# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:34:33*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/826.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/826.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_288/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_288_S369_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_288/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_288_S369_L003_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|---|---|
| Analysis date: | Mon May 29 21:34:32 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 76,813,571 |
| Mapped reads | 71,673,943 / 93.31% |
| Unmapped reads | 5,139,628 / 6.69% |
| Mapped paired reads | 71,673,943 / 93.31% |
| Mapped reads, first in pair | 35,848,088 / 46.67% |
| Mapped reads,  second in pair | 35,825,855 / 46.64% |
| Mapped reads, both in pair | 70,124,963 / 91.29% |
| Mapped reads, singletons | 1,548,980 / 2.02% |
| Read min/max/mean length | 30 / 151 / 148.16 |
| Duplicated reads (flagged) | 11,741,297 / 15.29% |
| Clipped reads | 16,595,515 / 21.6% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 3,043,834,028 / 30.73% |
| Number/percentage of C's | 1,908,824,343 / 19.27% |
| Number/percentage of T's | 3,050,659,576 / 30.8% |
| Number/percentage of G's | 1,901,041,541 / 19.19% |
| Number/percentage of N's | 35,014 / 0% |
| GC Percentage | 38.47% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 31.8608 |
| Standard Deviation | 270.9555 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.29 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 223,942.89 |
| Standard Deviation | 2,248,251.98 |
| P25/Median/P75 | 312 / 410 / 536 |

## 2.6. Mismatches and indels

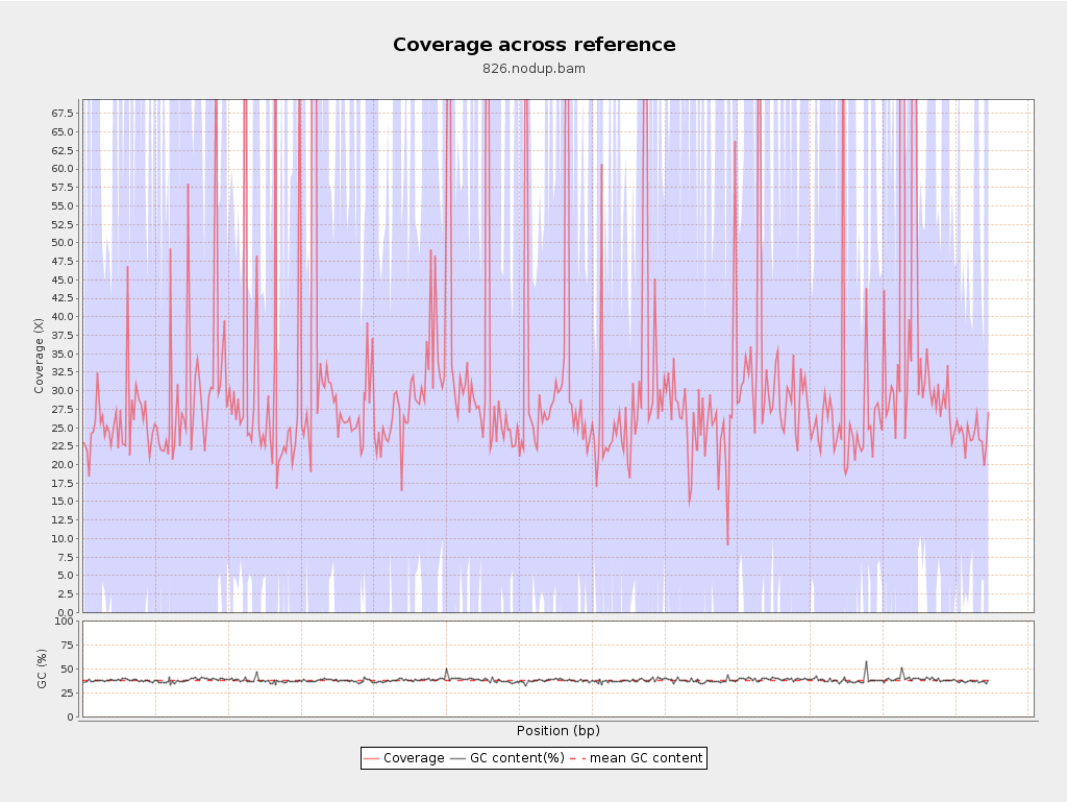
| | |
|---|---|
| General error rate | 2.37% |
| Mismatches | 216,797,745 |
| Insertions | 6,689,761 |
| Mapped reads with at least one insertion | 8.38% |
| Deletions | 6,638,374 |
| Mapped reads with at least one deletion | 8.23% |
| Homopolymer indels | 56.37% |

## 2.7. Chromosome stats

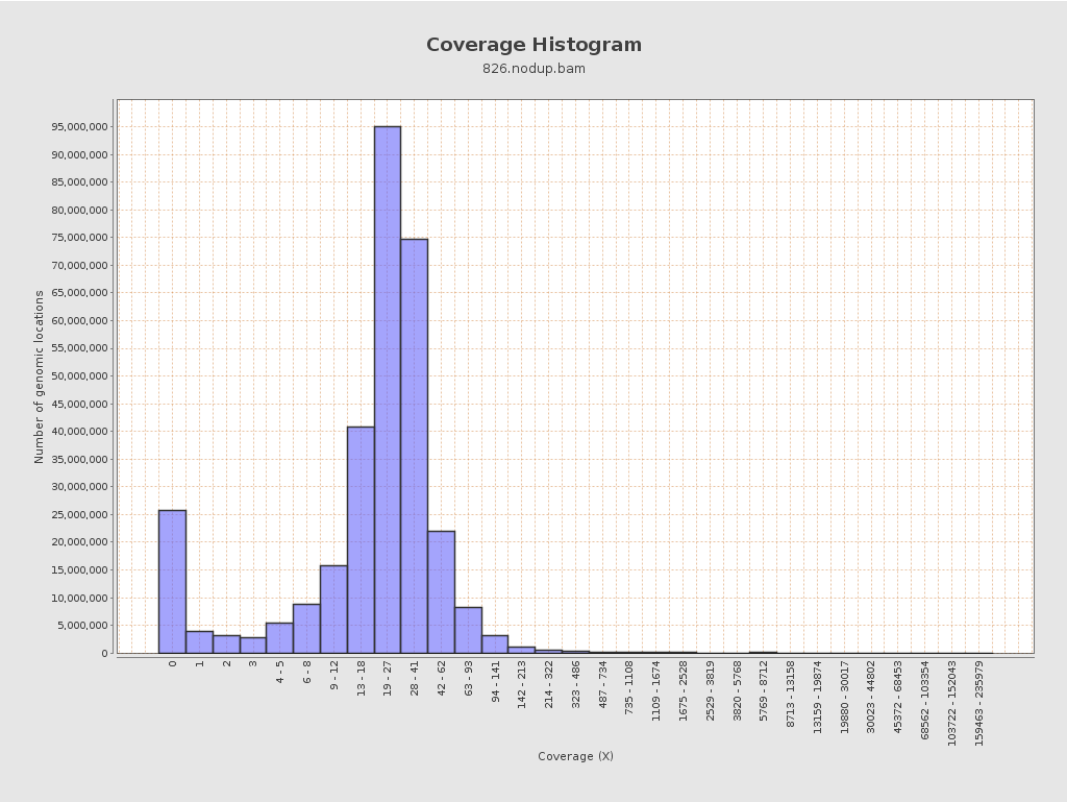
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 753274713 | 25.342 | 84.9005 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 1172365742 | 32.0334 | 280.1511 |
| LT669790.1 | 30422129 | 1066670868 | 35.0623 | 301.6922 |
| LT669791.1 | 52758100 | 1666457009 | 31.5868 | 249.065 |
| LT669792.1 | 28376109 | 880871559 | 31.0427 | 309.1142 |
| LT669793.1 | 33388210 | 983419440 | 29.4541 | 192.8645 |
| LT669794.1 | 50579949 | 1522120236 | 30.0934 | 229.0918 |
| LT669795.1 | 49795044 | 1883999764 | 37.8351 | 378.6602 |

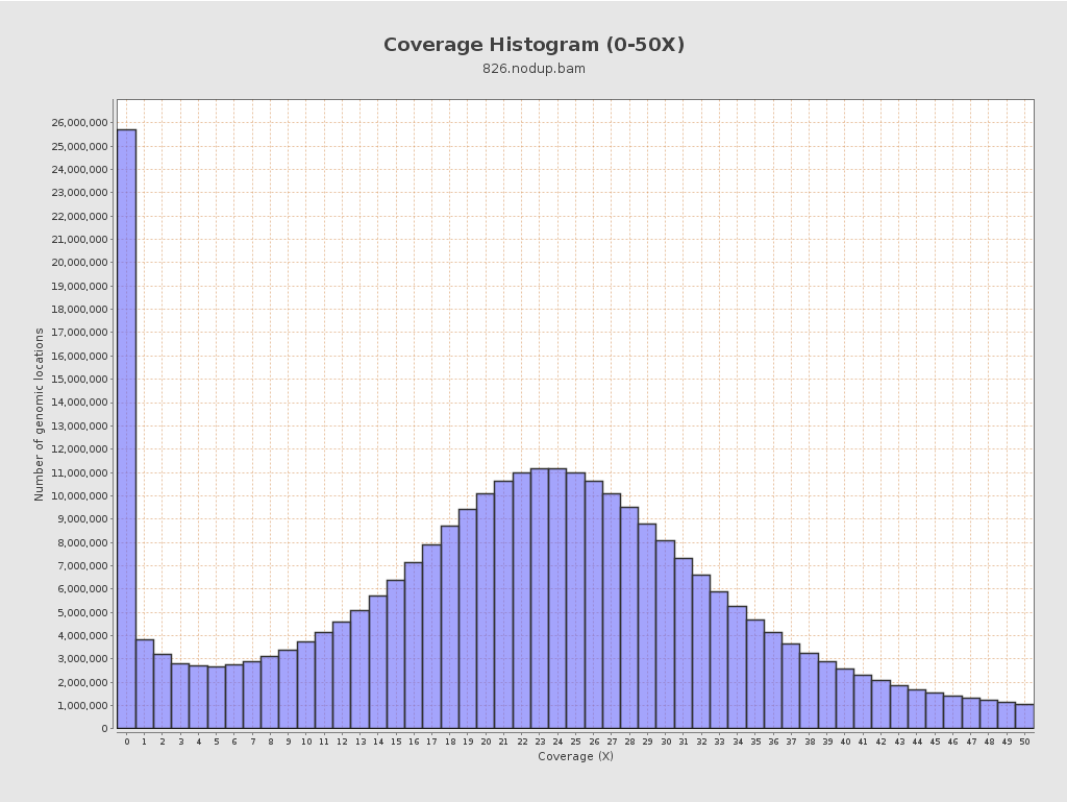
# 3. Results : Coverage across reference



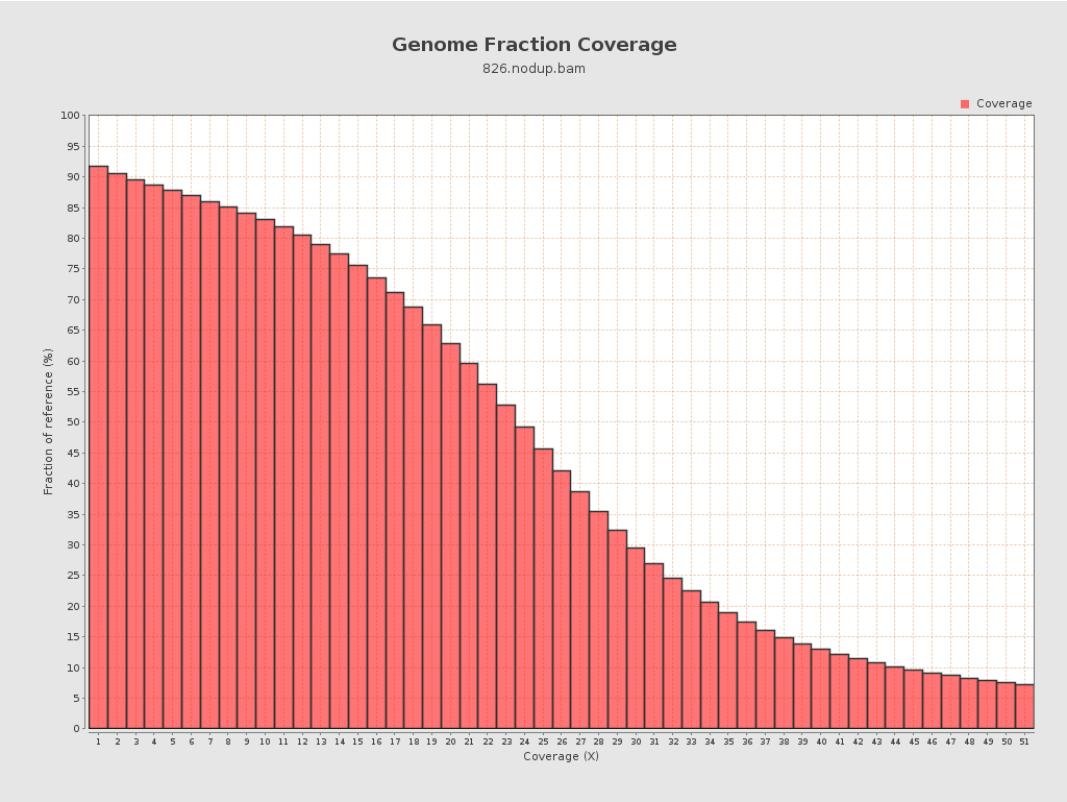
# 4. Results : Coverage Histogram



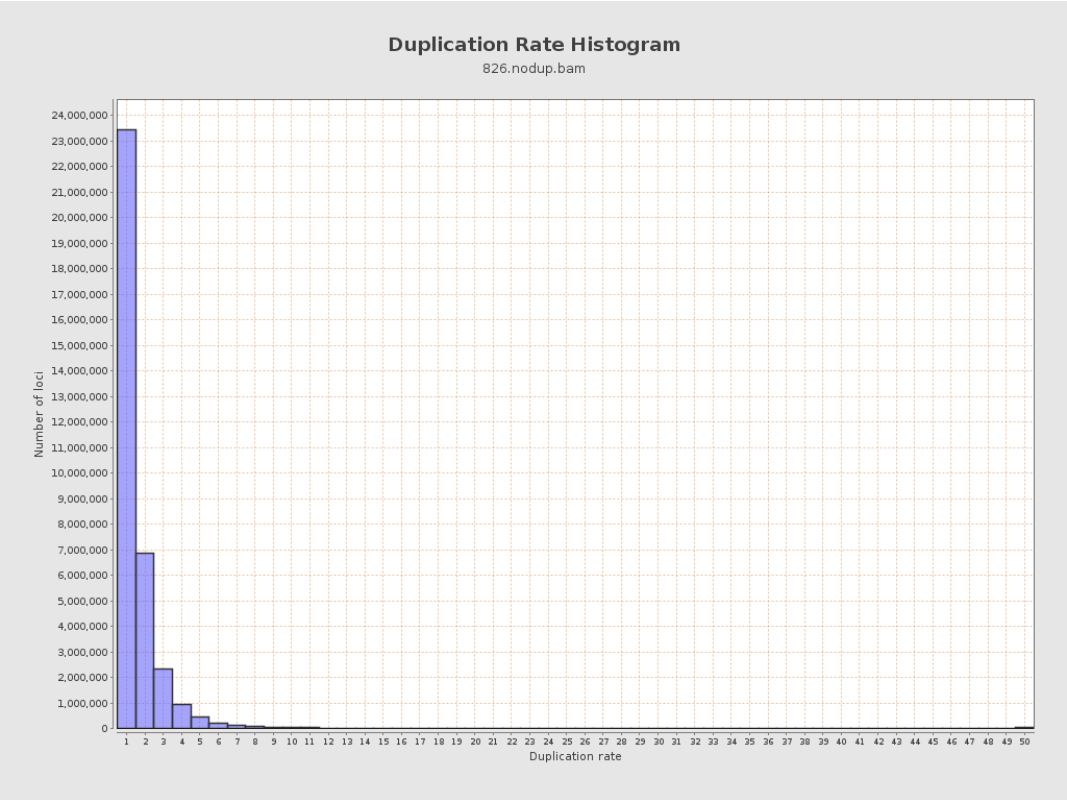
# 5. Results : Coverage Histogram (0-50X)



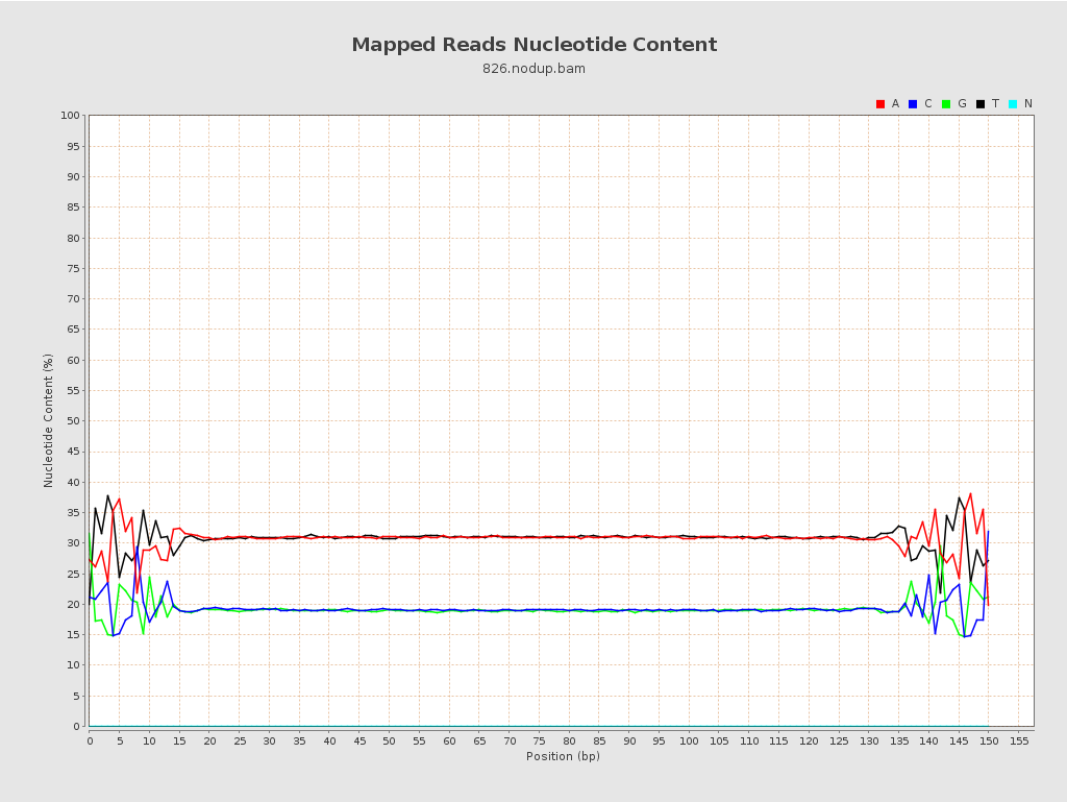
# 6. Results : Genome Fraction Coverage



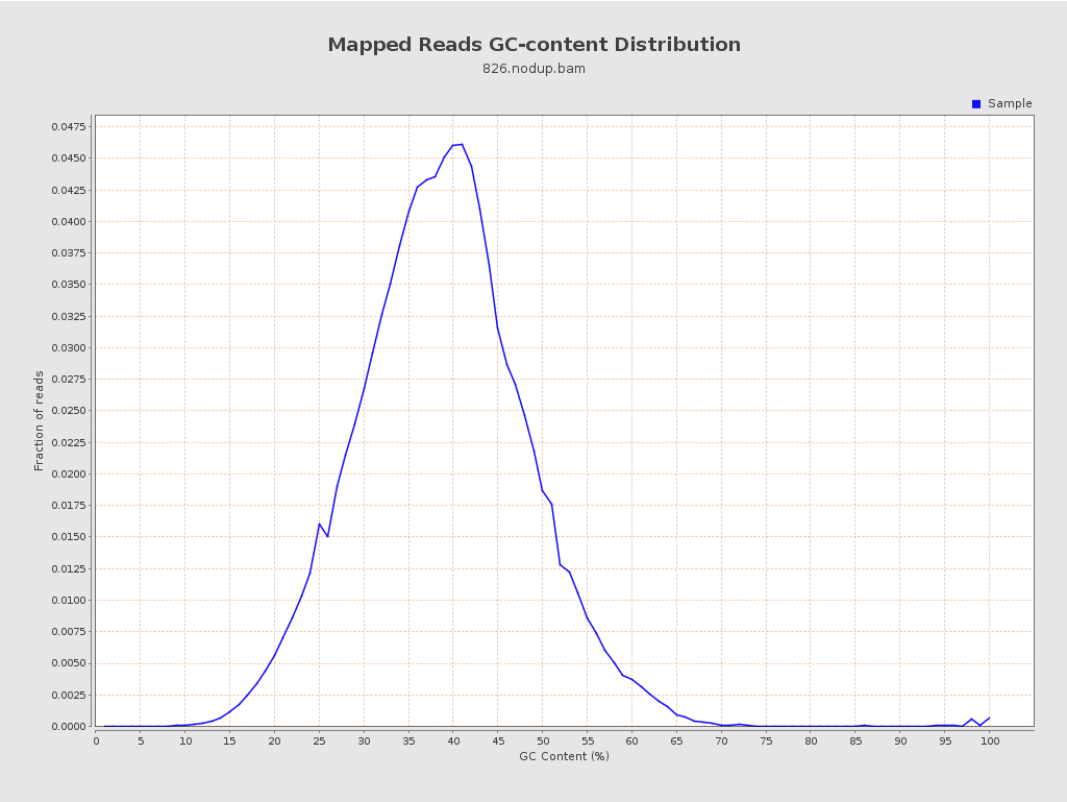
# 7. Results : Duplication Rate Histogram



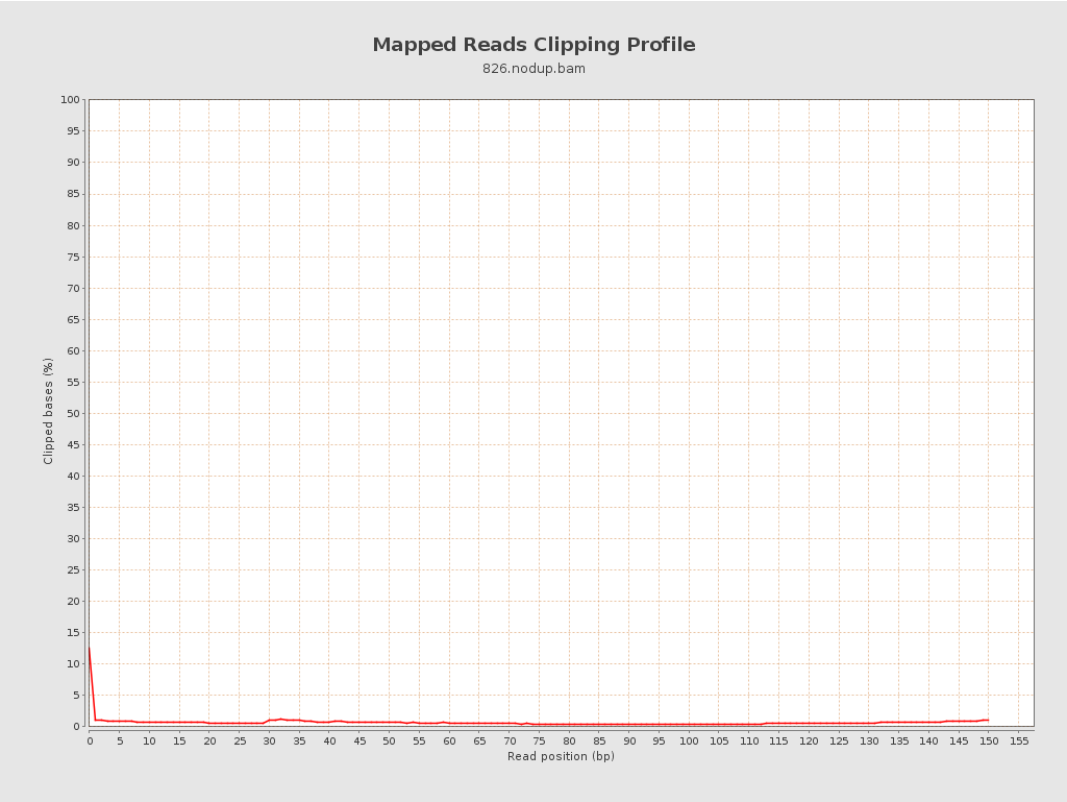
# 8. Results : Mapped Reads Nucleotide Content



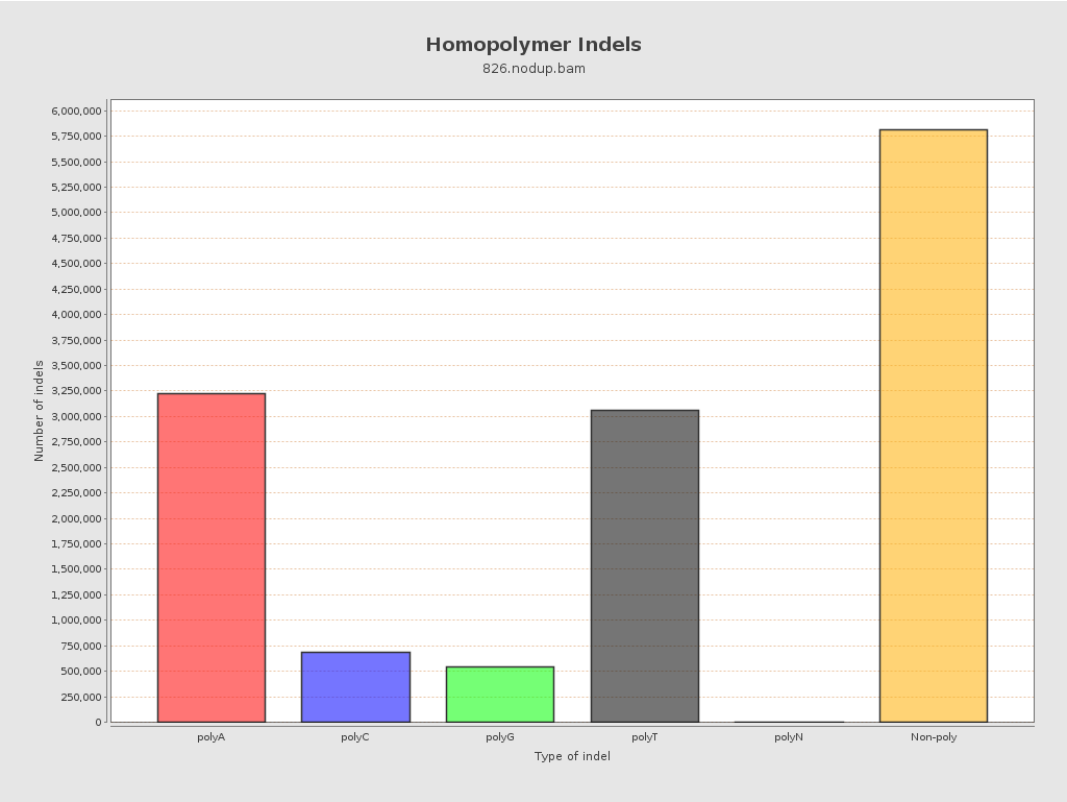
# 9. Results : Mapped Reads GC-content Distribution



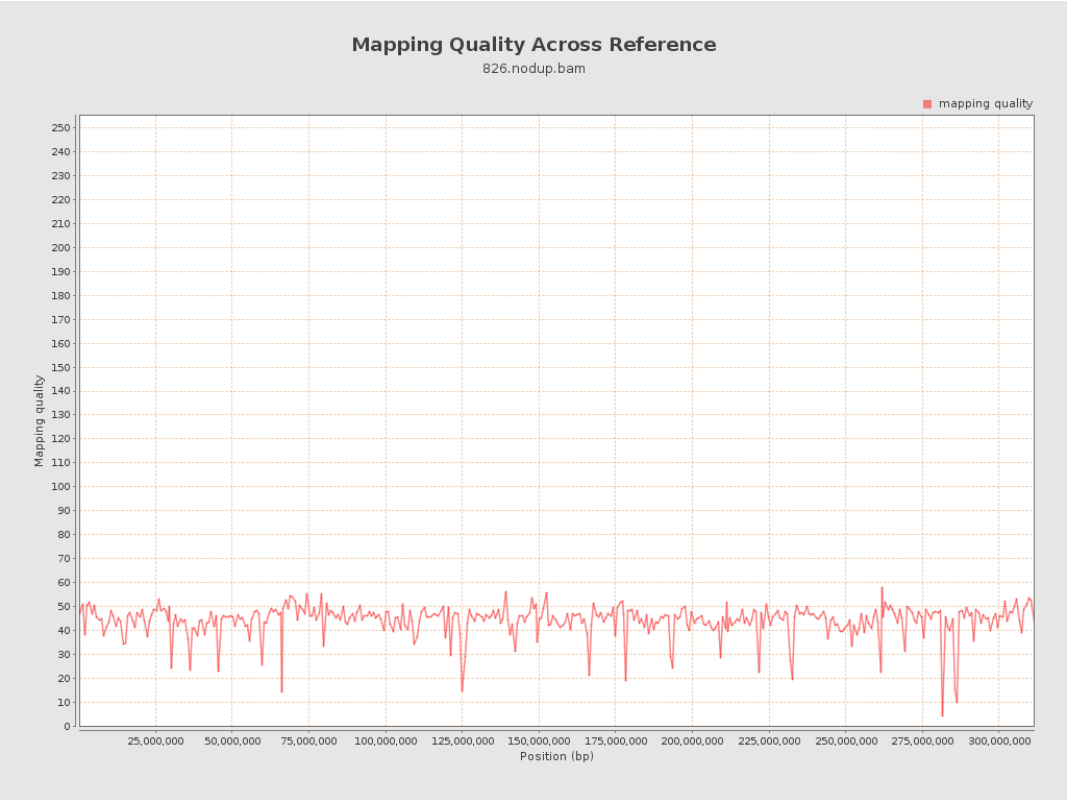
# 10. Results : Mapped Reads Clipping Profile



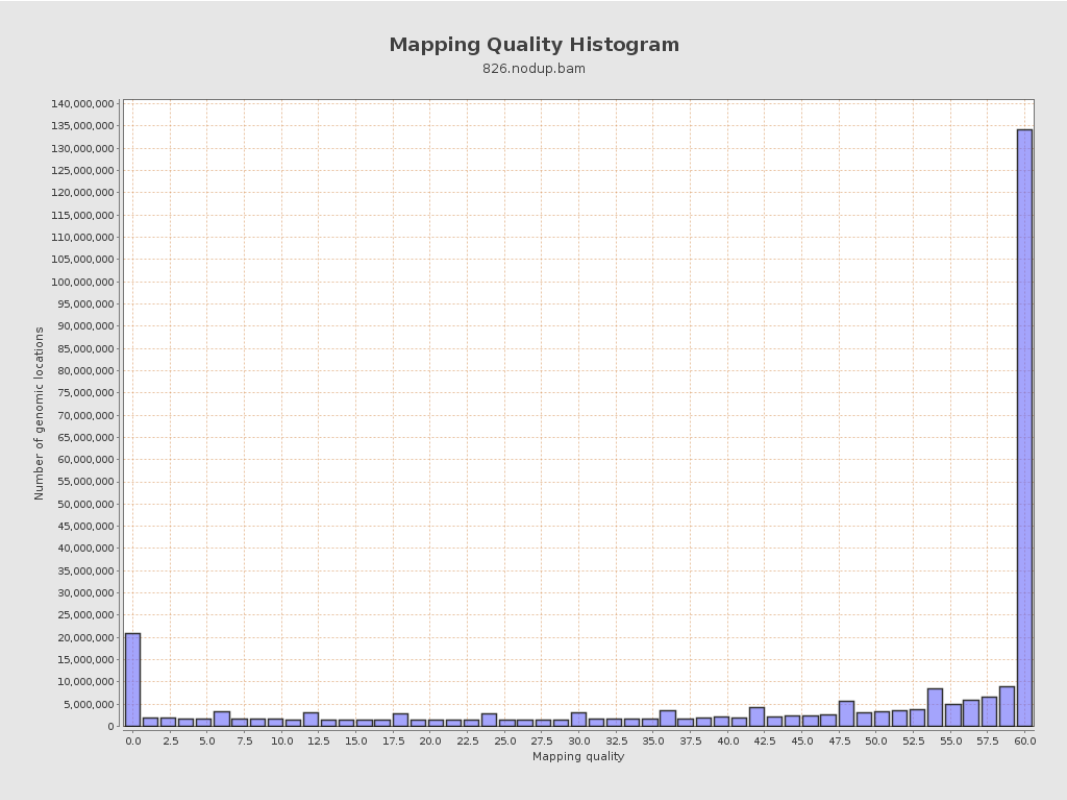
# 11. Results : Homopolymer Indels



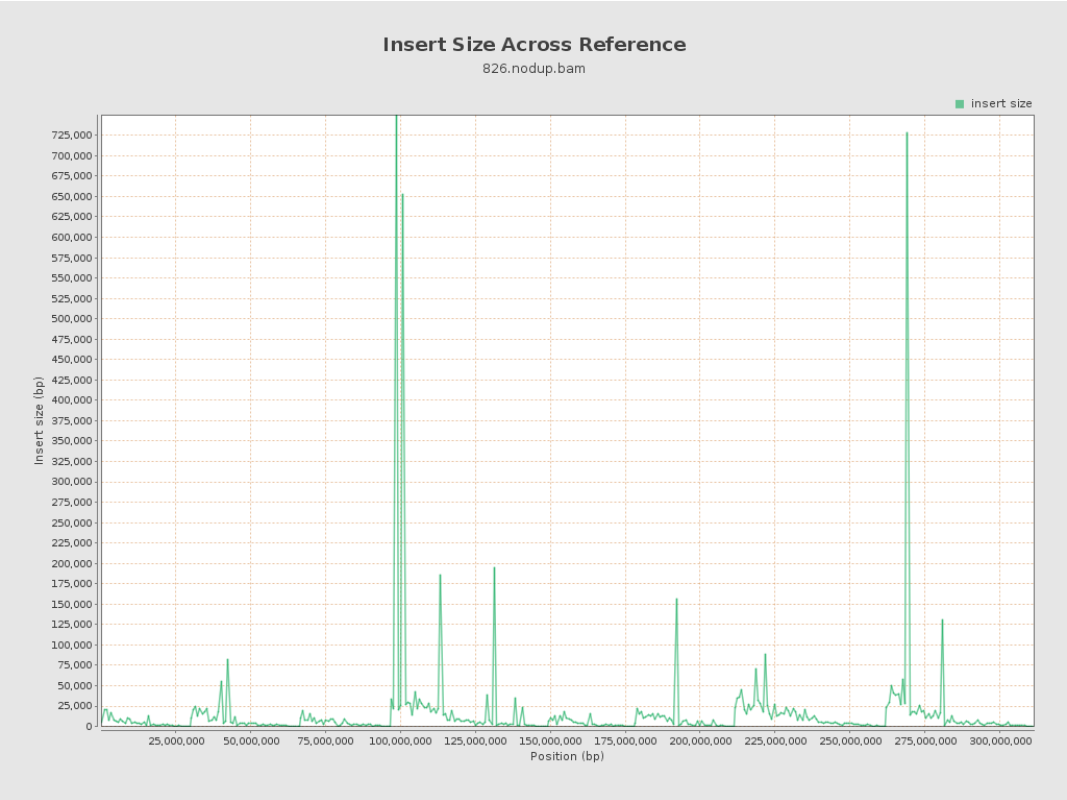
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram