# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:27:38*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/506.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/506.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_275/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_275_S356_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_275/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_275_S356_L003_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|---|---|
| Analysis date: | Mon May 29 21:27:38 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 58,575,380 |
| Mapped reads | 51,422,805 / 87.79% |
| Unmapped reads | 7,152,575 / 12.21% |
| Mapped paired reads | 51,422,805 / 87.79% |
| Mapped reads, first in pair | 25,743,788 / 43.95% |
| Mapped reads,  second in pair | 25,679,017 / 43.84% |
| Mapped reads, both in pair | 50,316,398 / 85.9% |
| Mapped reads, singletons | 1,106,407 / 1.89% |
| Read min/max/mean length | 30 / 151 / 148.06 |
| Duplicated reads (flagged) | 7,011,129 / 11.97% |
| Clipped reads | 12,513,828 / 21.36% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 2,170,859,593 / 30.78% |
| Number/percentage of C's | 1,356,811,156 / 19.24% |
| Number/percentage of T's | 2,168,220,645 / 30.74% |
| Number/percentage of G's | 1,357,882,223 / 19.25% |
| Number/percentage of N's | 25,562 / 0% |
| GC Percentage | 38.49% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 22.6939 |
| Standard Deviation | 202.9563 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.54 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 234,603.53 |
| Standard Deviation | 2,285,909.25 |
| P25/Median/P75 | 308 / 408 / 532 |

## 2.6. Mismatches and indels

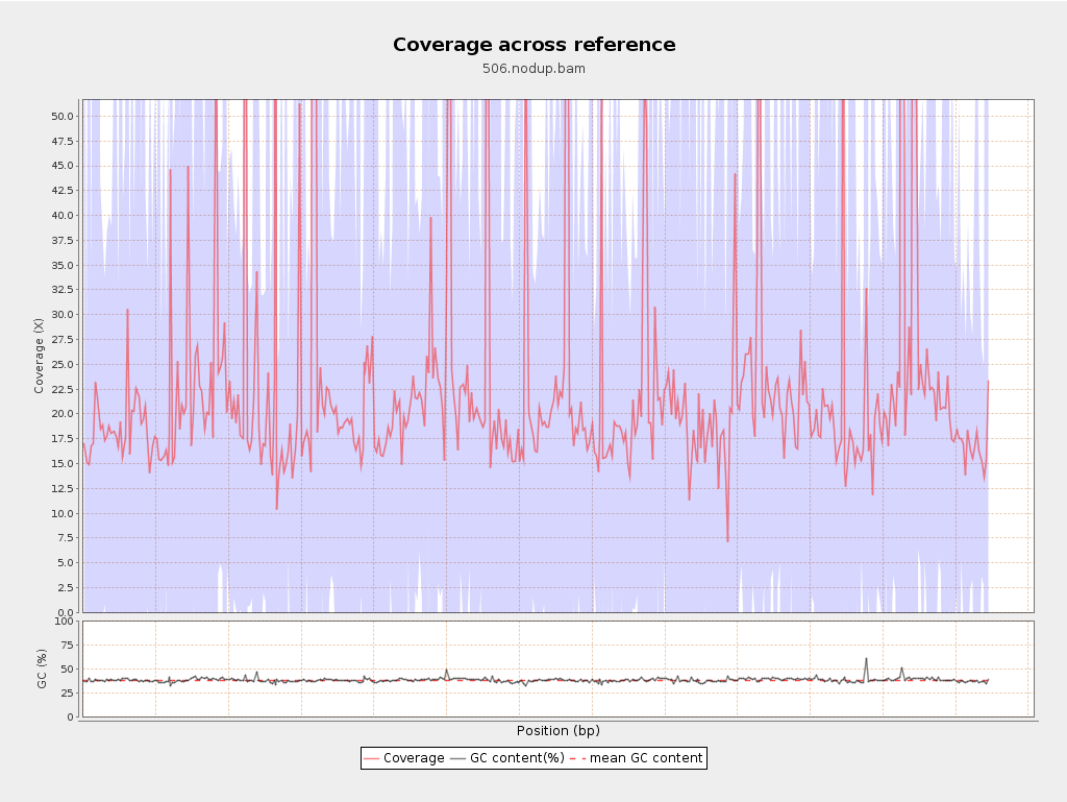
| | |
|---|---|
| General error rate | 2.39% |
| Mismatches | 155,120,655 |
| Insertions | 4,888,945 |
| Mapped reads with at least one insertion | 8.54% |
| Deletions | 5,016,844 |
| Mapped reads with at least one deletion | 8.65% |
| Homopolymer indels | 56.48% |

## 2.7. Chromosome stats

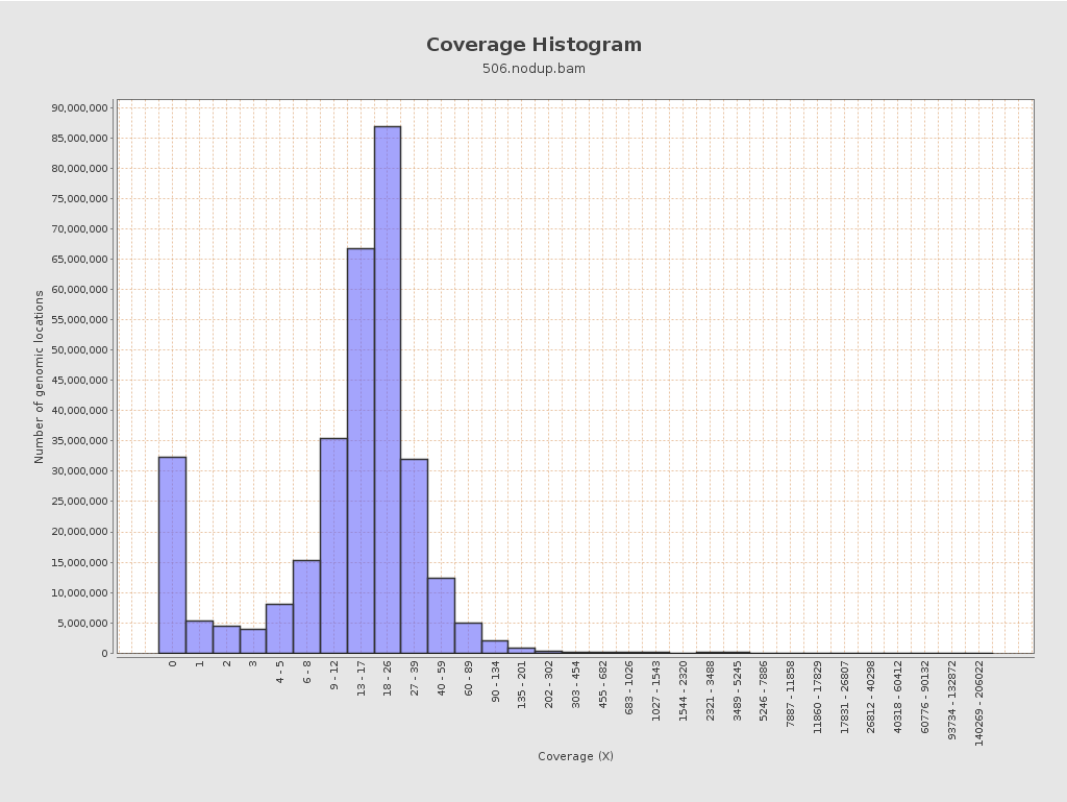
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 541028258 | 18.2015 | 71.5765 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 893662867 | 24.4182 | 219.56 |
| LT669790.1 | 30422129 | 734048397 | 24.1288 | 202.6402 |
| LT669791.1 | 52758100 | 1193774643 | 22.6273 | 201.4266 |
| LT669792.1 | 28376109 | 633389261 | 22.3212 | 238.0031 |
| LT669793.1 | 33388210 | 704190964 | 21.091 | 110.7994 |
| LT669794.1 | 50579949 | 1131745300 | 22.3754 | 199.4358 |
| LT669795.1 | 49795044 | 1240528936 | 24.9127 | 265.1354 |

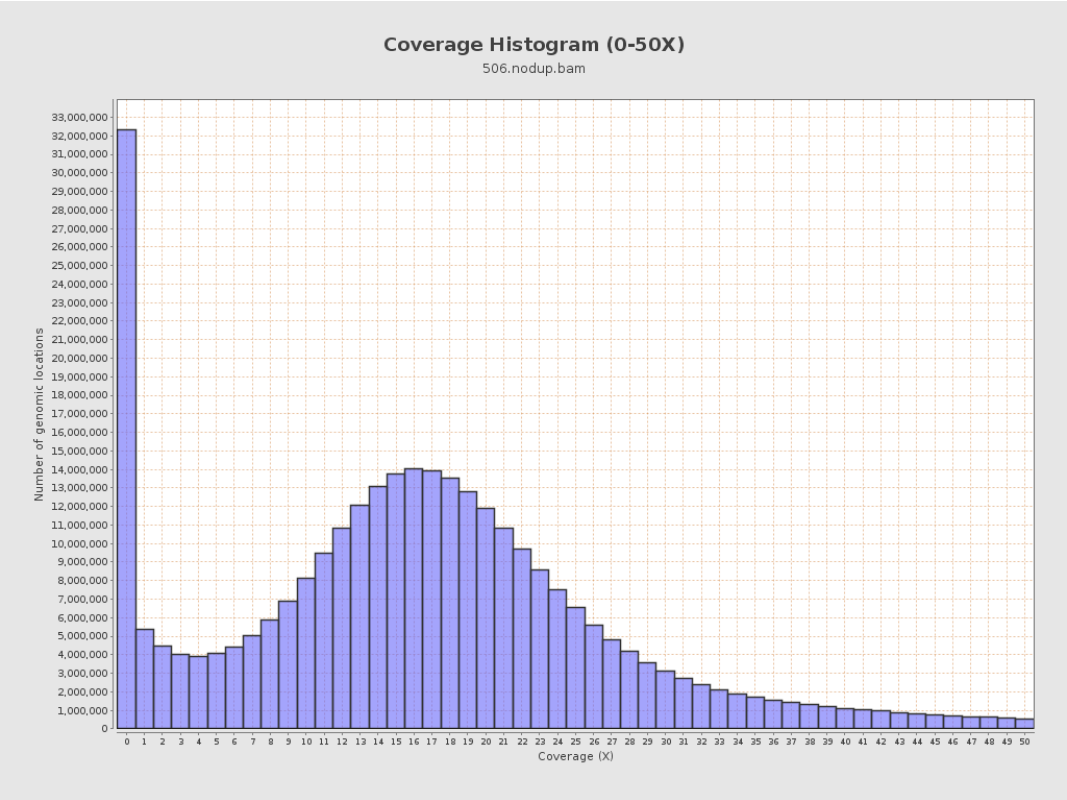
# 3. Results : Coverage across reference



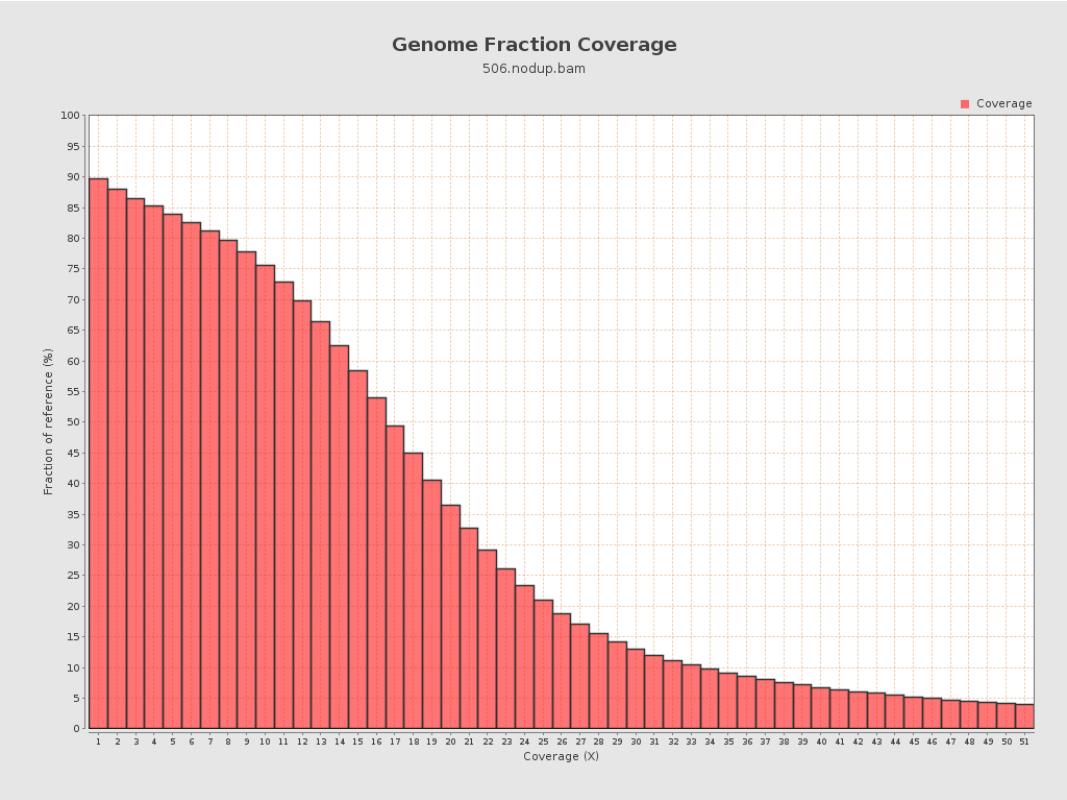
# 4. Results : Coverage Histogram



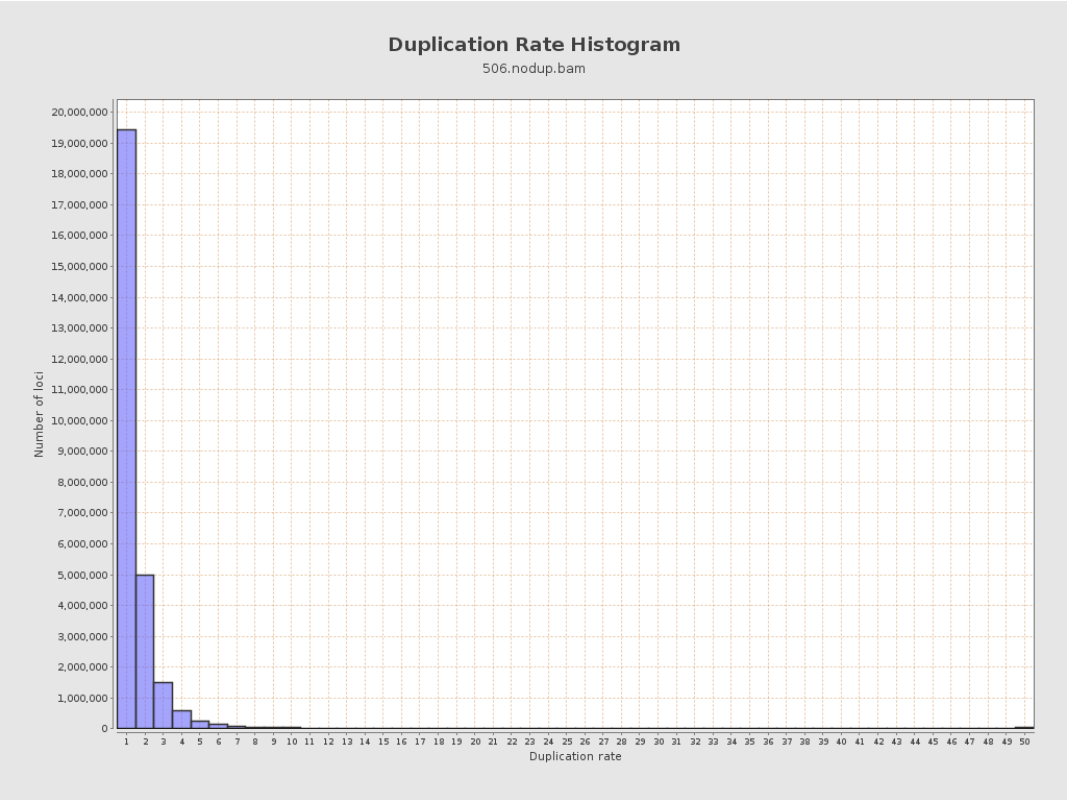
# 5. Results : Coverage Histogram (0-50X)



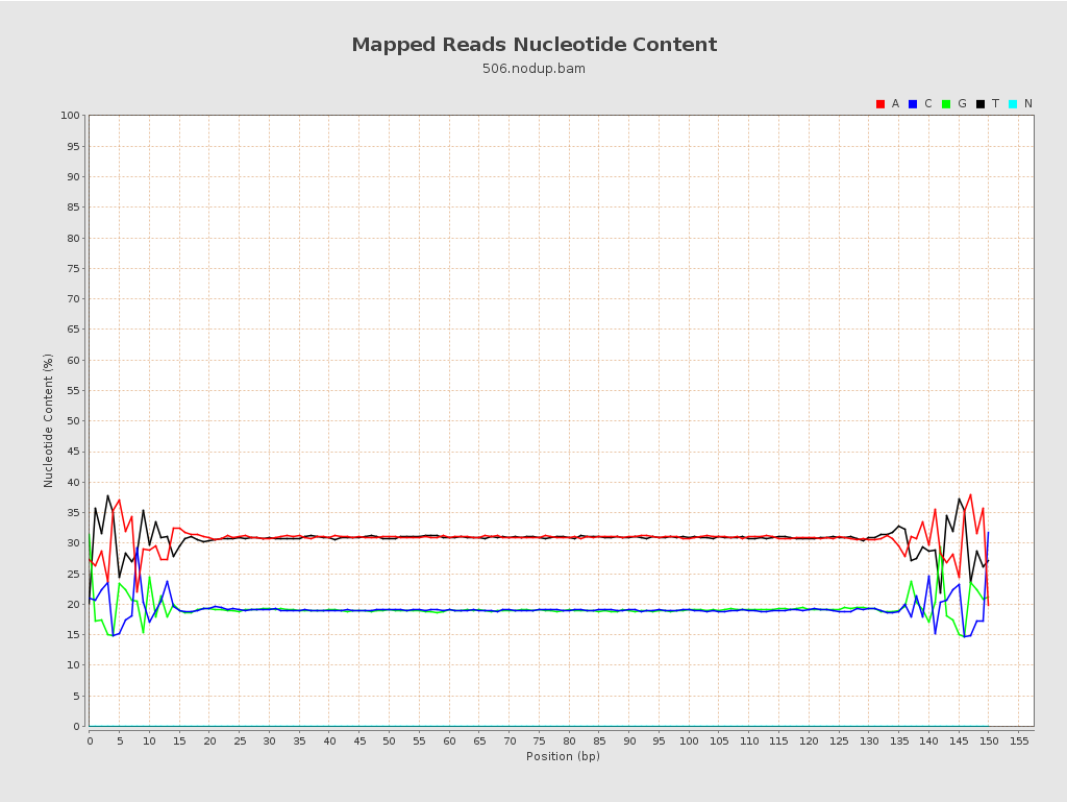
# 6. Results : Genome Fraction Coverage



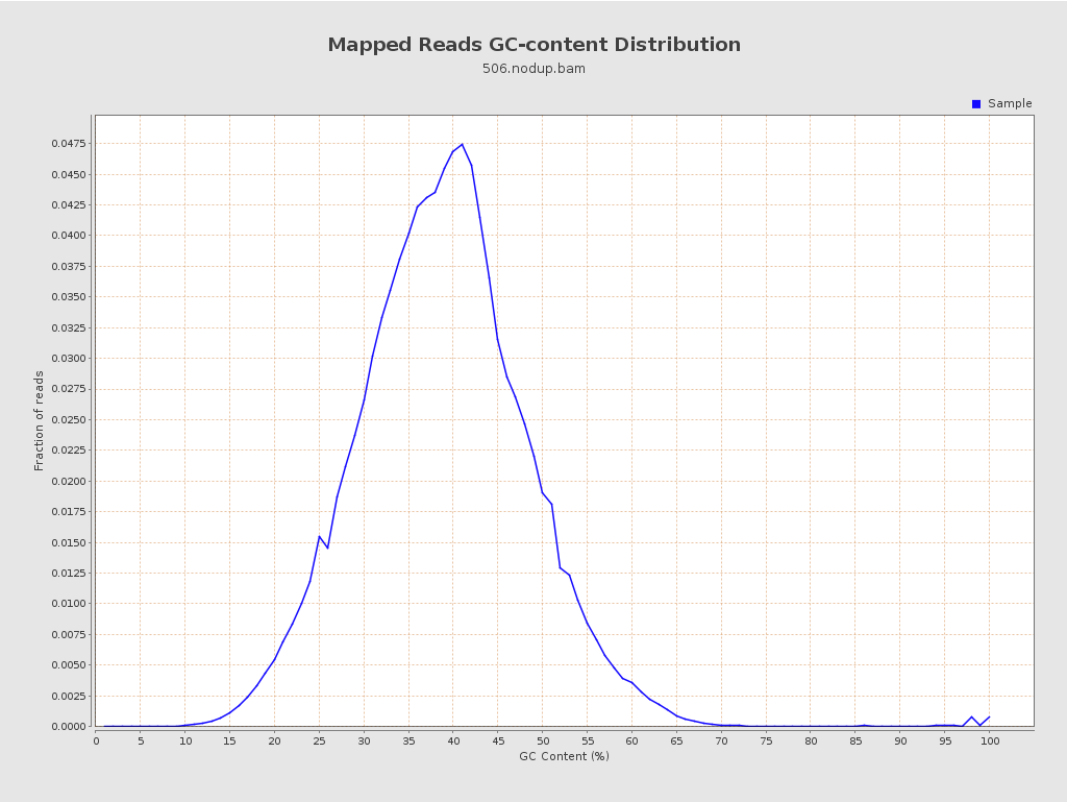
# 7. Results : Duplication Rate Histogram



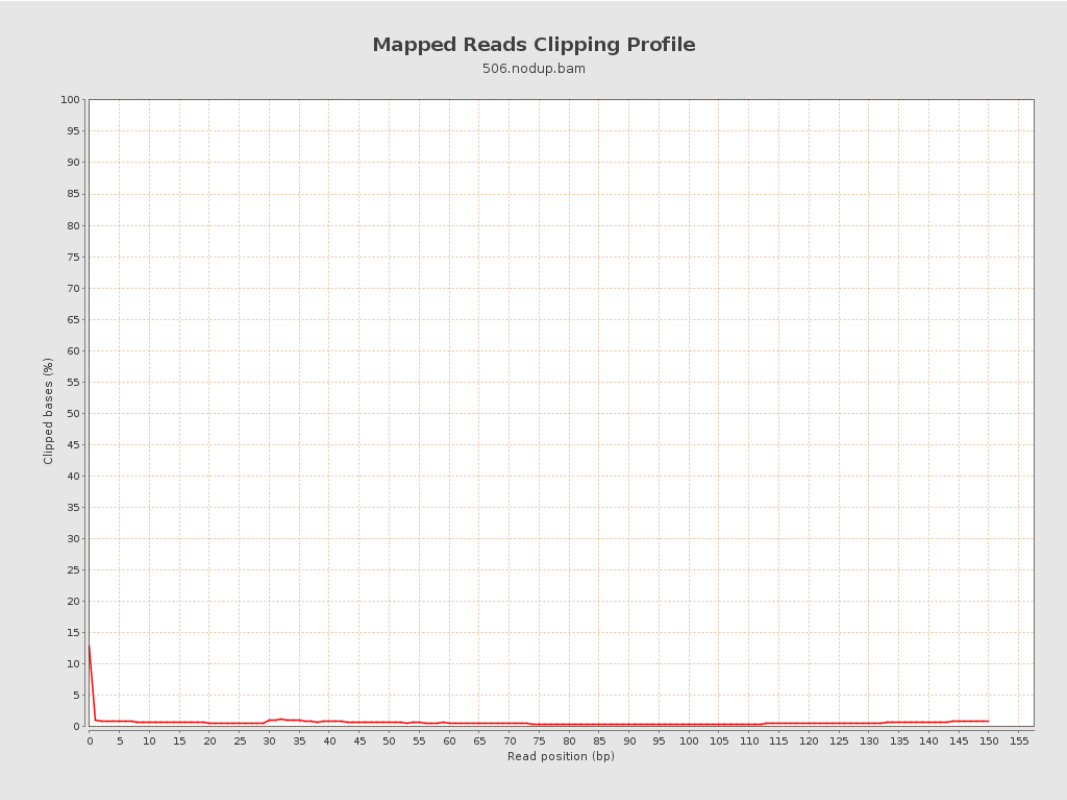
# 8. Results : Mapped Reads Nucleotide Content



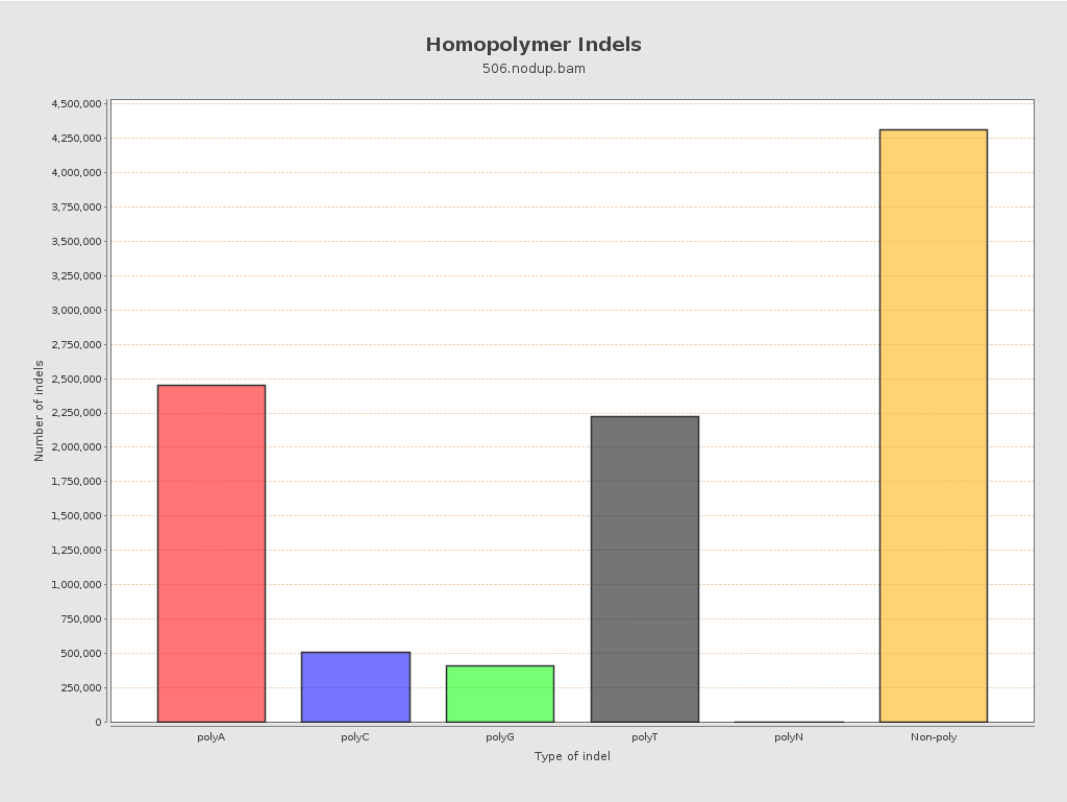
# 9. Results : Mapped Reads GC-content Distribution



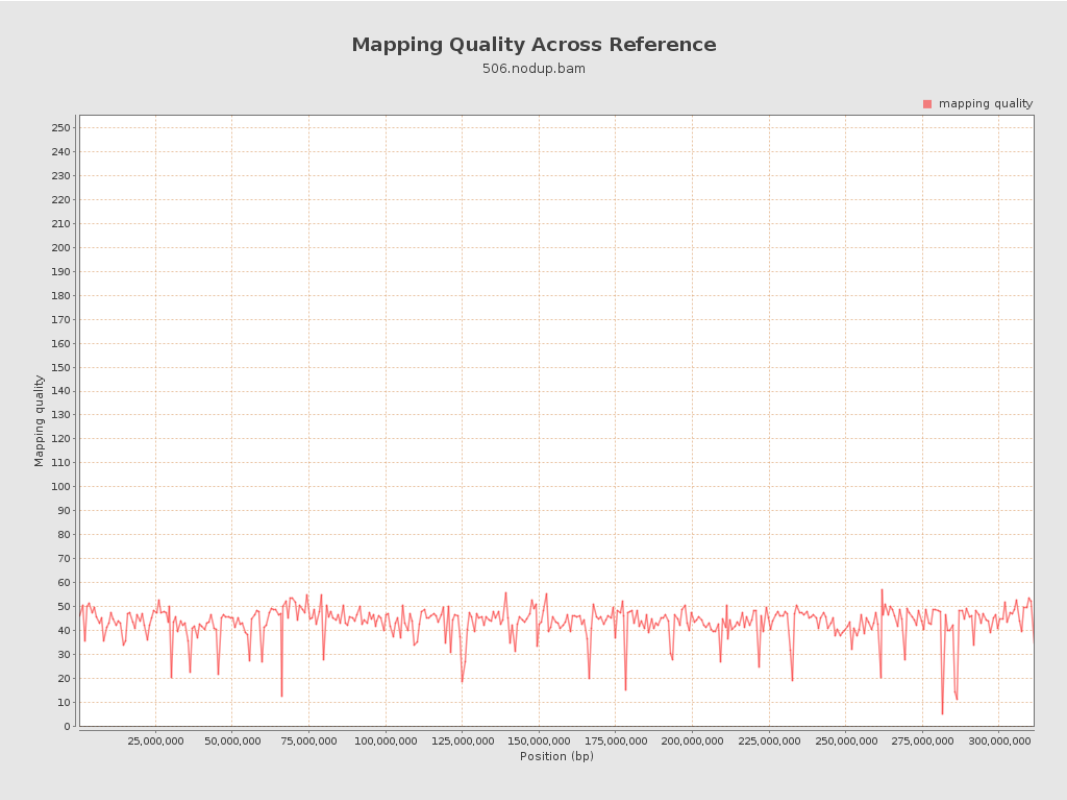
# 10. Results : Mapped Reads Clipping Profile



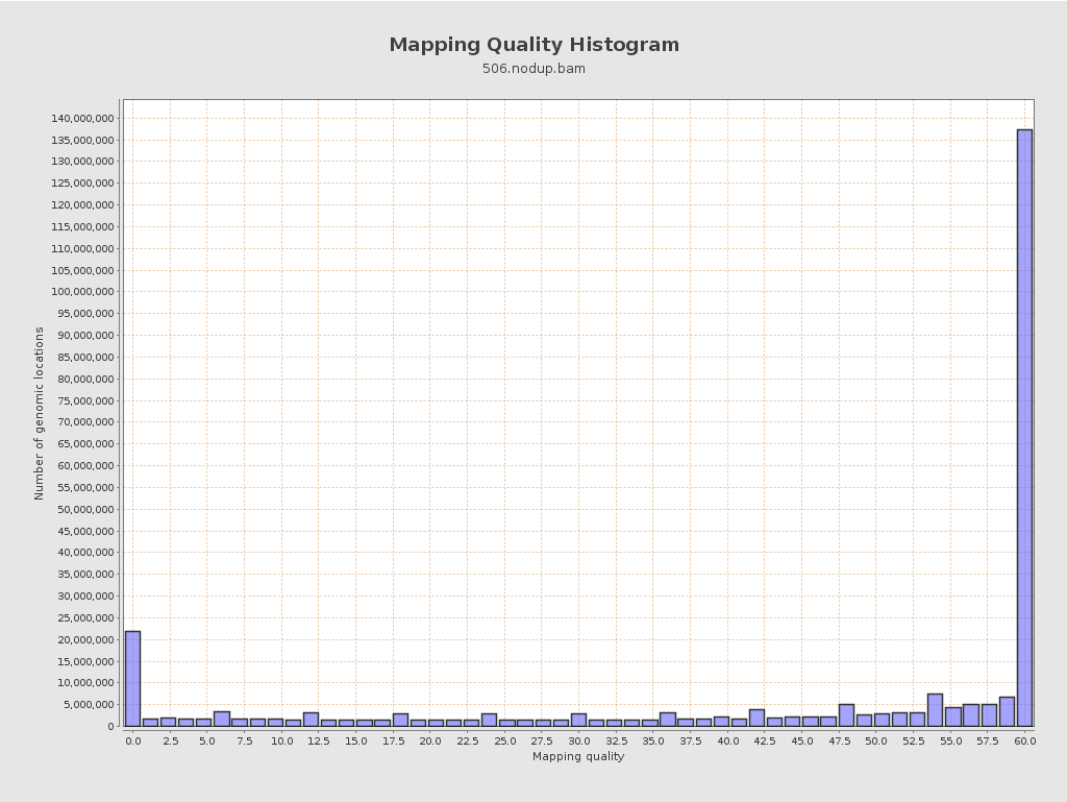
# 11. Results : Homopolymer Indels



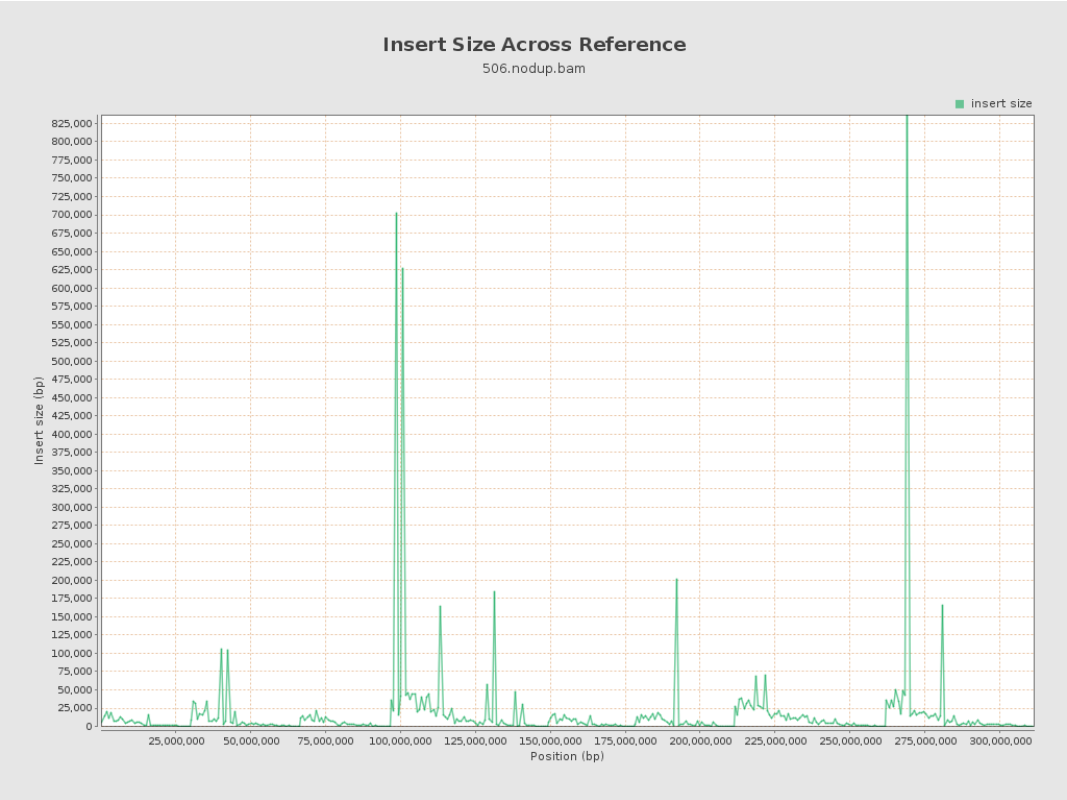
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram