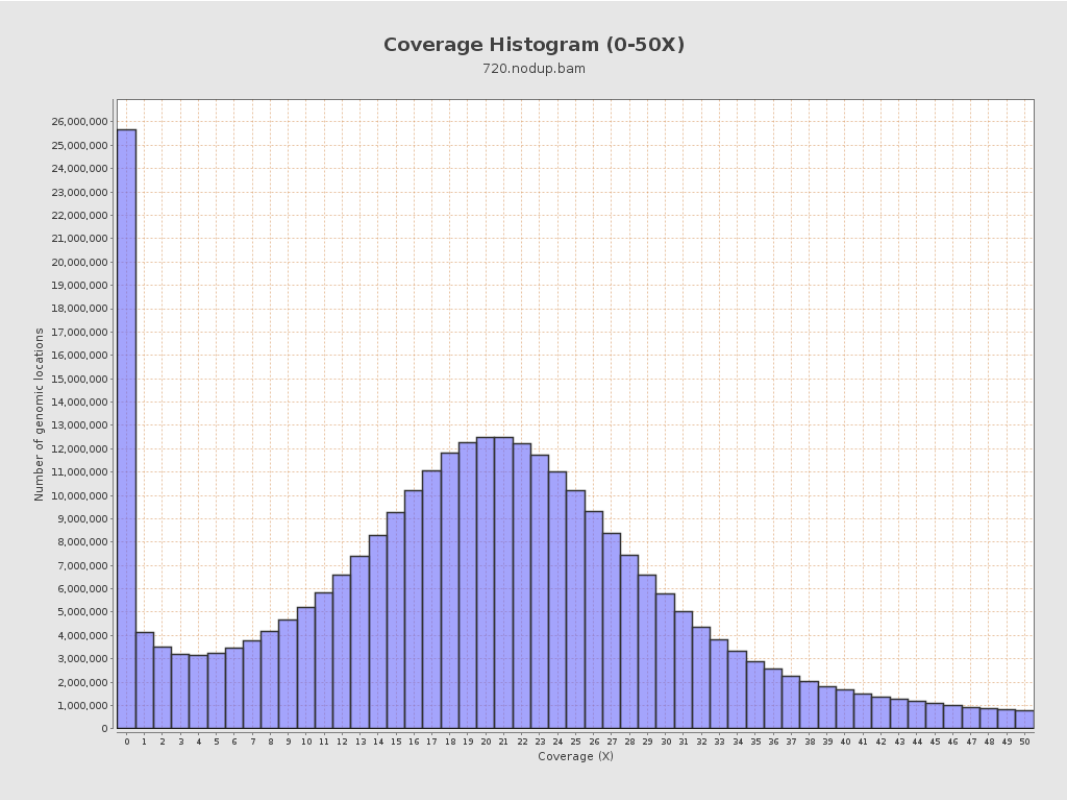
# 3. Results : Coverage across reference



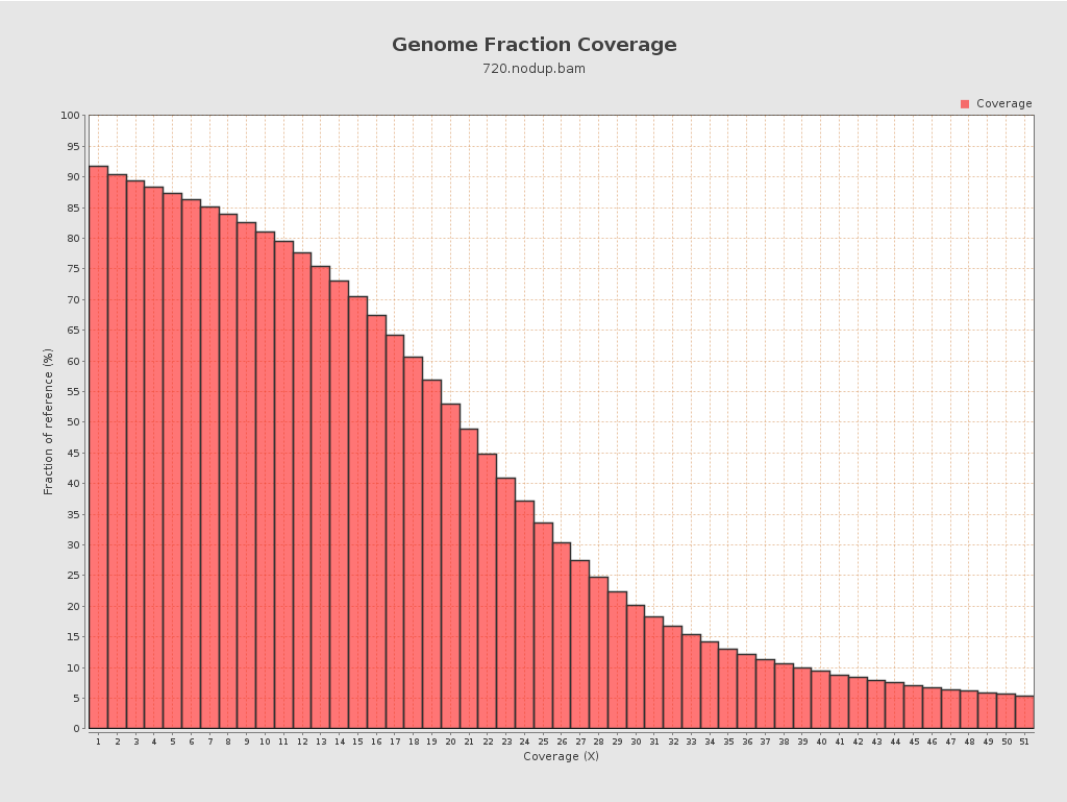
# 4. Results : Coverage Histogram



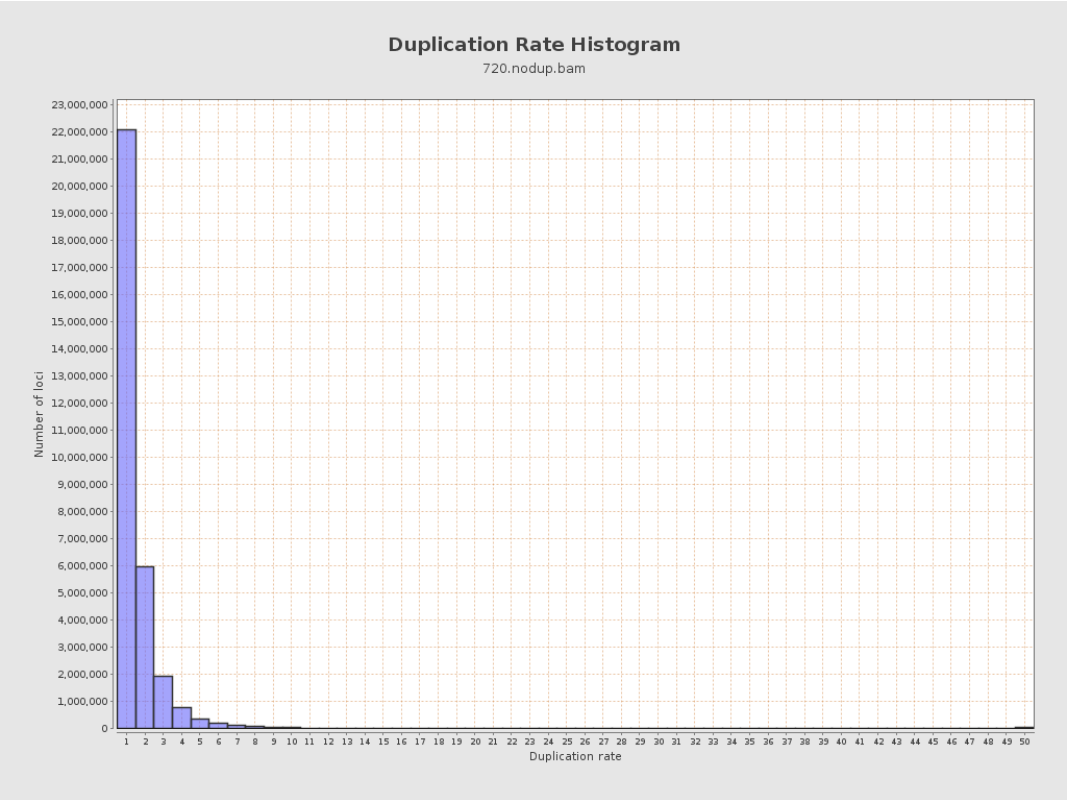
# 5. Results : Coverage Histogram (0-50X)



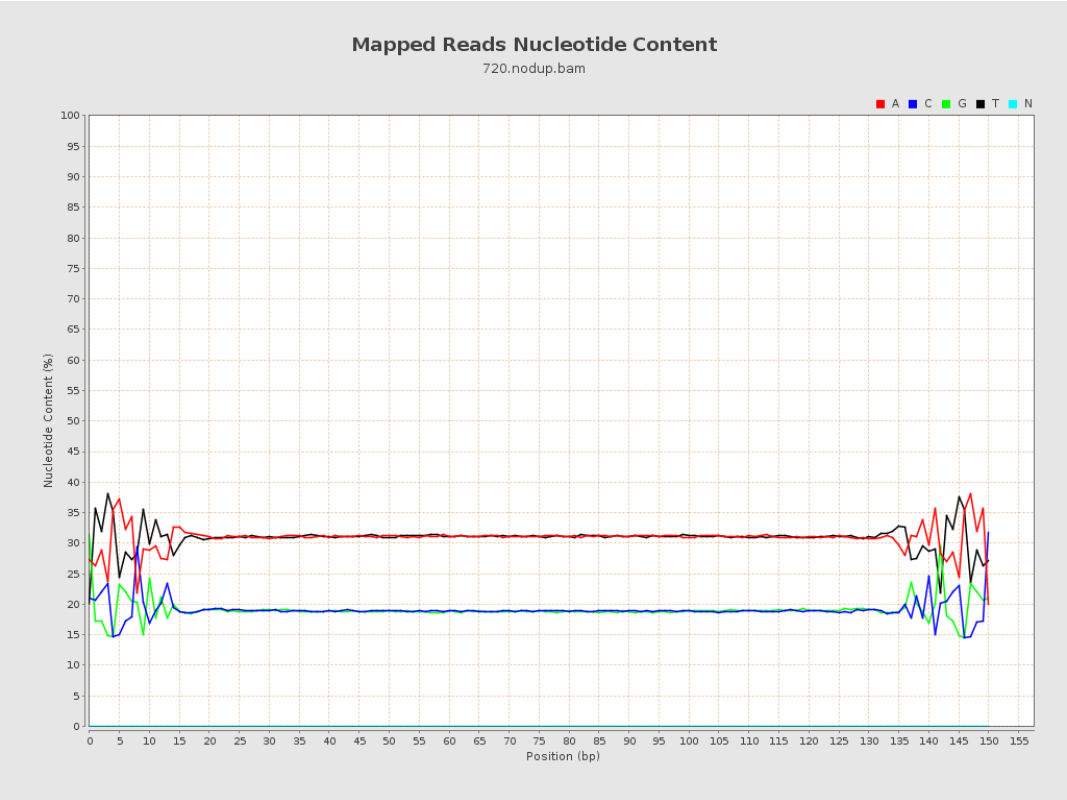
# 6. Results : Genome Fraction Coverage



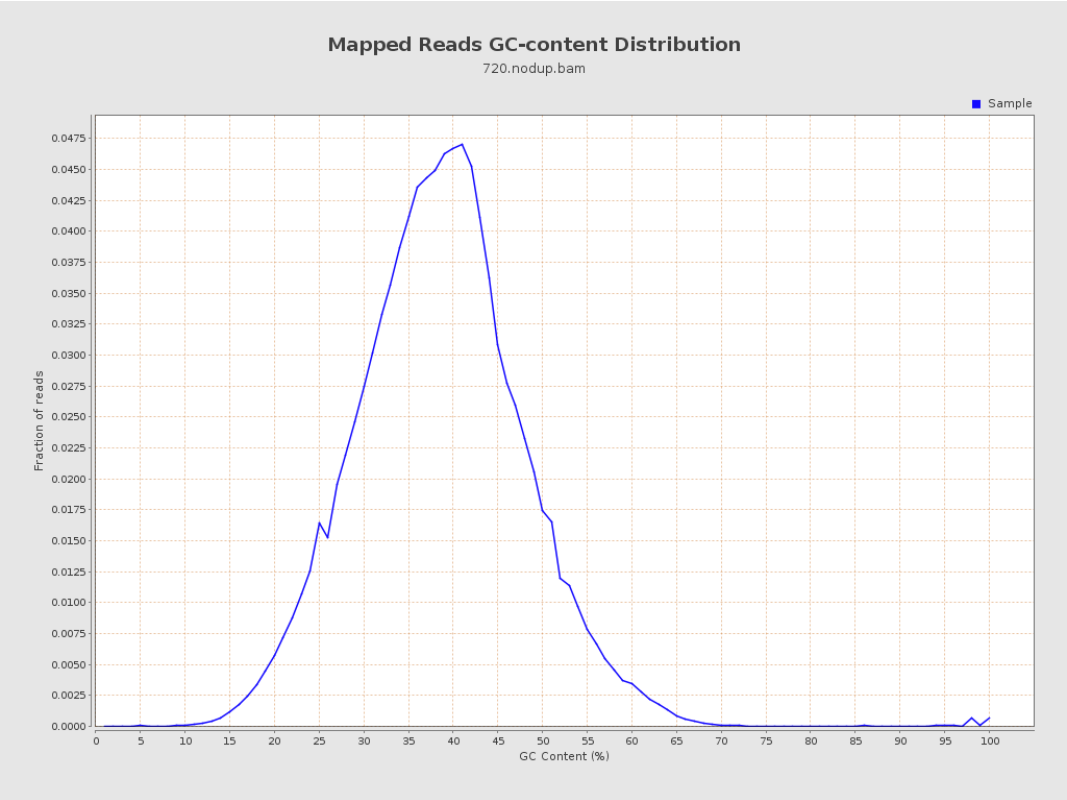
# 7. Results : Duplication Rate Histogram



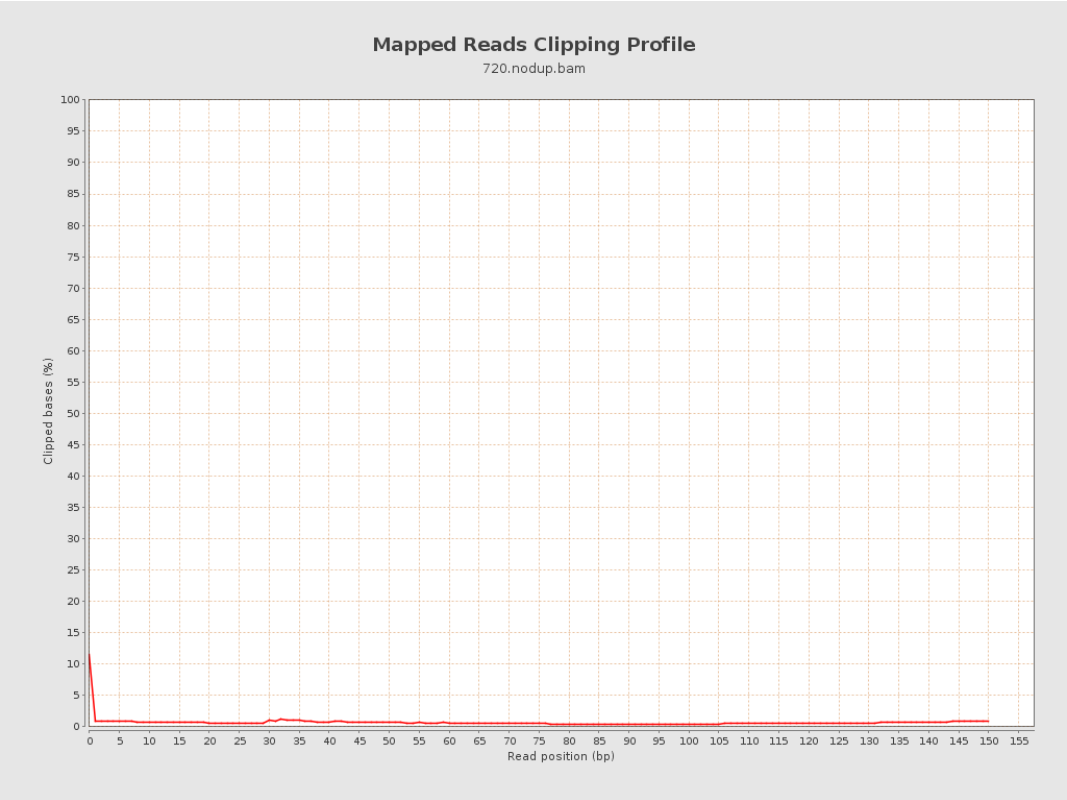
# 8. Results : Mapped Reads Nucleotide Content



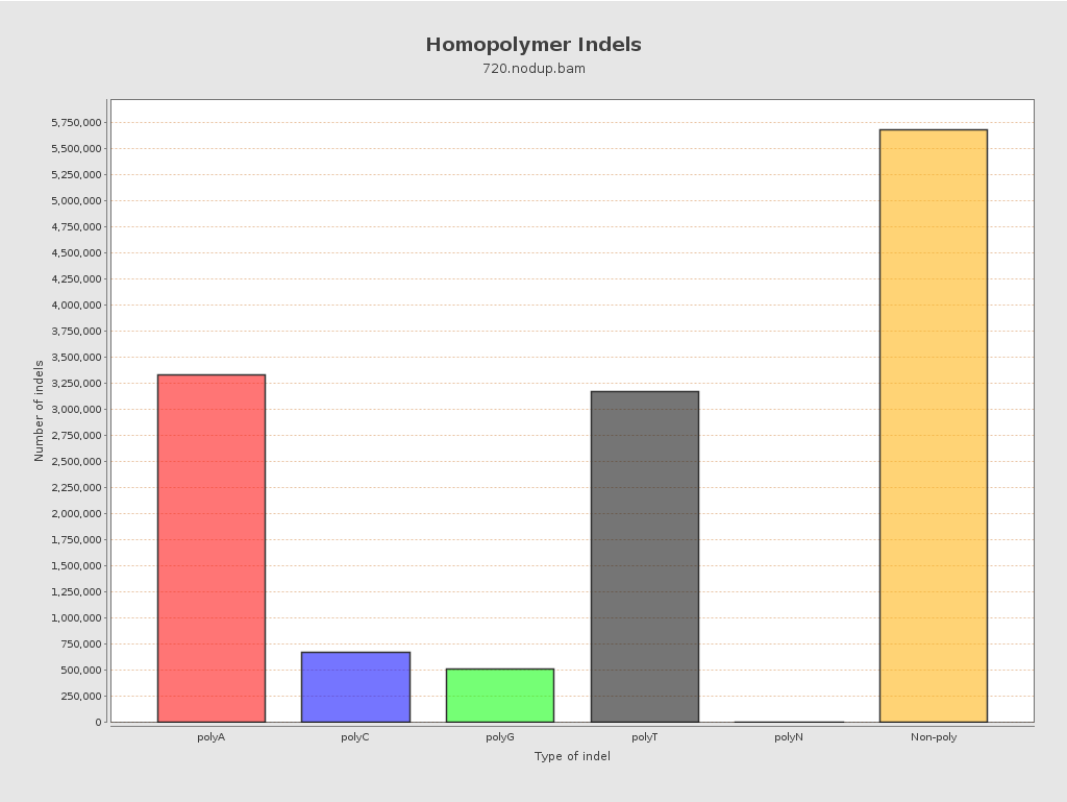
# 9. Results : Mapped Reads GC-content Distribution



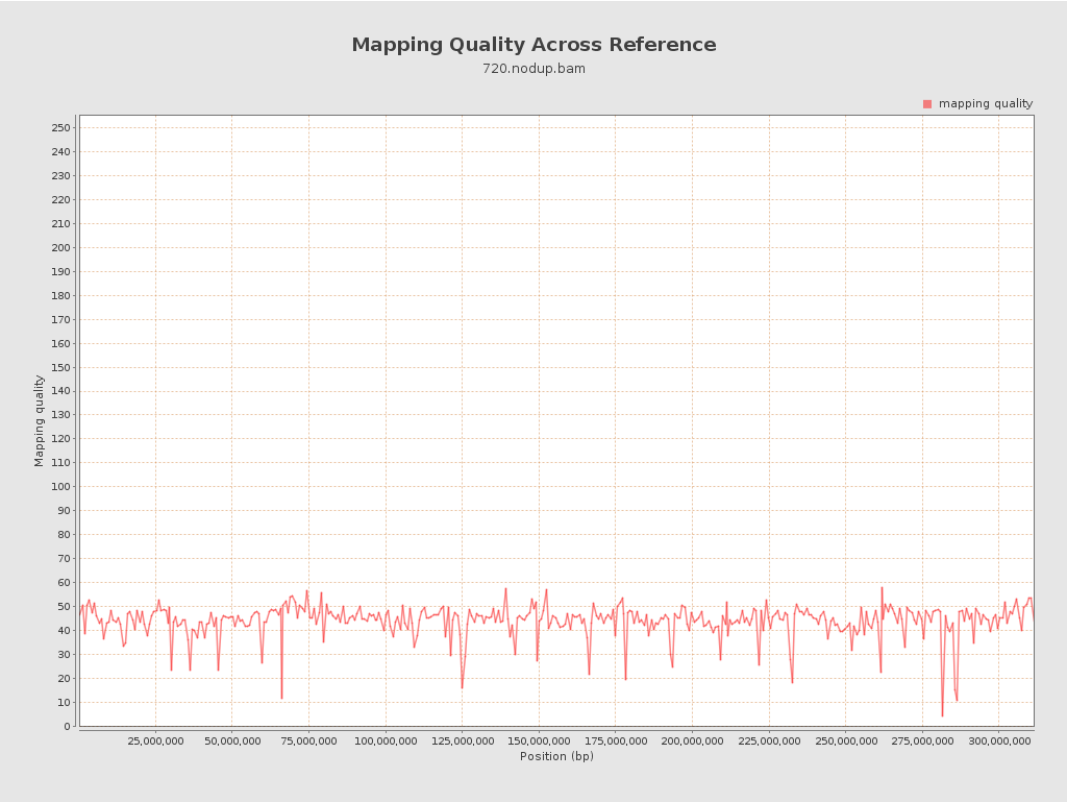
# 10. Results : Mapped Reads Clipping Profile



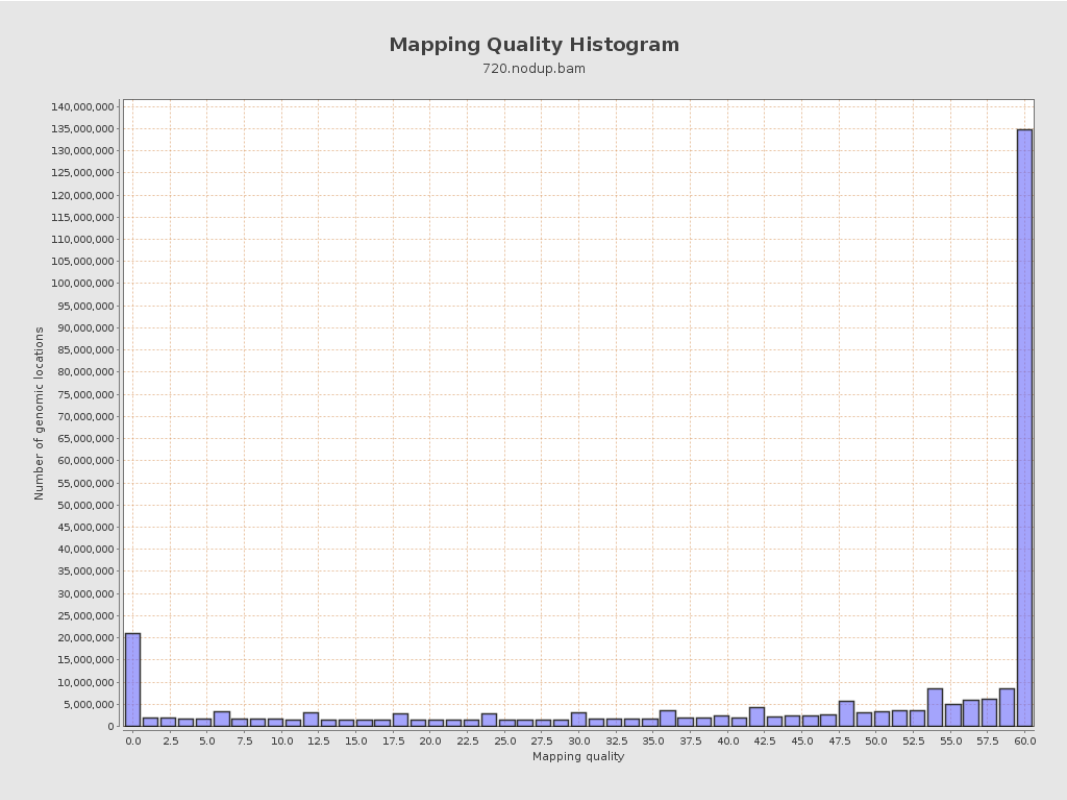
# 11. Results : Homopolymer Indels



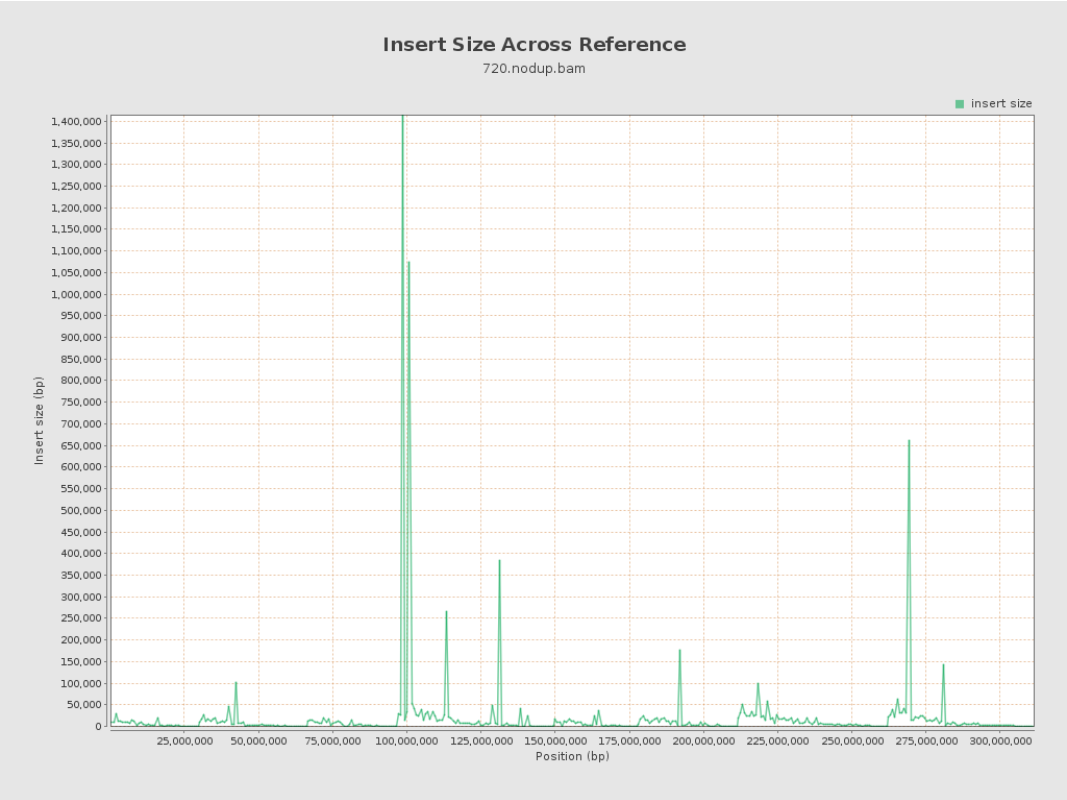
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram