# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:36:02*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/863.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/863.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_452/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_452_S427_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_452/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_452_S427_L004_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|---|---|
| Analysis date: | Mon May 29 21:36:01 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 77,214,386 |
| Mapped reads | 71,888,466 / 93.1% |
| Unmapped reads | 5,325,920 / 6.9% |
| Mapped paired reads | 71,888,466 / 93.1% |
| Mapped reads, first in pair | 36,034,094 / 46.67% |
| Mapped reads,  second in pair | 35,854,372 / 46.43% |
| Mapped reads, both in pair | 70,186,647 / 90.9% |
| Mapped reads, singletons | 1,701,819 / 2.2% |
| Read min/max/mean length | 30 / 151 / 148.12 |
| Duplicated reads (flagged) | 10,881,245 / 14.09% |
| Clipped reads | 16,090,133 / 20.84% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 3,092,302,237 / 31.07% |
| Number/percentage of C's | 1,884,373,308 / 18.93% |
| Number/percentage of T's | 3,091,943,777 / 31.07% |
| Number/percentage of G's | 1,883,979,906 / 18.93% |
| Number/percentage of N's | 34,956 / 0% |
| GC Percentage | 37.86% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 32.0189 |
| Standard Deviation | 240.6285 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.56 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 246,951.1 |
| Standard Deviation | 2,375,415.34 |
| P25/Median/P75 | 355 / 467 / 612 |

## 2.6. Mismatches and indels

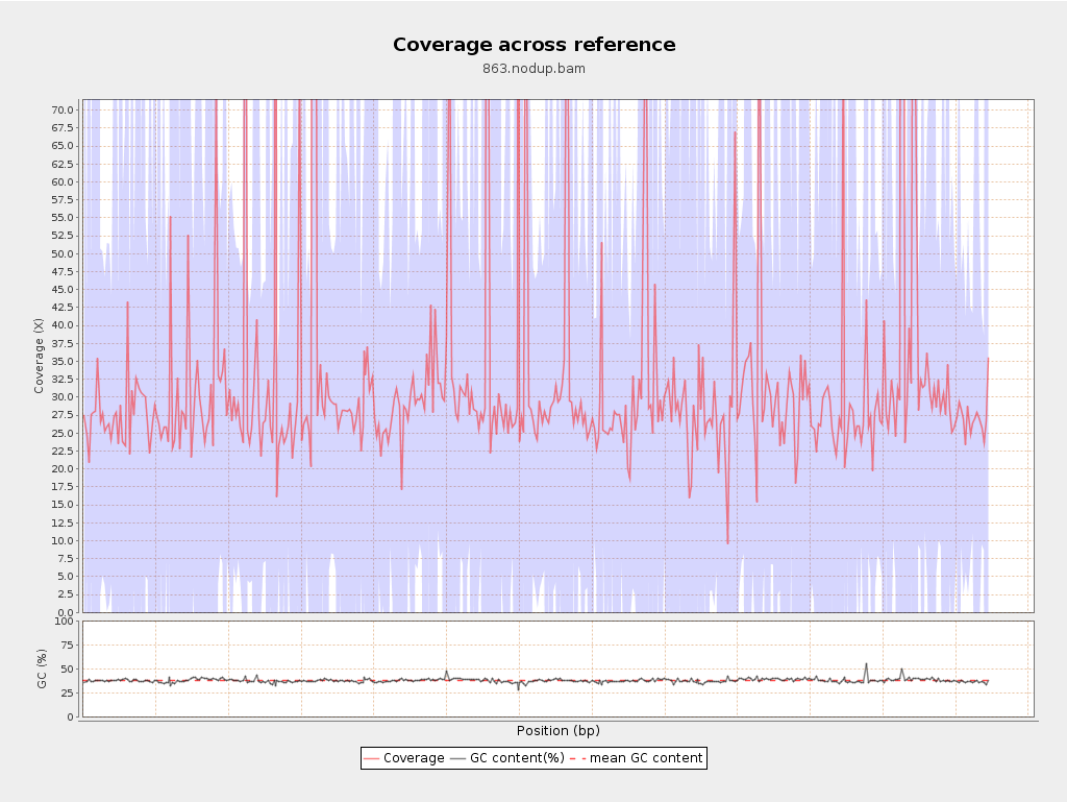
| | |
|---|---|
| General error rate | 2.29% |
| Mismatches | 208,582,464 |
| Insertions | 6,835,295 |
| Mapped reads with at least one insertion | 8.52% |
| Deletions | 6,907,855 |
| Mapped reads with at least one deletion | 8.54% |
| Homopolymer indels | 57.39% |

## 2.7. Chromosome stats

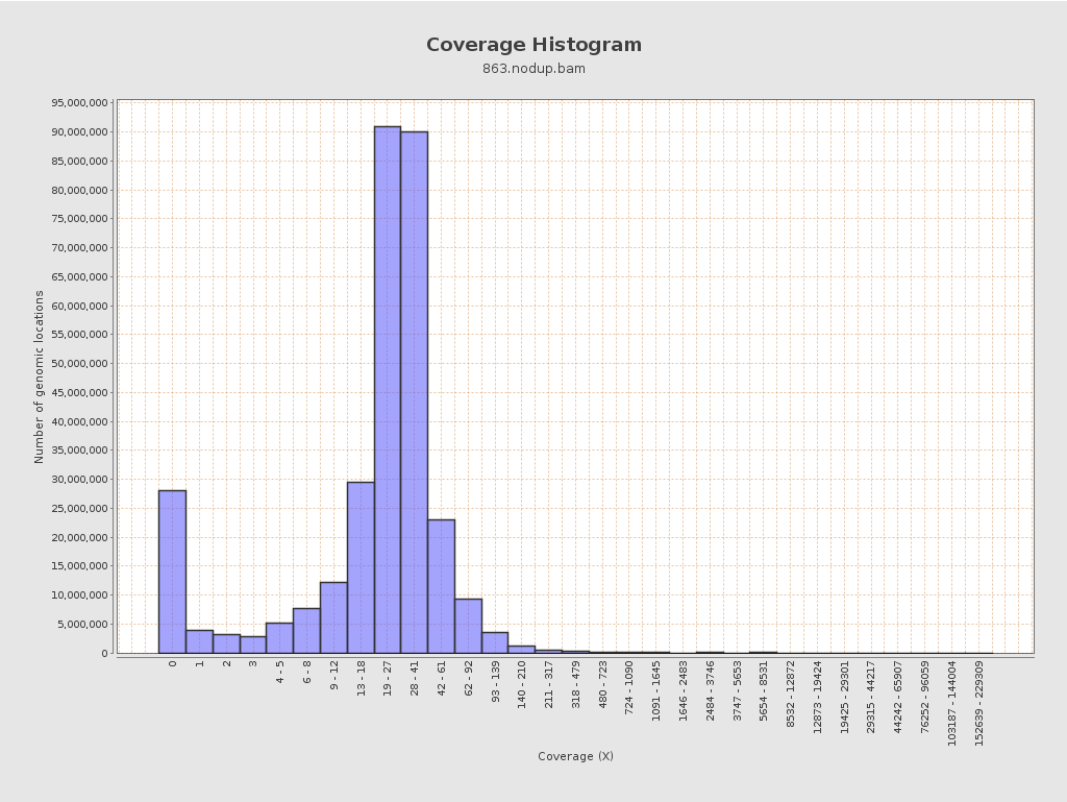
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 812064182 | 27.3198 | 84.083 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 1207111972 | 32.9828 | 271.0931 |
| LT669790.1 | 30422129 | 1101289973 | 36.2003 | 306.3459 |
| LT669791.1 | 52758100 | 1666913416 | 31.5954 | 232.3264 |
| LT669792.1 | 28376109 | 920401138 | 32.4358 | 263.3518 |
| LT669793.1 | 33388210 | 1001833981 | 30.0056 | 166.8005 |
| LT669794.1 | 50579949 | 1543049809 | 30.5071 | 228.7087 |
| LT669795.1 | 49795044 | 1725784759 | 34.6578 | 279.7778 |

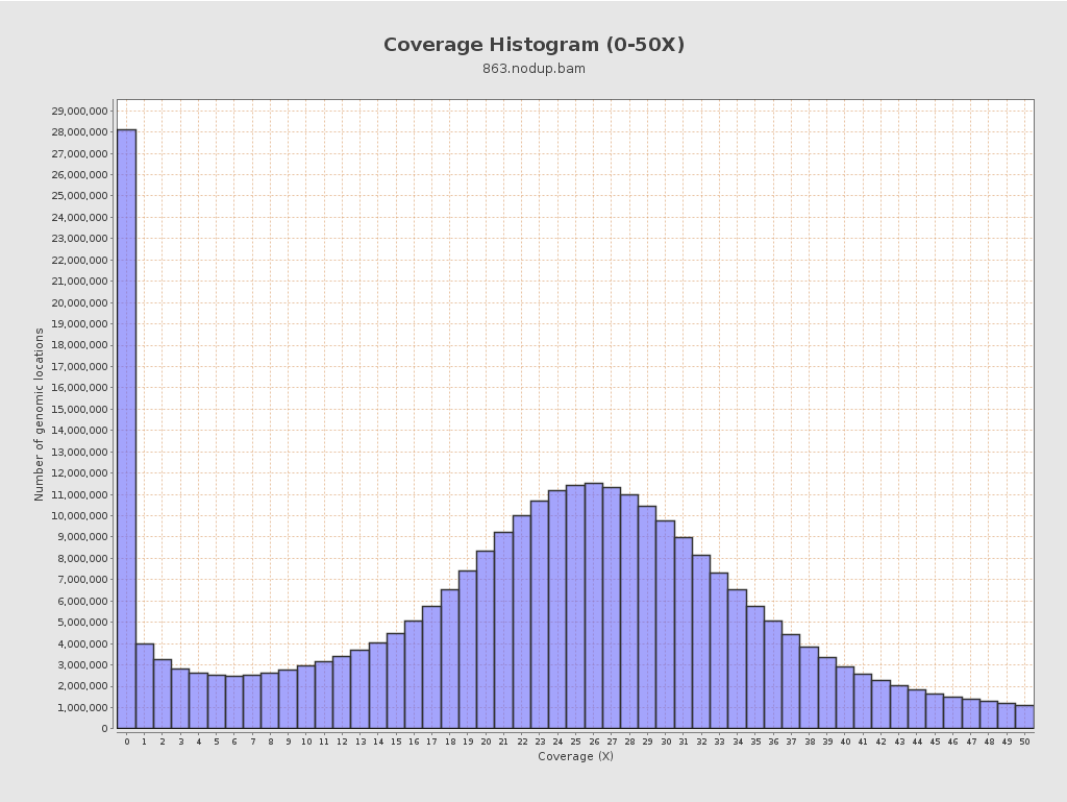
# 3. Results : Coverage across reference



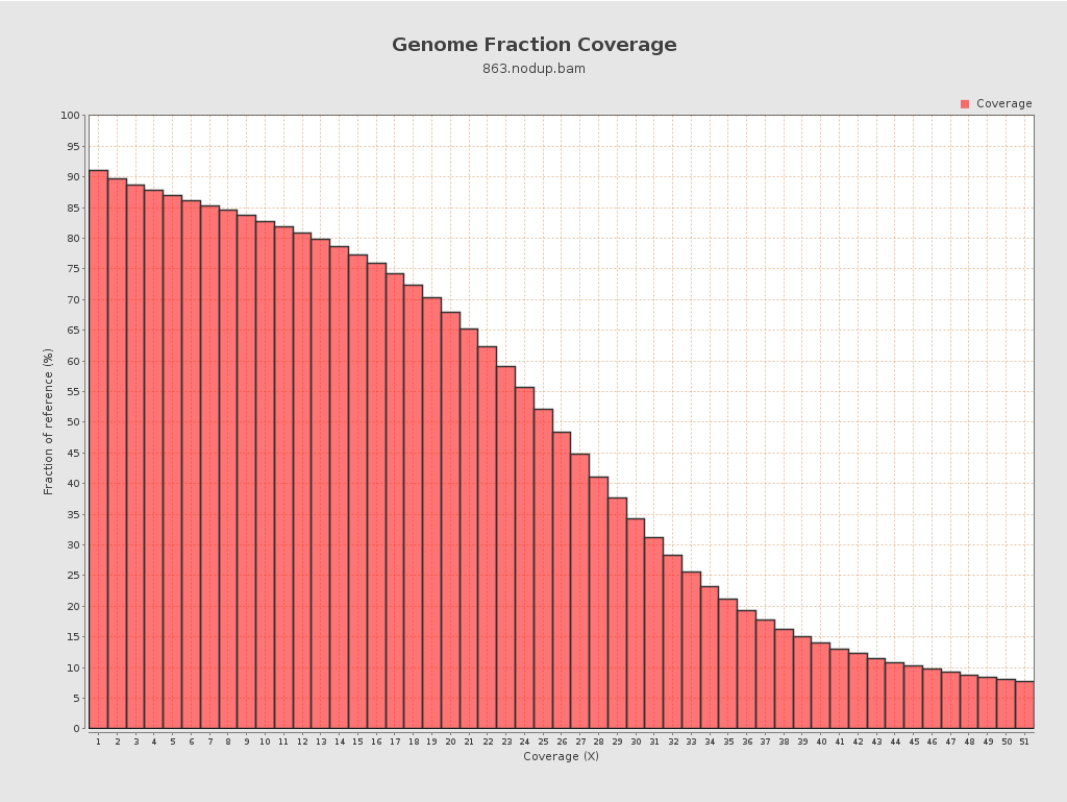
# 4. Results : Coverage Histogram



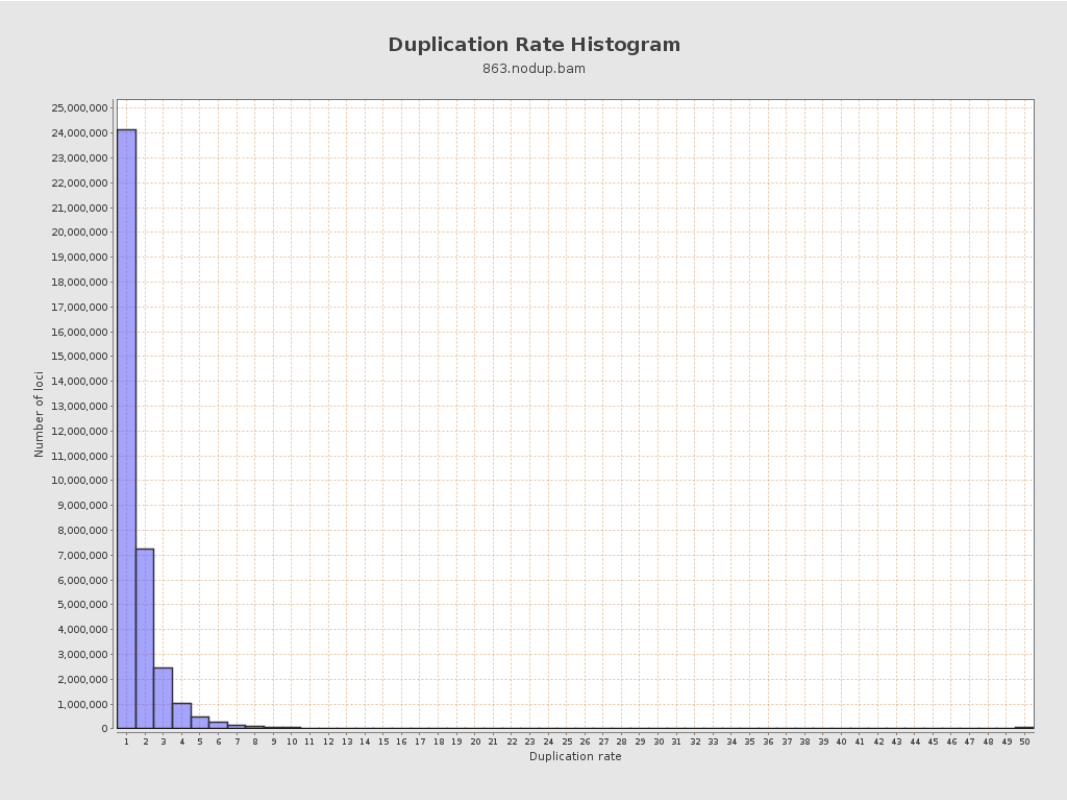
# 5. Results : Coverage Histogram (0-50X)



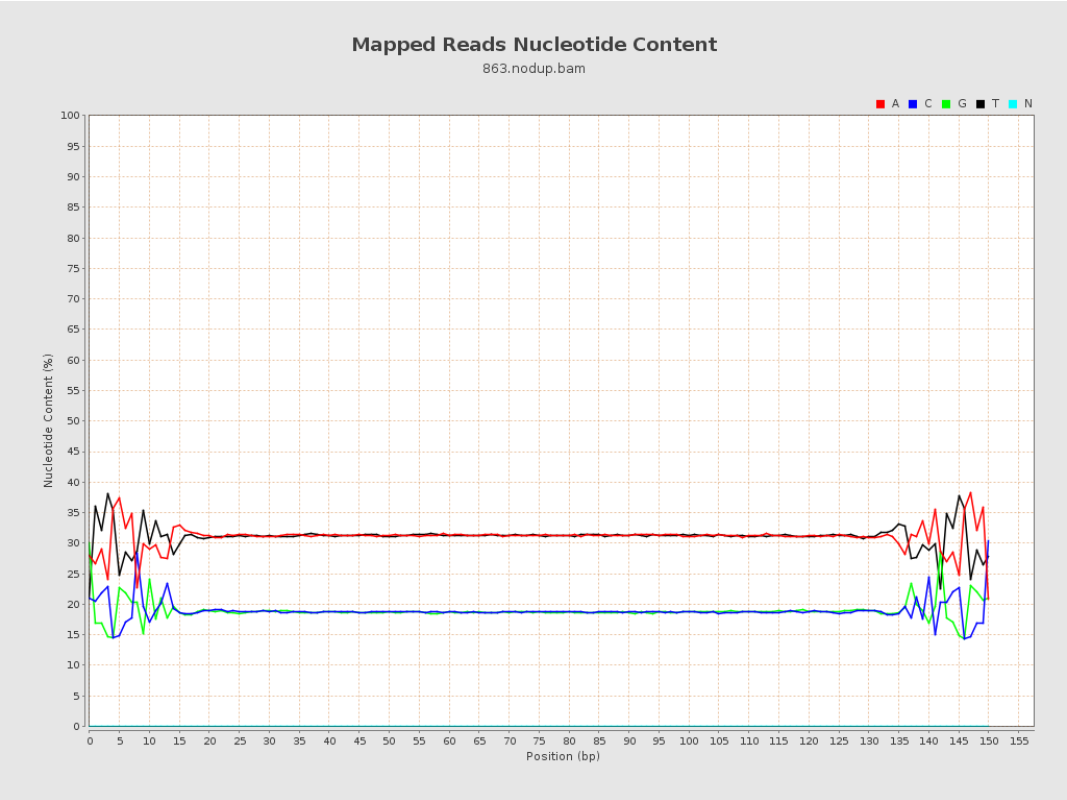
# 6. Results : Genome Fraction Coverage



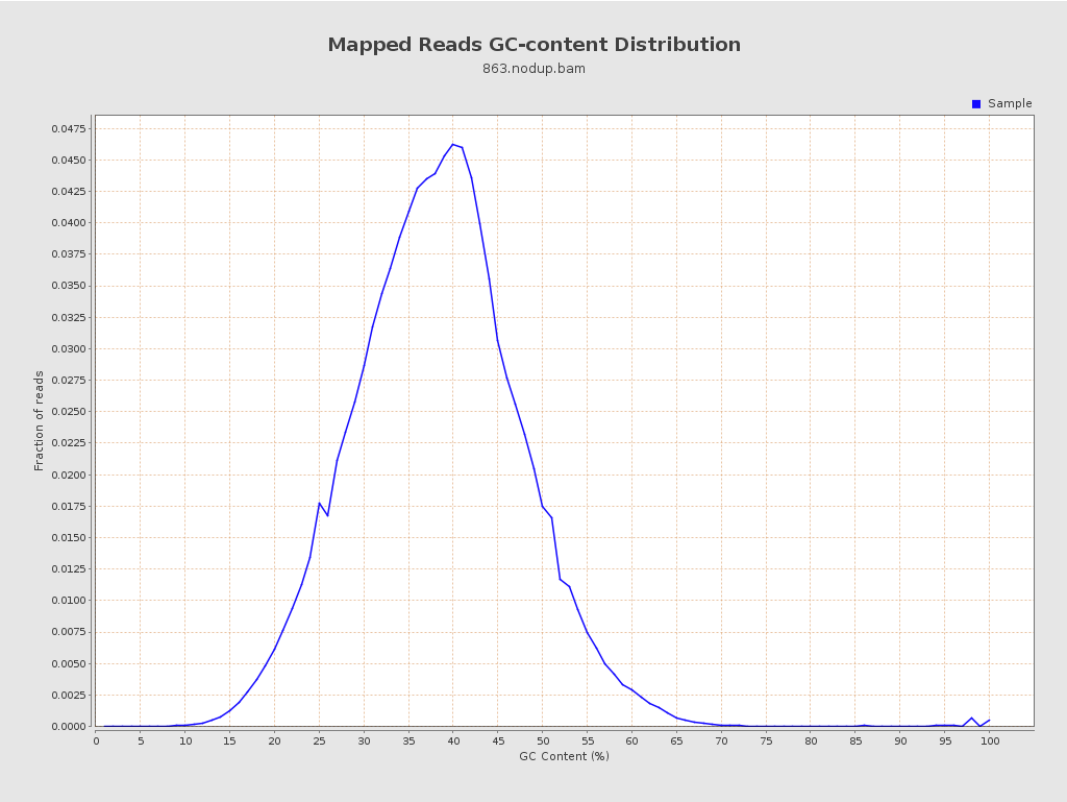
# 7. Results : Duplication Rate Histogram



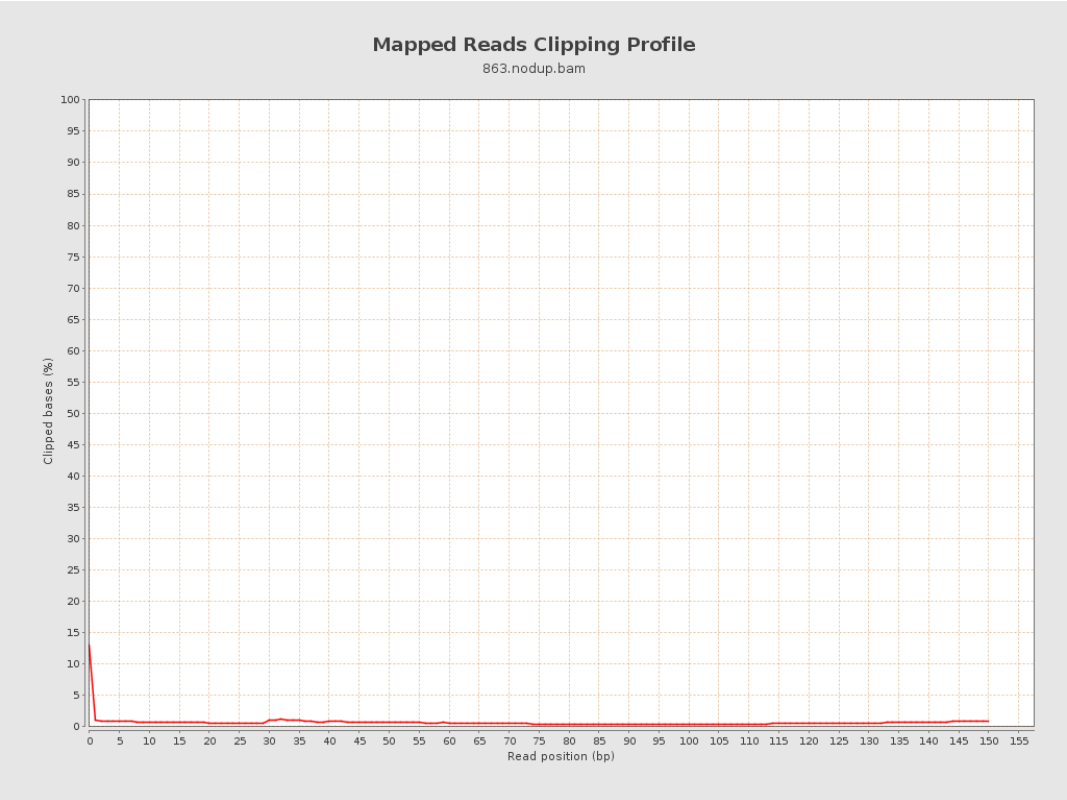
# 8. Results : Mapped Reads Nucleotide Content



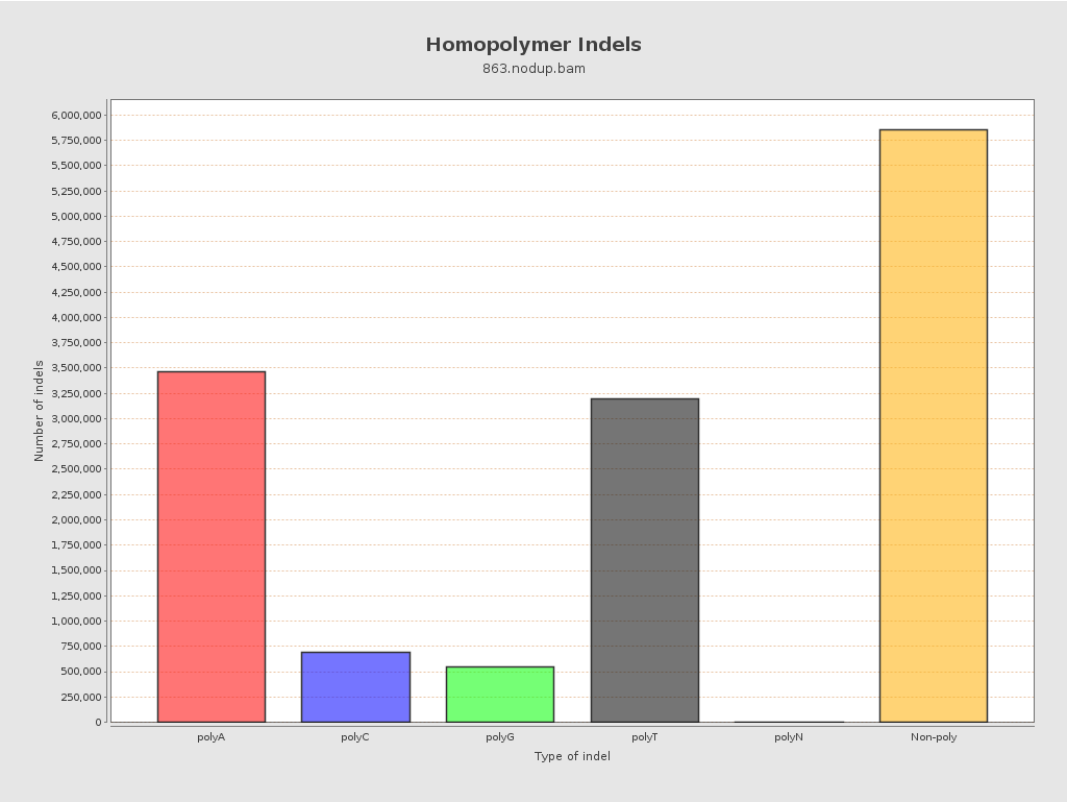
# 9. Results : Mapped Reads GC-content Distribution



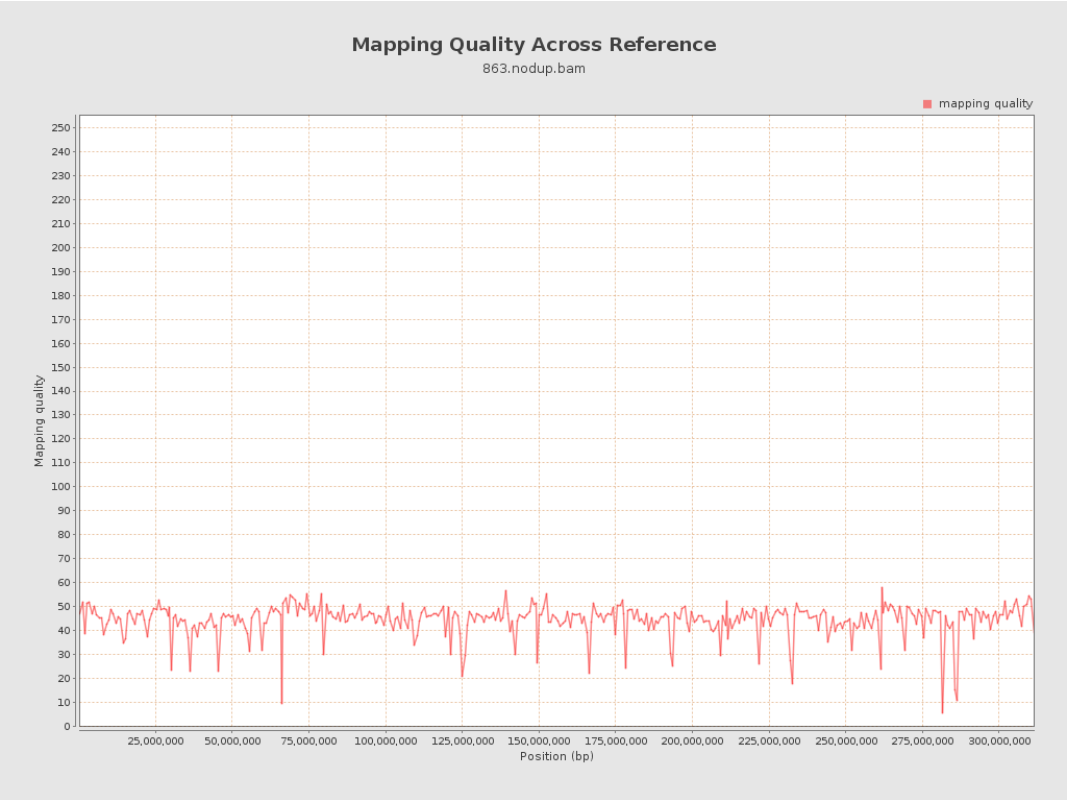
# 10. Results : Mapped Reads Clipping Profile



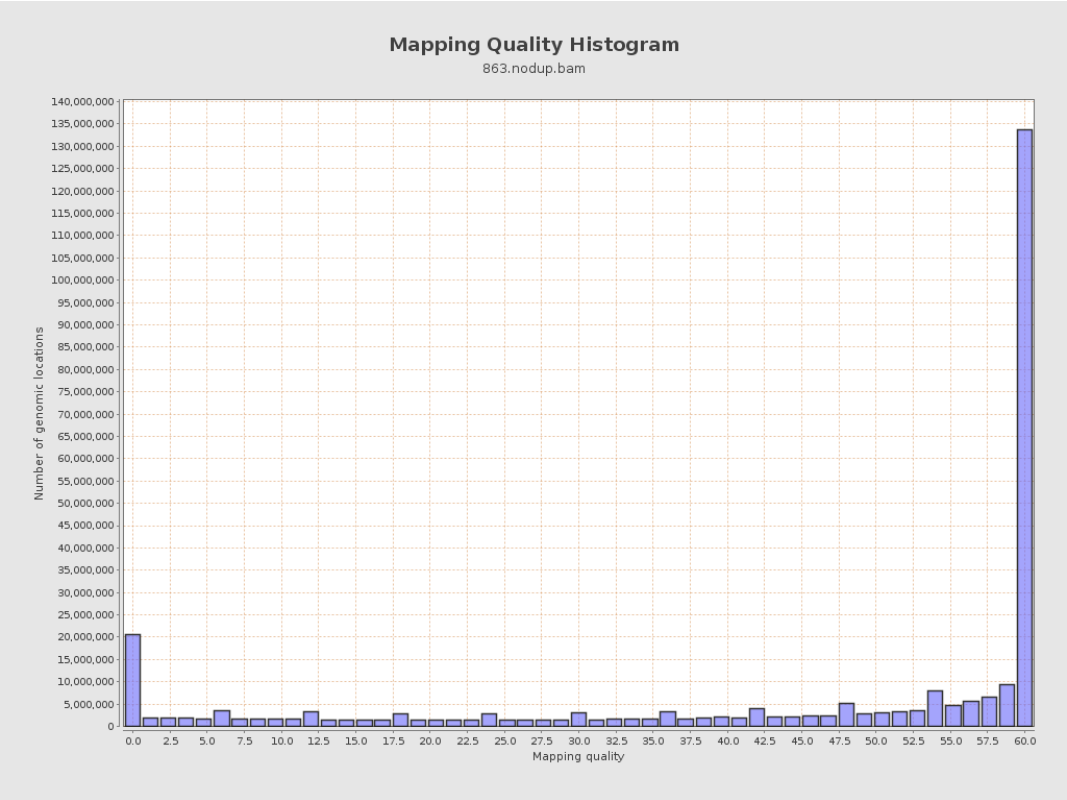
# 11. Results : Homopolymer Indels



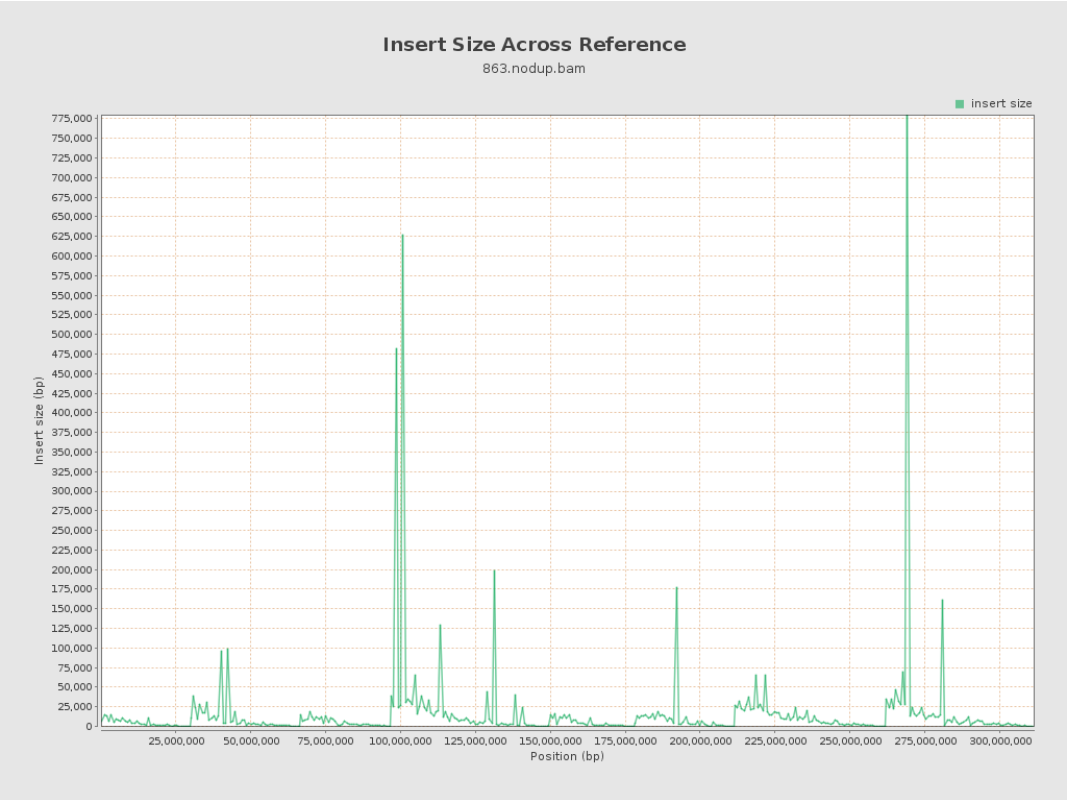
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram