# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:24:42*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/868.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/868.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_276/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_276_S357_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_276/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_276_S357_L003_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|---|---|
| Analysis date: | Mon May 29 21:24:41 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 49,722,051 |
| Mapped reads | 44,396,913 / 89.29% |
| Unmapped reads | 5,325,138 / 10.71% |
| Mapped paired reads | 44,396,913 / 89.29% |
| Mapped reads, first in pair | 22,253,423 / 44.76% |
| Mapped reads,  second in pair | 22,143,490 / 44.53% |
| Mapped reads, both in pair | 42,718,315 / 85.91% |
| Mapped reads, singletons | 1,678,598 / 3.38% |
| Read min/max/mean length | 30 / 151 / 147.98 |
| Duplicated reads (flagged) | 7,536,939 / 15.16% |
| Clipped reads | 11,381,918 / 22.89% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,865,871,231 / 31.02% |
| Number/percentage of C's | 1,140,323,250 / 18.96% |
| Number/percentage of T's | 1,867,202,505 / 31.04% |
| Number/percentage of G's | 1,142,104,108 / 18.99% |
| Number/percentage of N's | 21,865 / 0% |
| GC Percentage | 37.94% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 19.3523 |
| Standard Deviation | 214.2349 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.38 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 286,467.37 |
| Standard Deviation | 2,602,361.56 |
| P25/Median/P75 | 338 / 448 / 581 |

## 2.6. Mismatches and indels

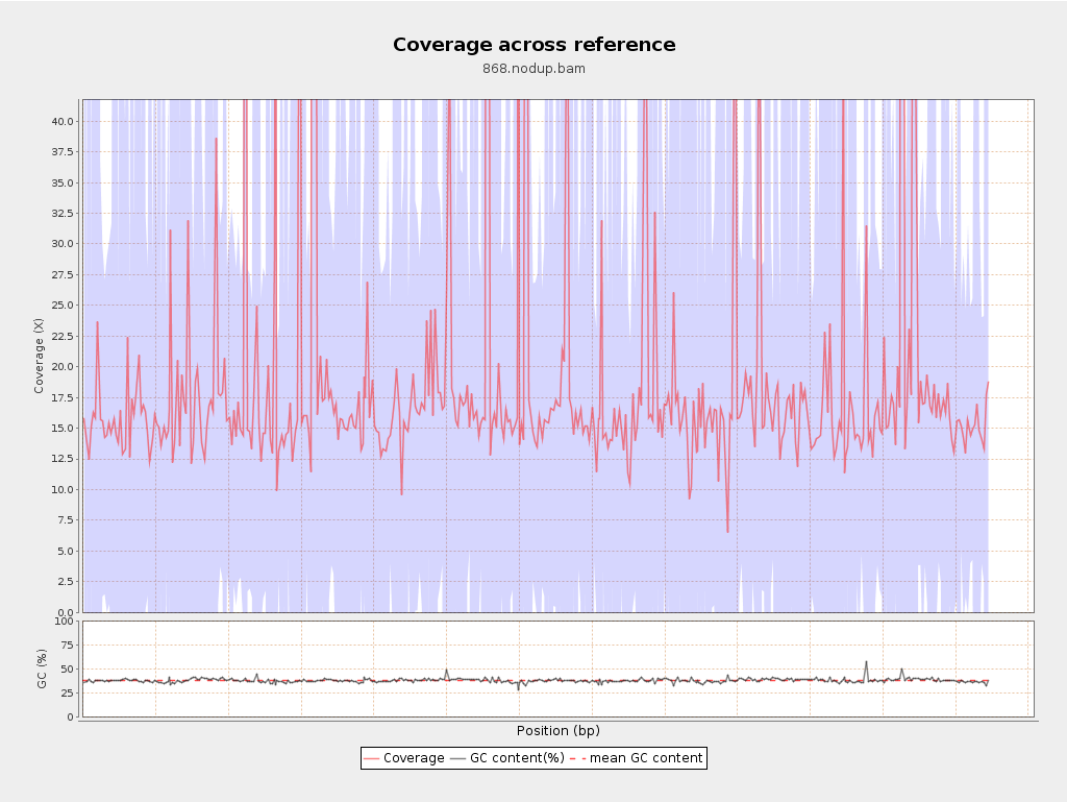
| | |
|---|---|
| General error rate | 2.42% |
| Mismatches | 132,475,388 |
| Insertions | 4,629,618 |
| Mapped reads with at least one insertion | 9.25% |
| Deletions | 4,210,539 |
| Mapped reads with at least one deletion | 8.4% |
| Homopolymer indels | 57.79% |

## 2.7. Chromosome stats

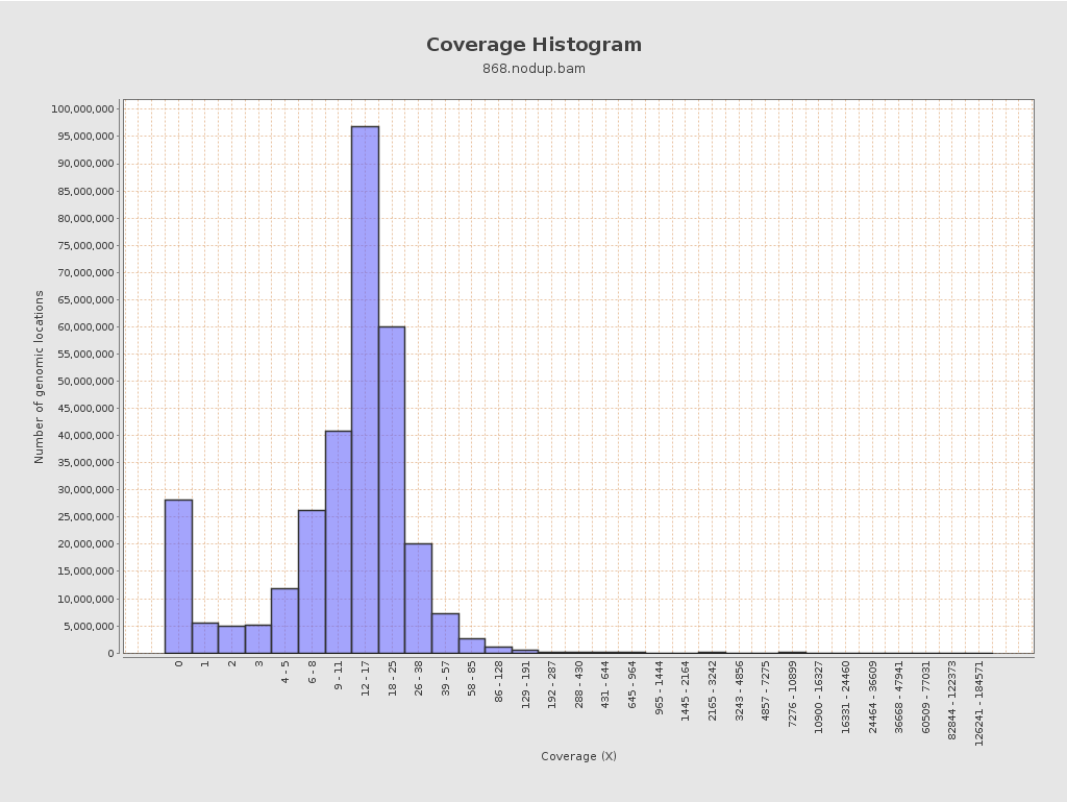
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 462773379 | 15.5688 | 89.5464 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 706178510 | 19.2955 | 218.6447 |
| LT669790.1 | 30422129 | 784389555 | 25.7835 | 339.894 |
| LT669791.1 | 52758100 | 1011612711 | 19.1745 | 243.3495 |
| LT669792.1 | 28376109 | 560729521 | 19.7606 | 207.9294 |
| LT669793.1 | 33388210 | 580434529 | 17.3844 | 130.637 |
| LT669794.1 | 50579949 | 901046625 | 17.8143 | 160.622 |
| LT669795.1 | 49795044 | 1023829313 | 20.5609 | 227.3104 |

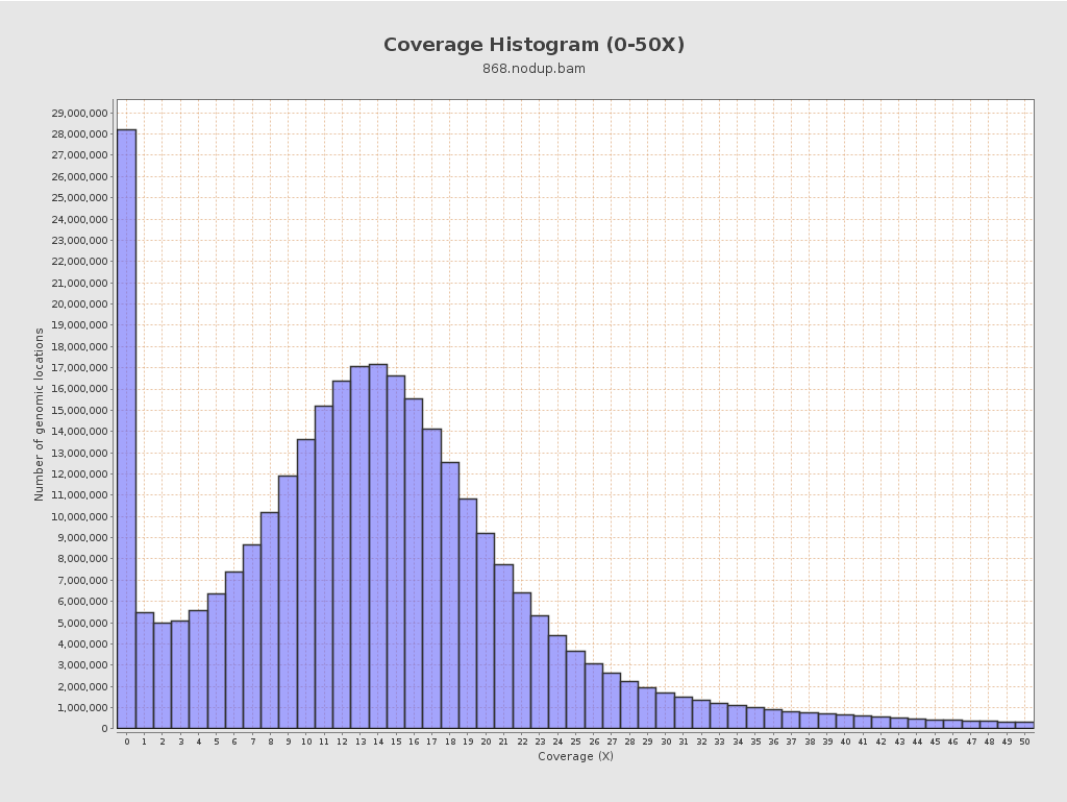
# 3. Results : Coverage across reference



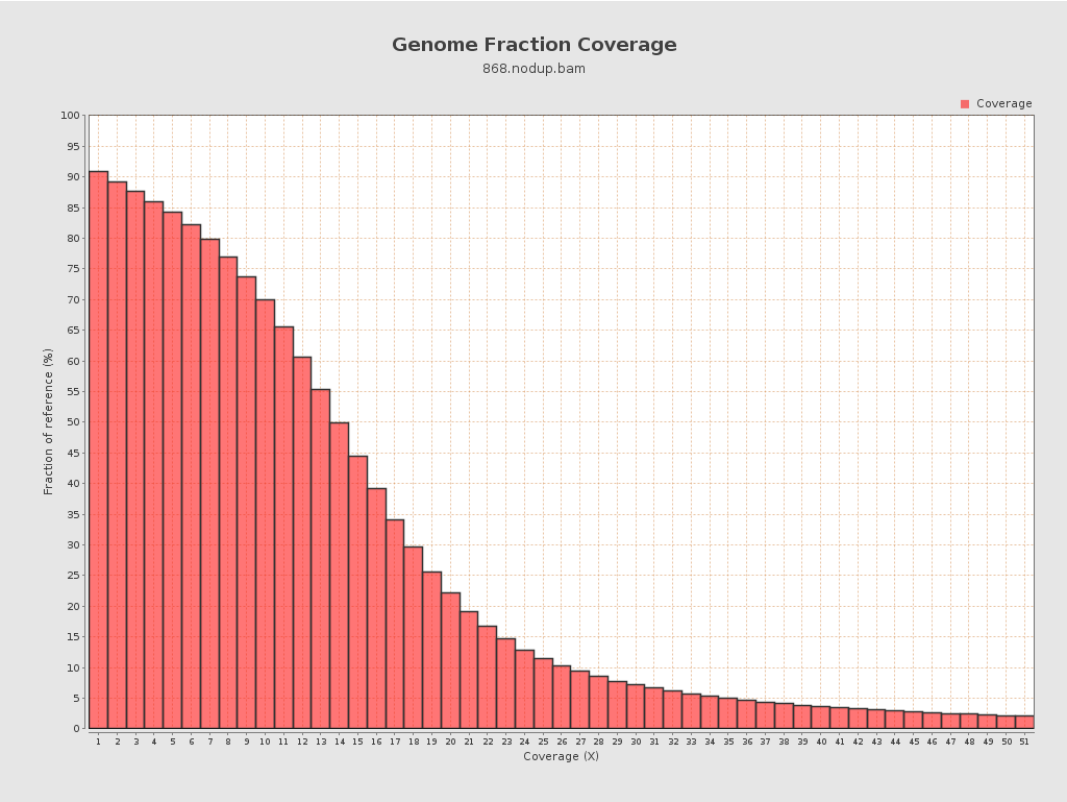
# 4. Results : Coverage Histogram



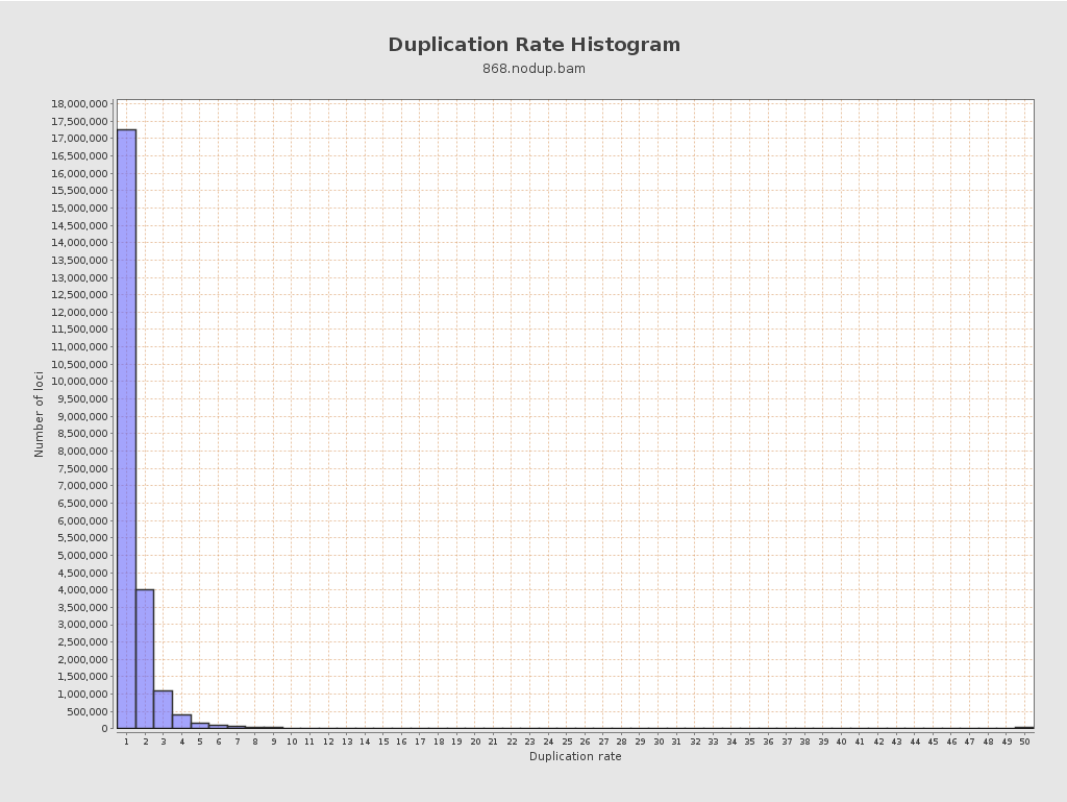
# 5. Results : Coverage Histogram (0-50X)



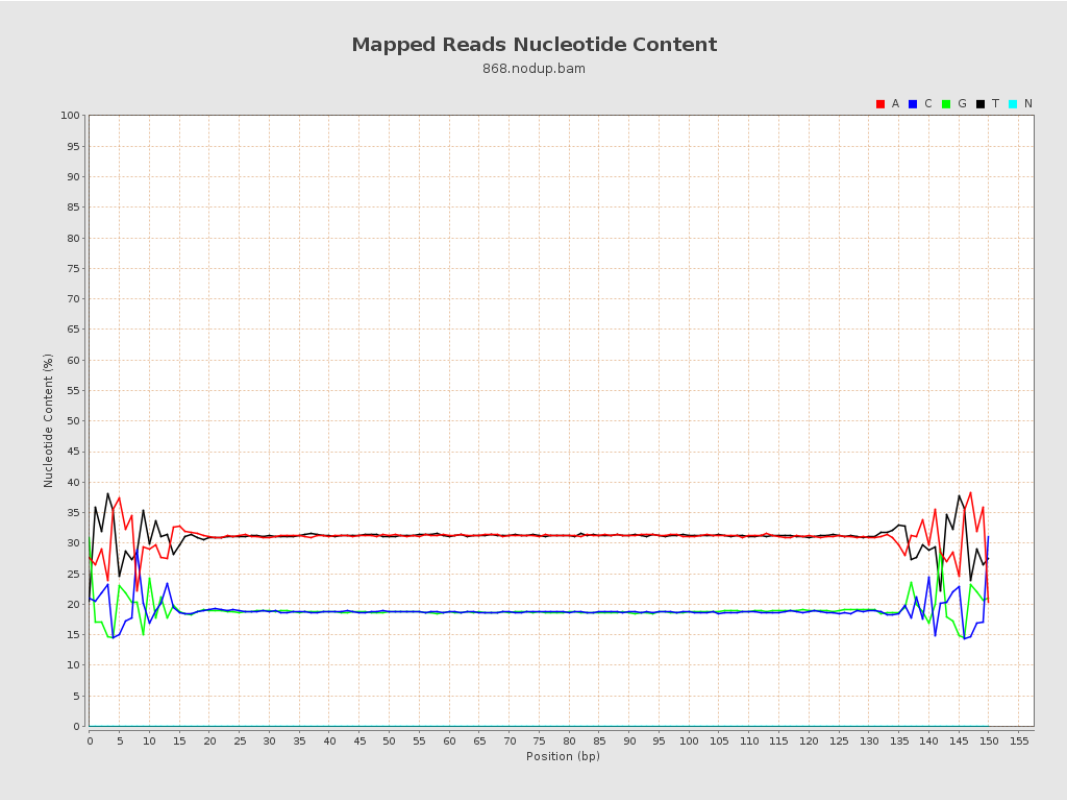
# 6. Results : Genome Fraction Coverage



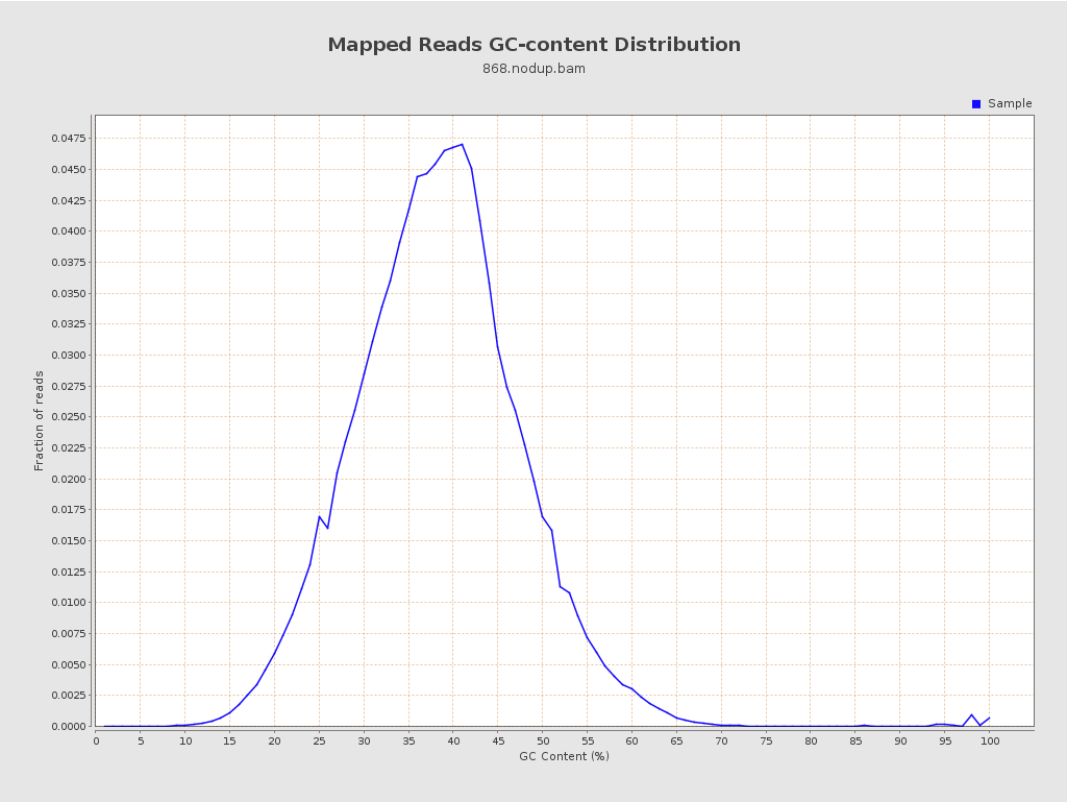
# 7. Results : Duplication Rate Histogram



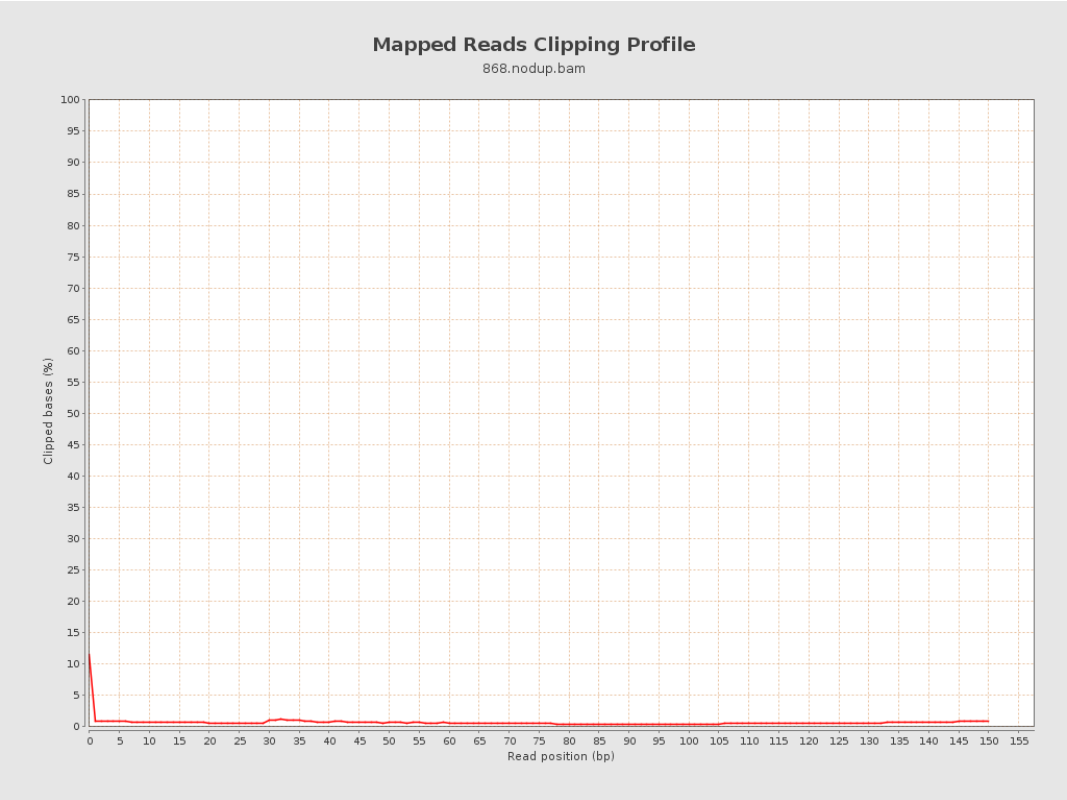
# 8. Results : Mapped Reads Nucleotide Content



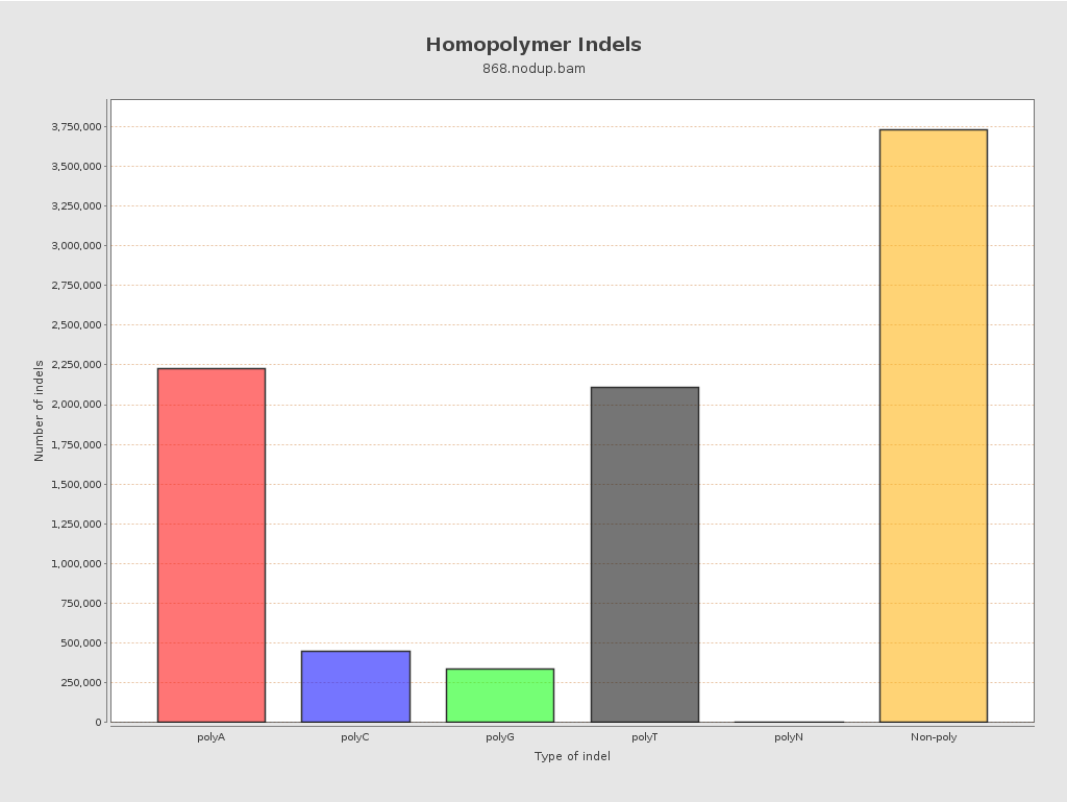
# 9. Results : Mapped Reads GC-content Distribution



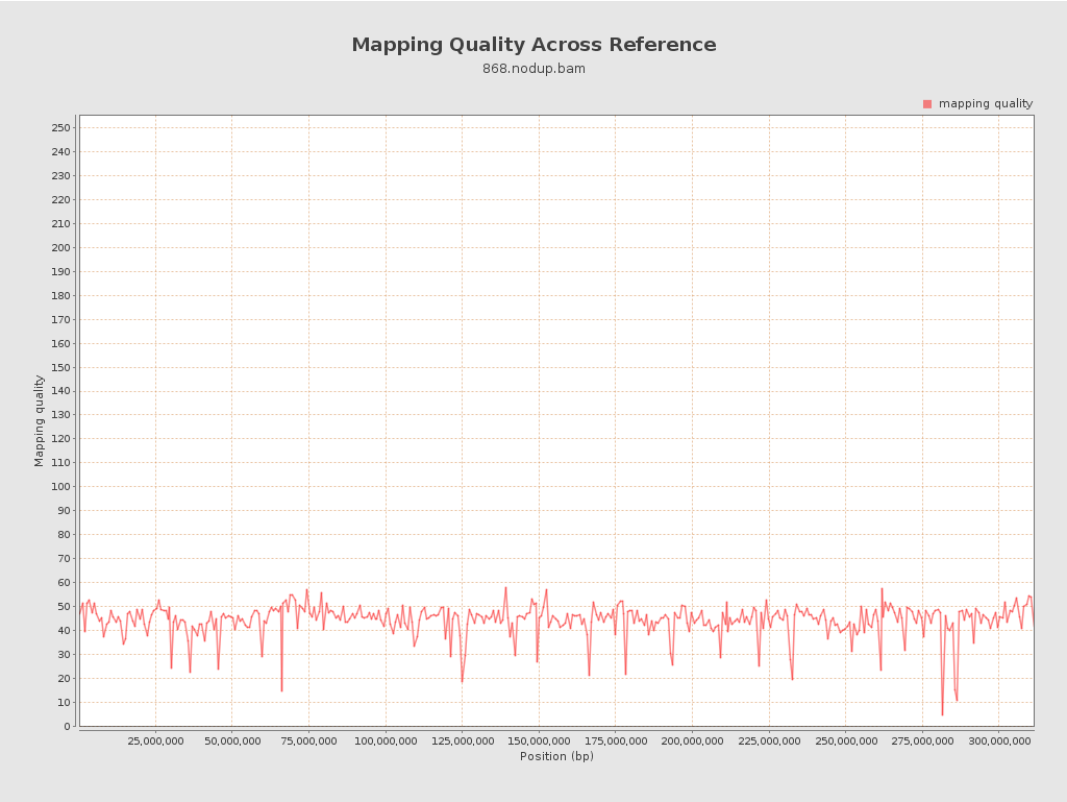
# 10. Results : Mapped Reads Clipping Profile



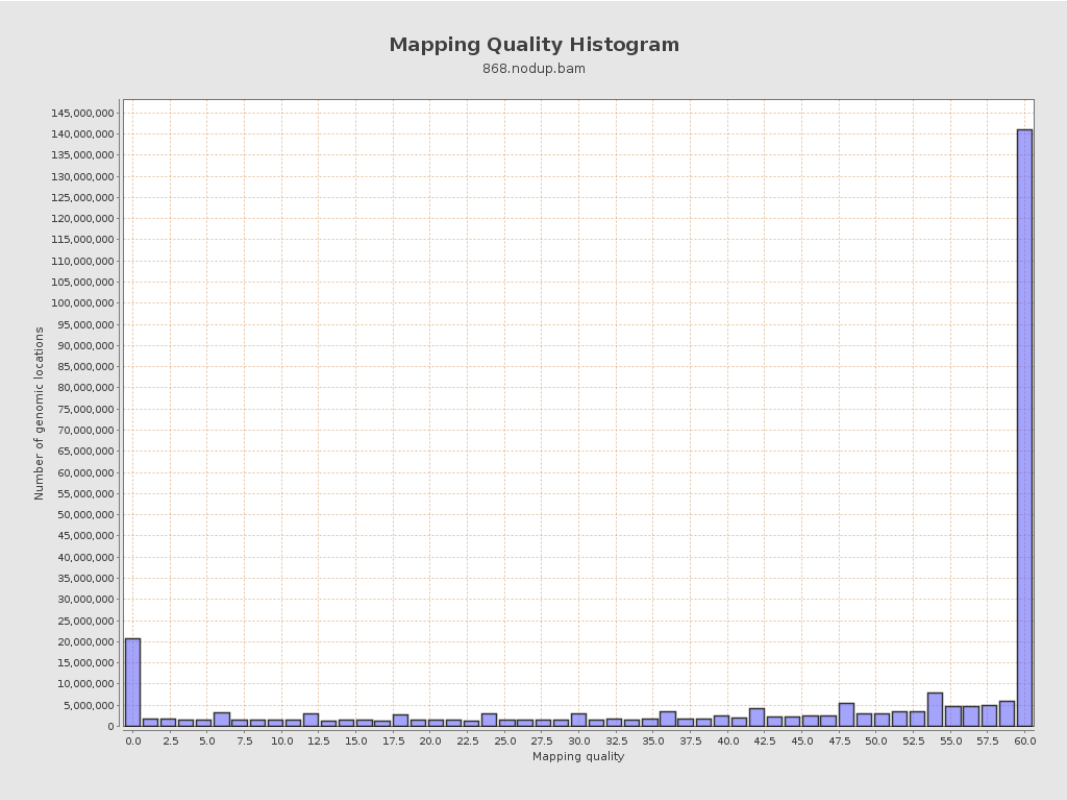
# 11. Results : Homopolymer Indels



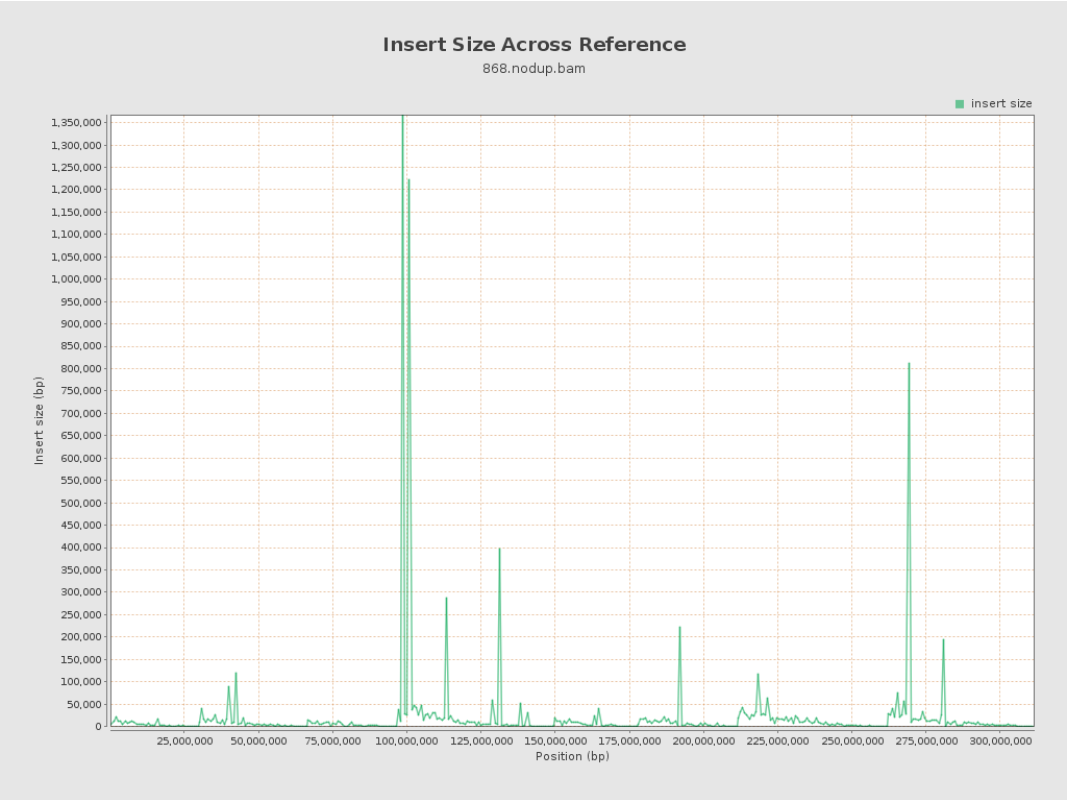
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram