# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:32:37*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/833.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/833.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_179/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_179_S269_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_179/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_179_S269_L002_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|---|---|
| Analysis date: | Mon May 29 21:32:36 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 65,083,853 |
| Mapped reads | 61,458,109 / 94.43% |
| Unmapped reads | 3,625,744 / 5.57% |
| Mapped paired reads | 61,458,109 / 94.43% |
| Mapped reads, first in pair | 30,815,344 / 47.35% |
| Mapped reads,  second in pair | 30,642,765 / 47.08% |
| Mapped reads, both in pair | 60,182,222 / 92.47% |
| Mapped reads, singletons | 1,275,887 / 1.96% |
| Read min/max/mean length | 30 / 151 / 148.17 |
| Duplicated reads (flagged) | 10,068,472 / 15.47% |
| Clipped reads | 13,588,171 / 20.88% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 2,632,586,791 / 30.77% |
| Number/percentage of C's | 1,645,975,513 / 19.24% |
| Number/percentage of T's | 2,638,260,074 / 30.84% |
| Number/percentage of G's | 1,637,536,939 / 19.14% |
| Number/percentage of N's | 35,657 / 0% |
| GC Percentage | 38.38% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 27.5215 |
| Standard Deviation | 244.028 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.66 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 233,346.08 |
| Standard Deviation | 2,278,750.29 |
| P25/Median/P75 | 344 / 448 / 584 |

## 2.6. Mismatches and indels

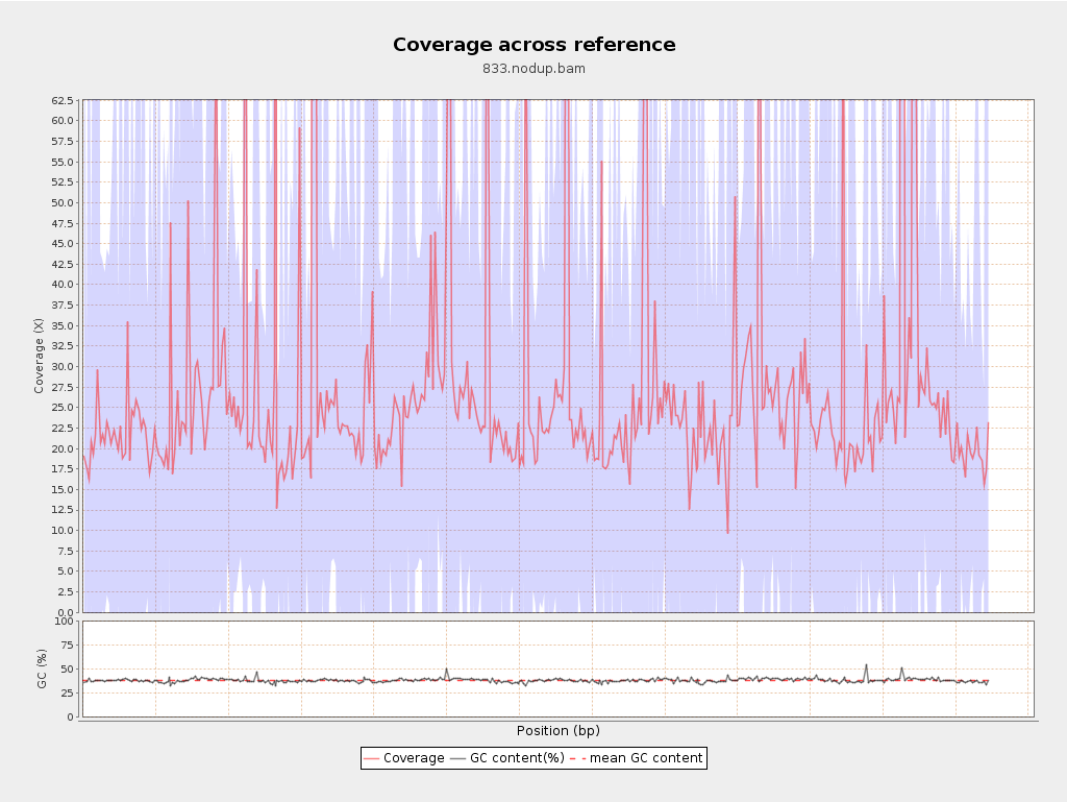
| | |
|---|---|
| General error rate | 2.41% |
| Mismatches | 190,410,575 |
| Insertions | 5,859,876 |
| Mapped reads with at least one insertion | 8.58% |
| Deletions | 6,005,468 |
| Mapped reads with at least one deletion | 8.69% |
| Homopolymer indels | 56.18% |

## 2.7. Chromosome stats

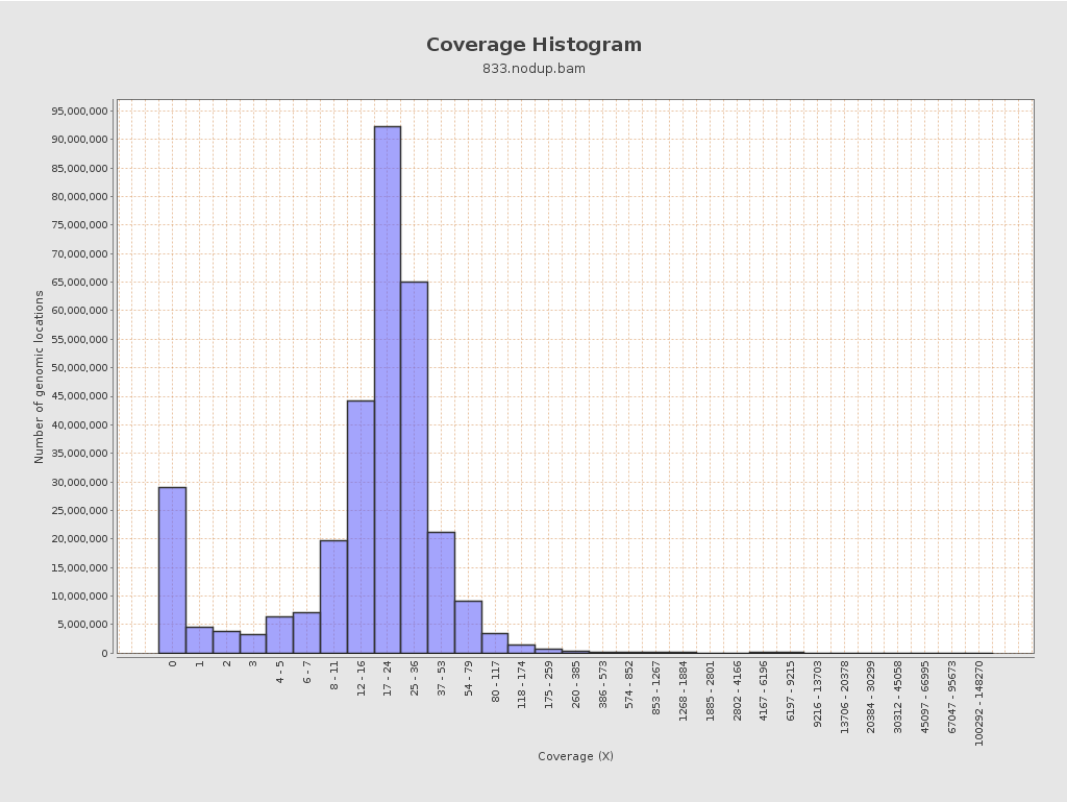
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 634416503 | 21.3433 | 62.1459 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 1055214745 | 28.8324 | 266.383 |
| LT669790.1 | 30422129 | 869270708 | 28.5736 | 241.992 |
| LT669791.1 | 52758100 | 1451923870 | 27.5204 | 207.9745 |
| LT669792.1 | 28376109 | 765210572 | 26.9667 | 325.7854 |
| LT669793.1 | 33388210 | 858728673 | 25.7195 | 177.6449 |
| LT669794.1 | 50579949 | 1349644847 | 26.6834 | 233.4995 |
| LT669795.1 | 49795044 | 1592431523 | 31.9797 | 315.5257 |

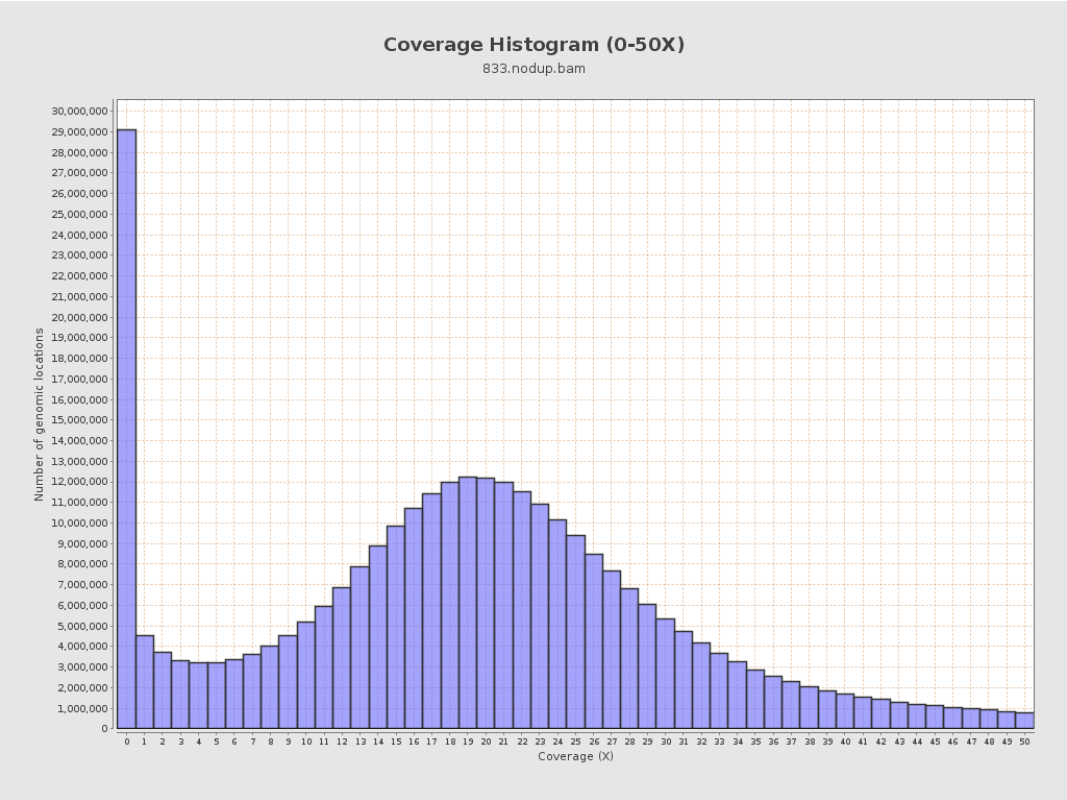
# 3. Results : Coverage across reference



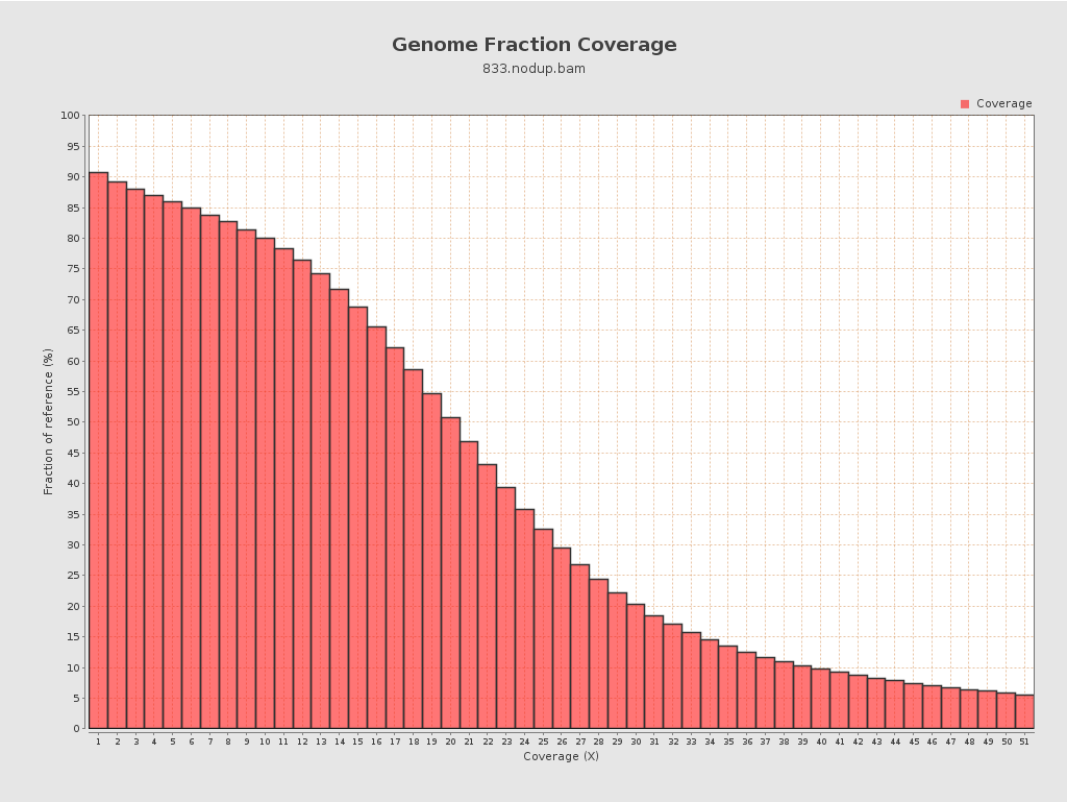
# 4. Results : Coverage Histogram



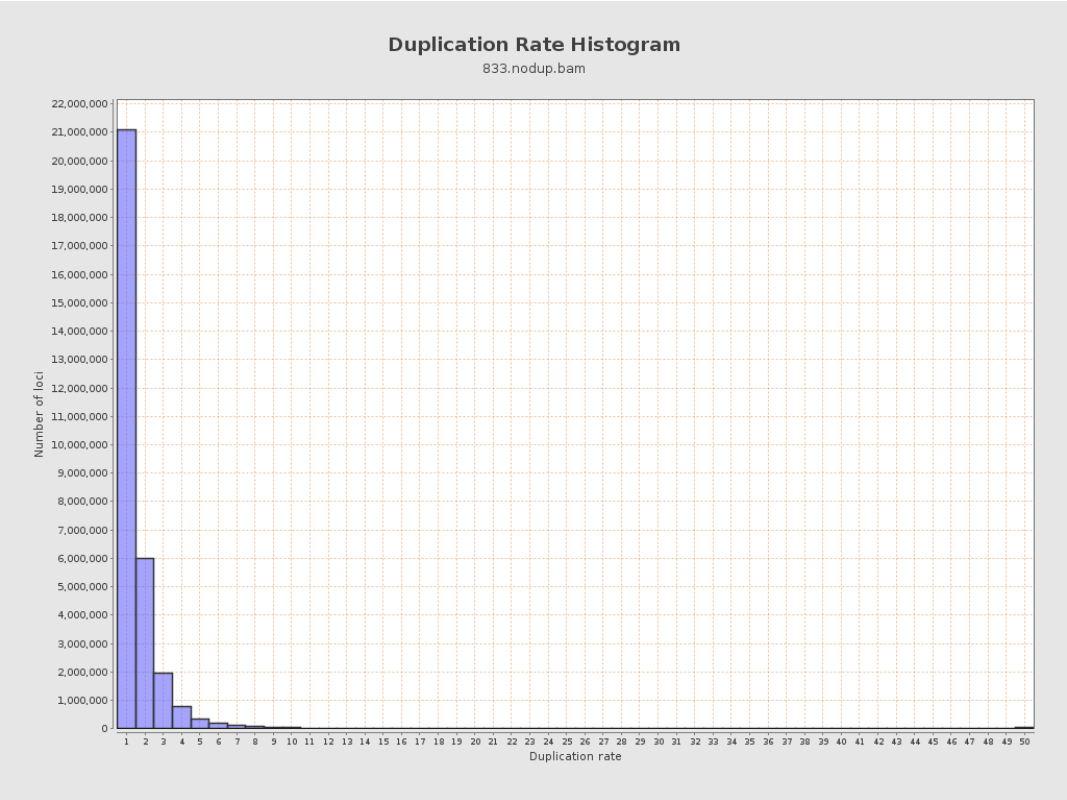
# 5. Results : Coverage Histogram (0-50X)



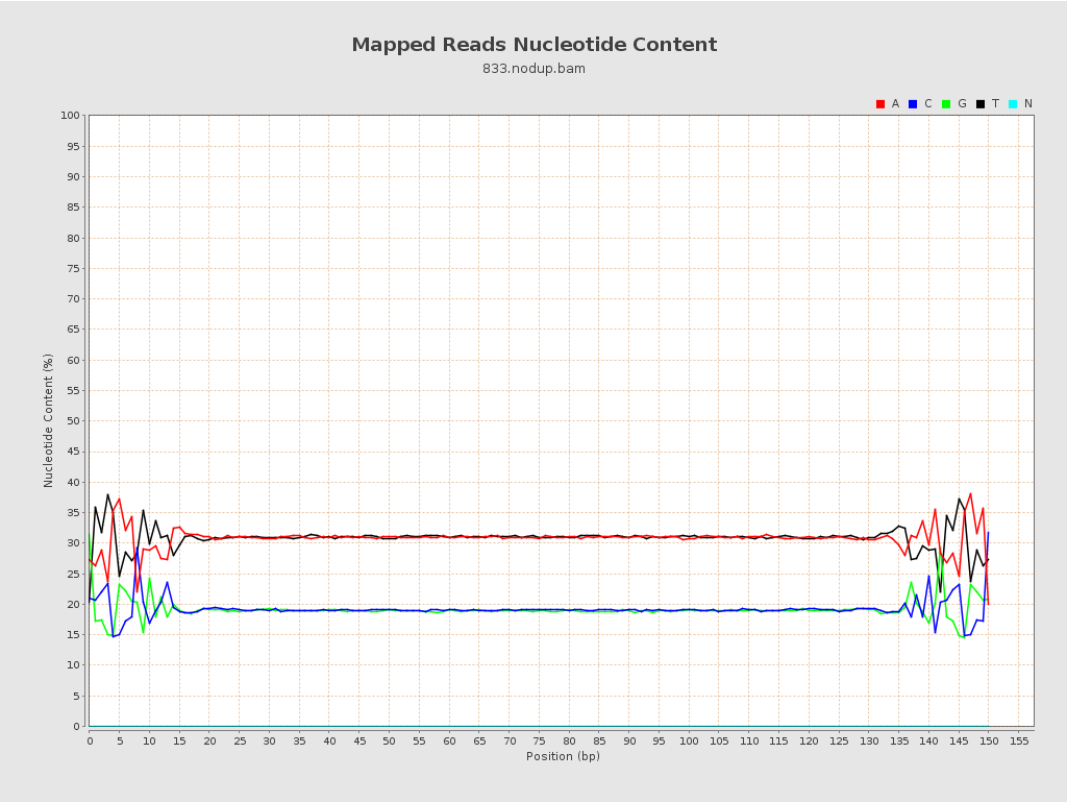
# 6. Results : Genome Fraction Coverage



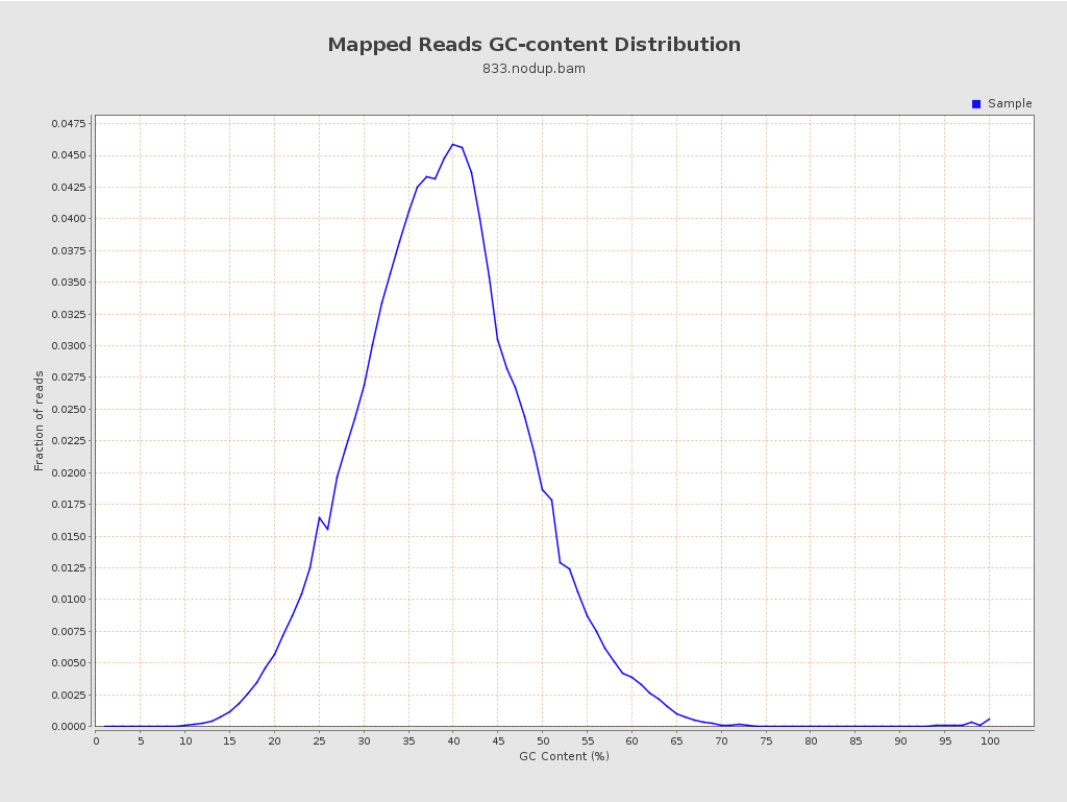
# 7. Results : Duplication Rate Histogram



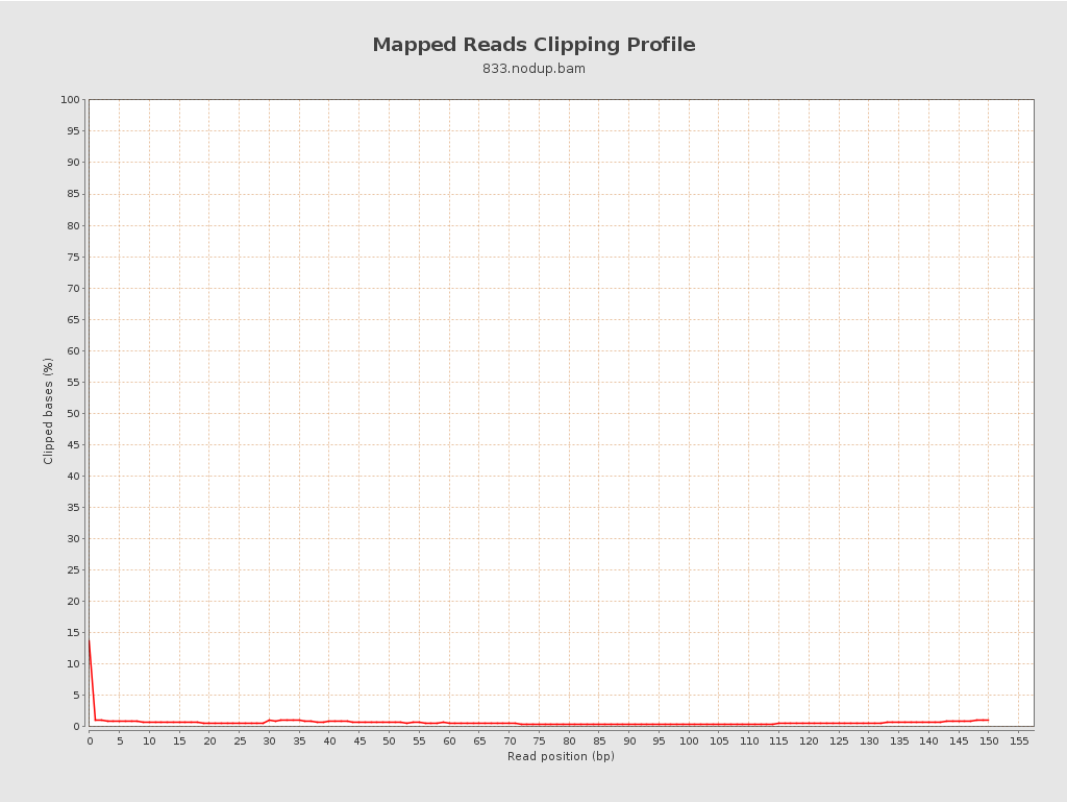
# 8. Results : Mapped Reads Nucleotide Content



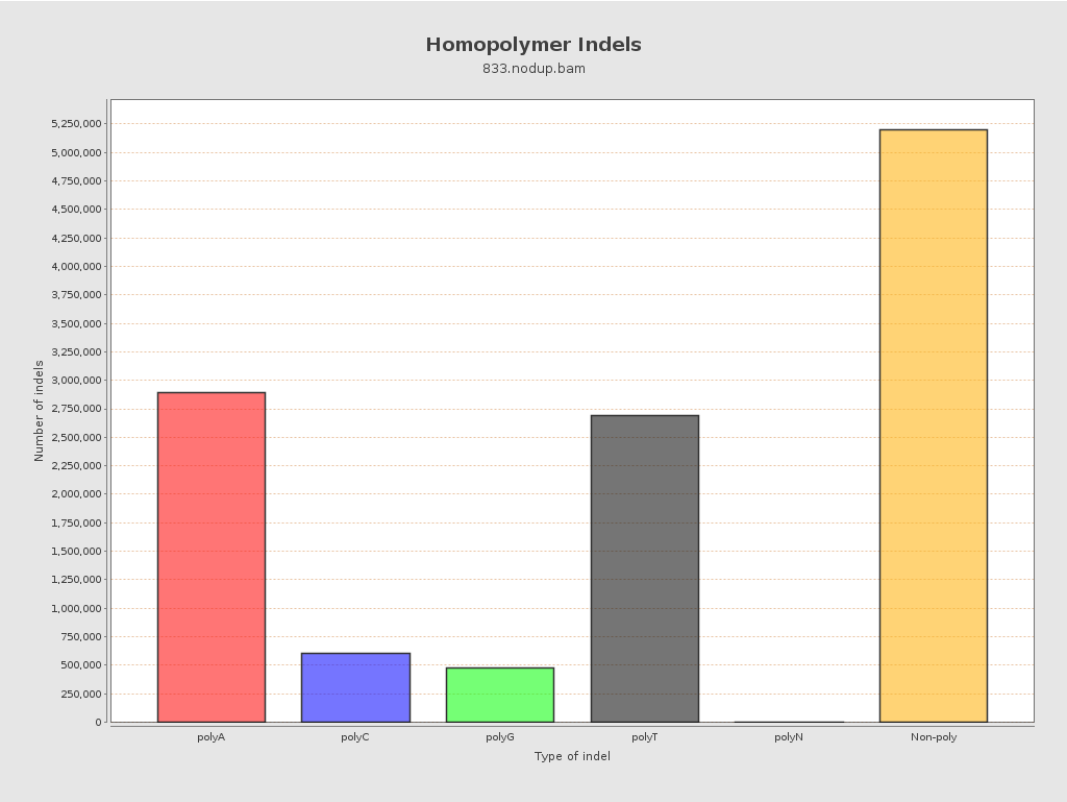
# 9. Results : Mapped Reads GC-content Distribution



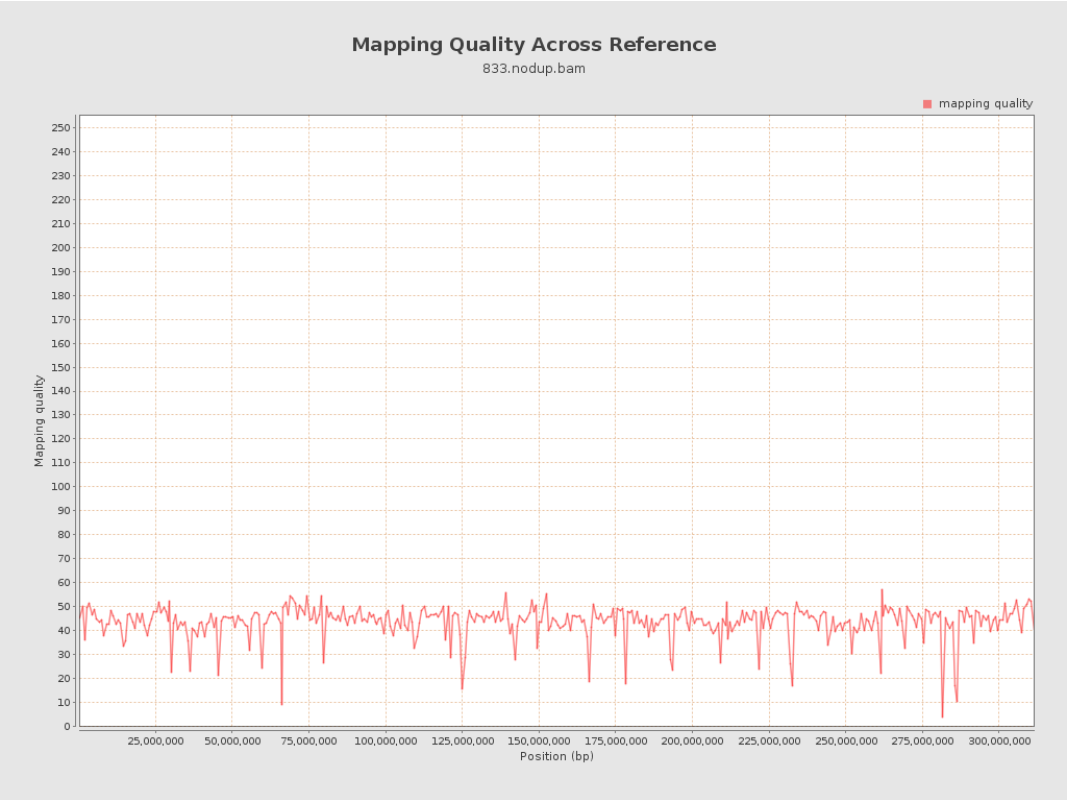
# 10. Results : Mapped Reads Clipping Profile



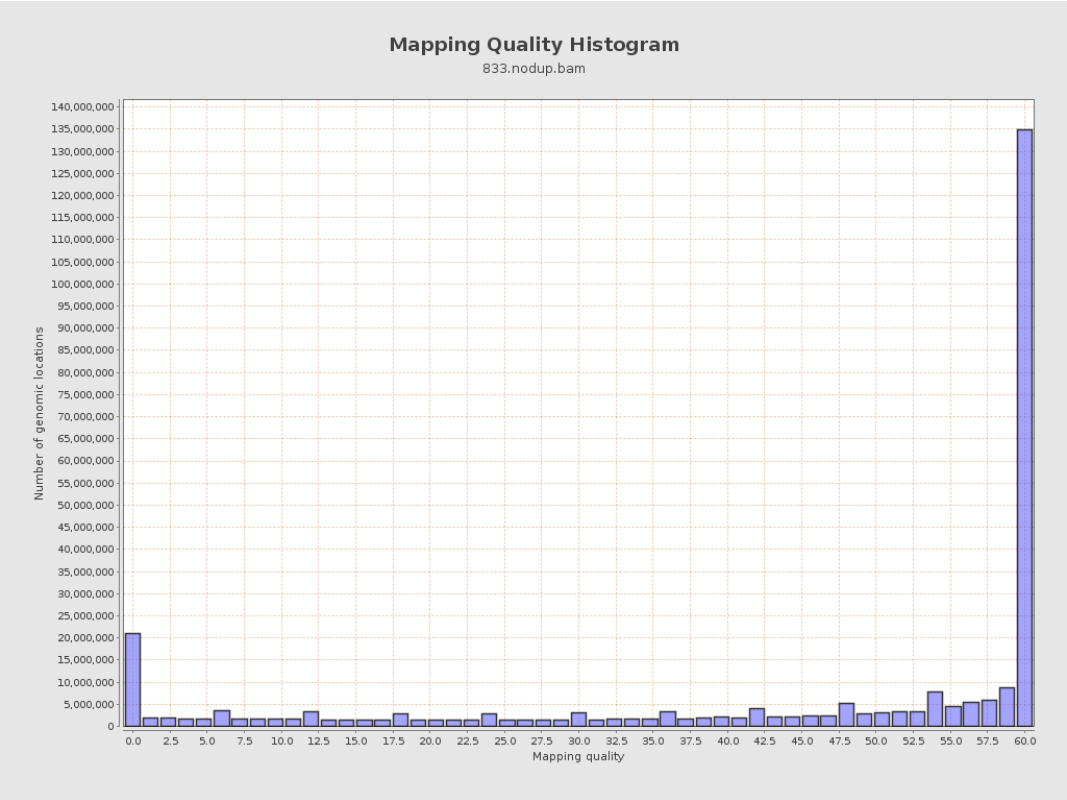
# 11. Results : Homopolymer Indels



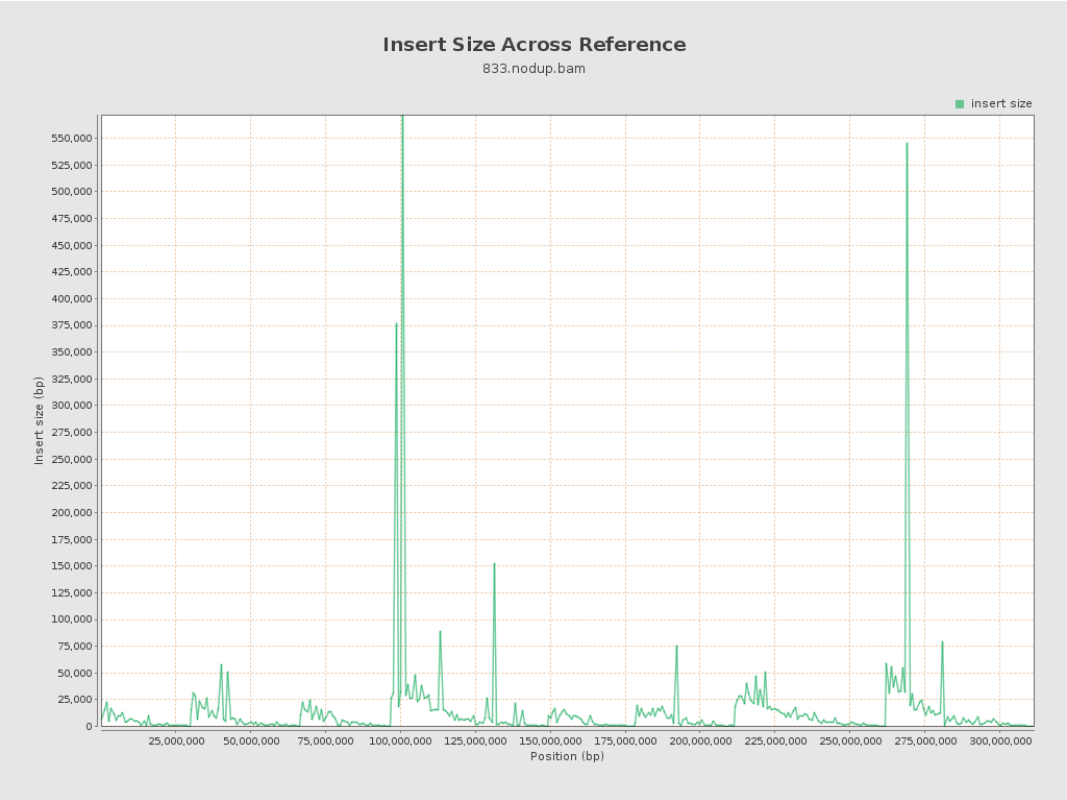
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram