# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:33:31*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1424
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1424 .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_112/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_112_S202_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_112/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_112_S202_L002_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| | |

| | |
|---|---|
| Number of windows: | 400 |
| Analysis date: | Mon May 29 21:33:30 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 74,804,060 |
| Mapped reads | 69,225,725 / 92.54% |
| Unmapped reads | 5,578,335 / 7.46% |
| Mapped paired reads | 69,225,725 / 92.54% |
| Mapped reads, first in pair | 34,662,495 / 46.34% |
| Mapped reads,  second in pair | 34,563,230 / 46.21% |
| Mapped reads, both in pair | 67,667,200 / 90.46% |
| Mapped reads, singletons | 1,558,525 / 2.08% |
| Read min/max/mean length | 30 / 151 / 148.12 |
| Duplicated reads (flagged) | 11,227,512 / 15.01% |
| Clipped reads | 15,394,652 / 20.58% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 2,964,938,331 / 30.89% |
| Number/percentage of C's | 1,833,274,389 / 19.1% |
| Number/percentage of T's | 2,967,799,901 / 30.92% |
| Number/percentage of G's | 1,831,499,202 / 19.08% |
| Number/percentage of N's | 39,951 / 0% |
| GC Percentage | 38.18% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 30.8778 |
| Standard Deviation | 239.3902 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.01 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 238,441.95 |
| Standard Deviation | 2,318,987.91 |
| P25/Median/P75 | 323 / 422 / 554 |

## 2.6. Mismatches and indels

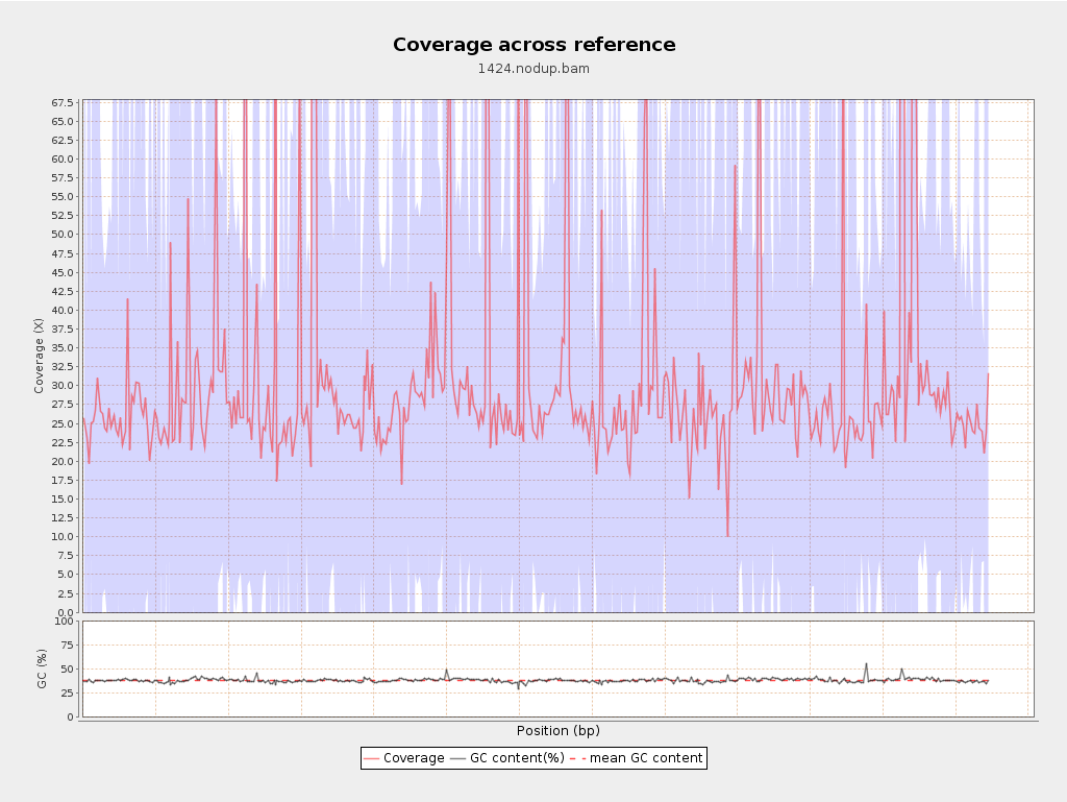
| | |
|---|---|
| General error rate | 2.32% |
| Mismatches | 204,571,953 |
| Insertions | 6,631,081 |
| Mapped reads with at least one insertion | 8.59% |
| Deletions | 6,682,372 |
| Mapped reads with at least one deletion | 8.56% |
| Homopolymer indels | 56.55% |

## 2.7. Chromosome stats

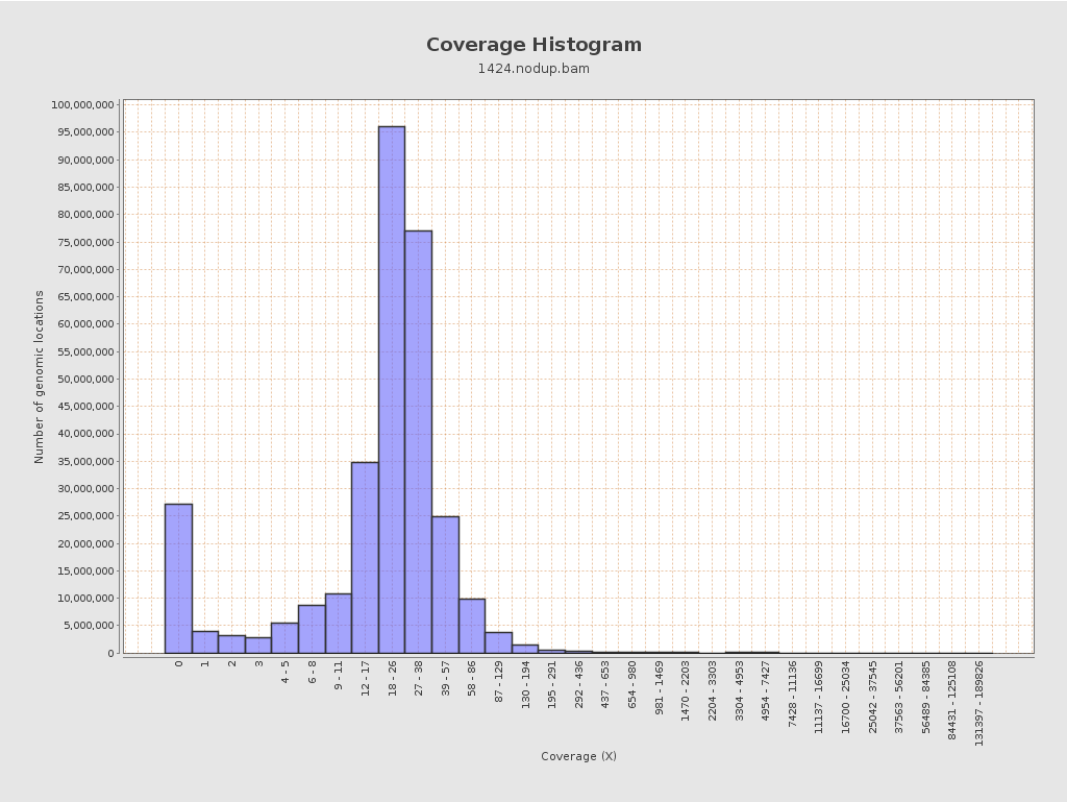
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 760948714 | 25.6002 | 79.4392 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 1166962759 | 31.8858 | 264.2547 |
| LT669790.1 | 30422129 | 1043806675 | 34.3108 | 270.5594 |
| LT669791.1 | 52758100 | 1602171854 | 30.3683 | 221.3165 |
| LT669792.1 | 28376109 | 873773556 | 30.7926 | 262.5726 |
| LT669793.1 | 33388210 | 952512614 | 28.5284 | 224.0727 |
| LT669794.1 | 50579949 | 1478207640 | 29.2252 | 197.5619 |
| LT669795.1 | 49795044 | 1744442178 | 35.0324 | 307.0866 |

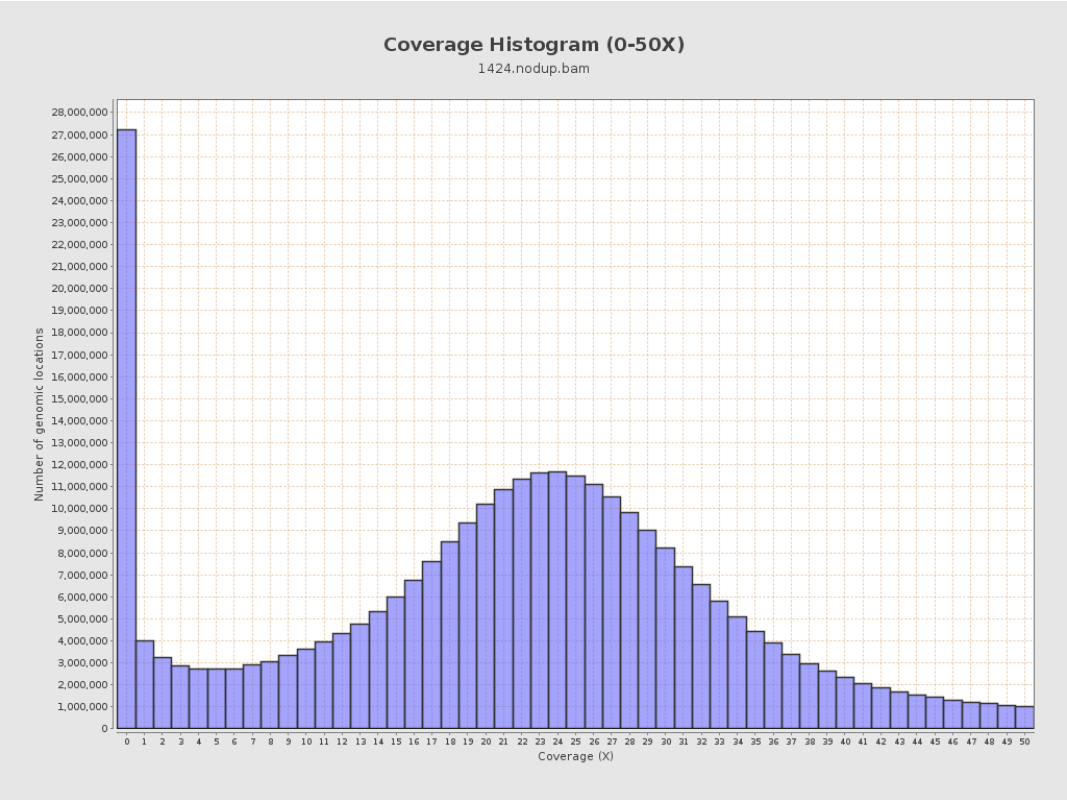
# 3. Results : Coverage across reference



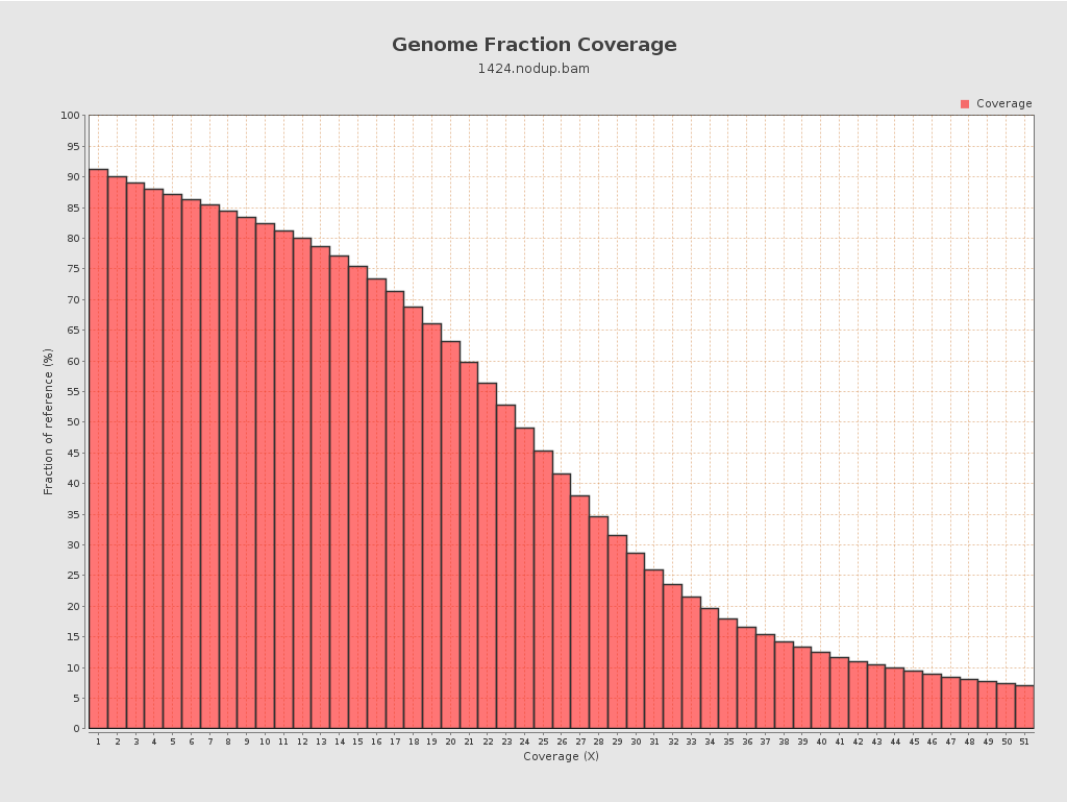
# 4. Results : Coverage Histogram



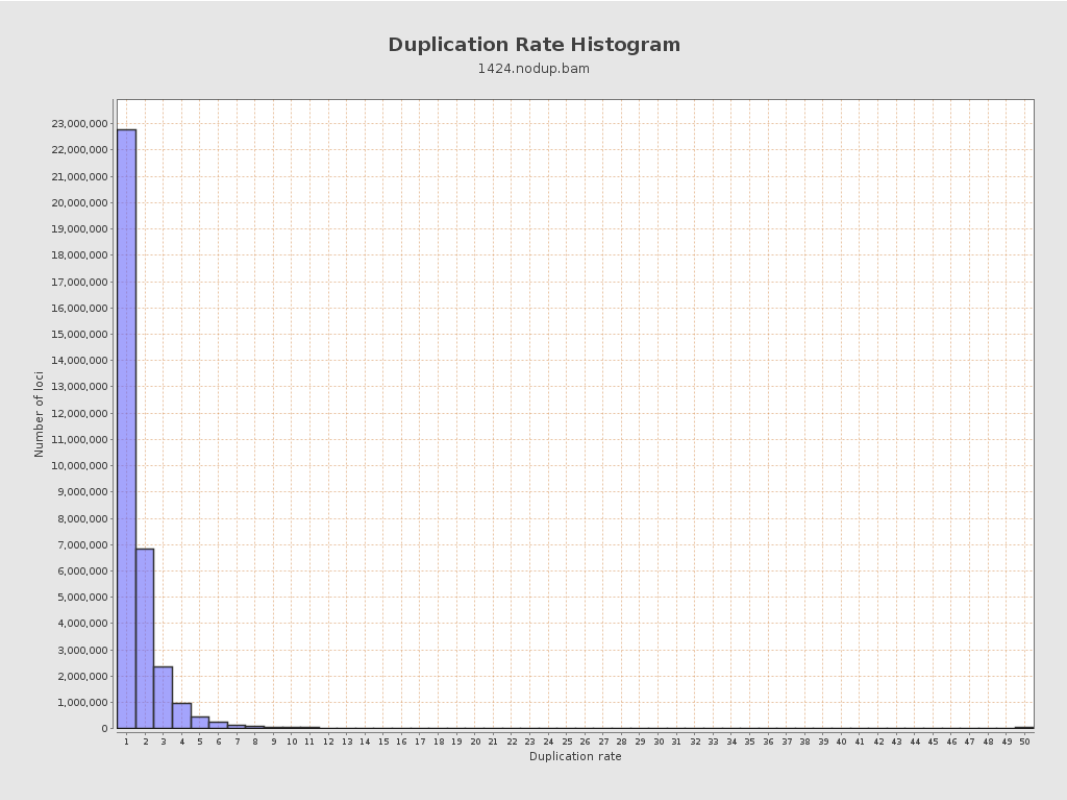
# 5. Results : Coverage Histogram (0-50X)



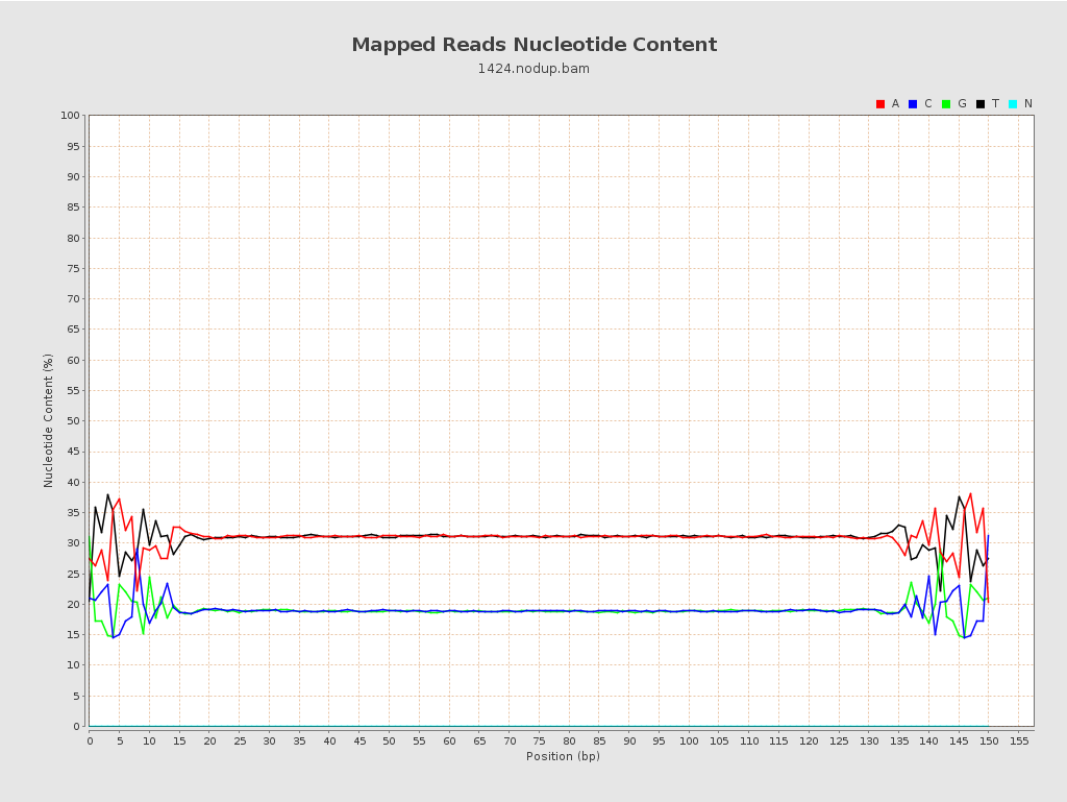
# 6. Results : Genome Fraction Coverage



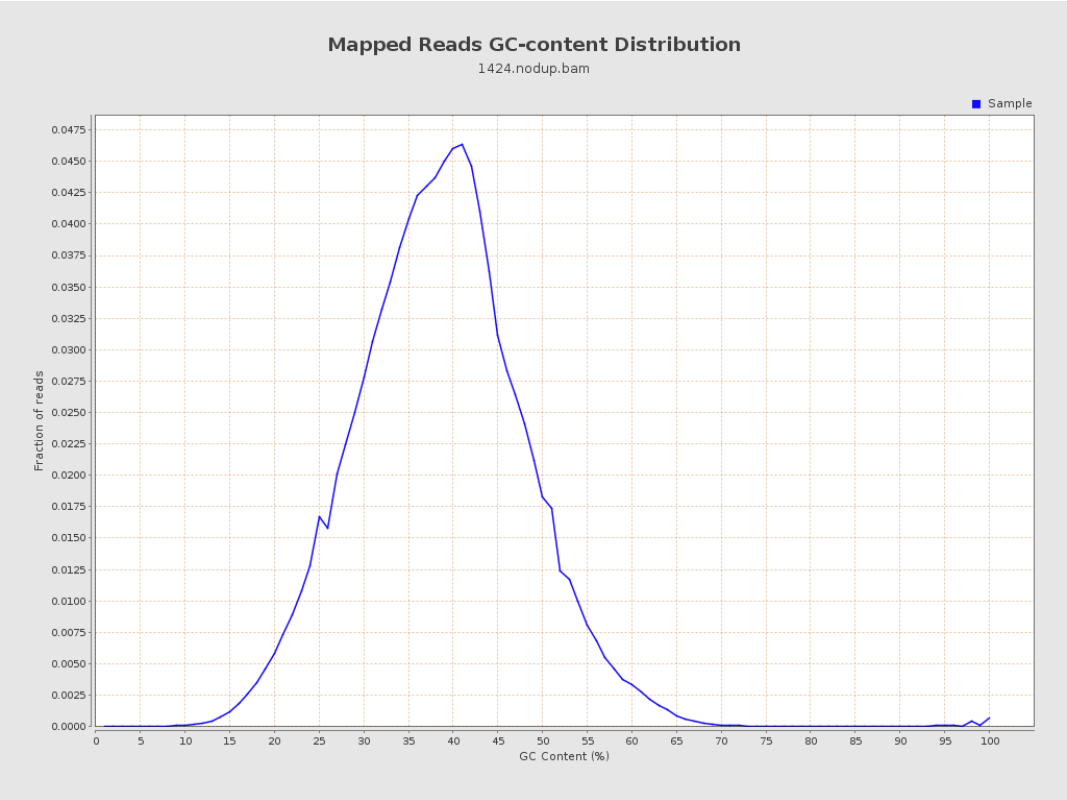
# 7. Results : Duplication Rate Histogram



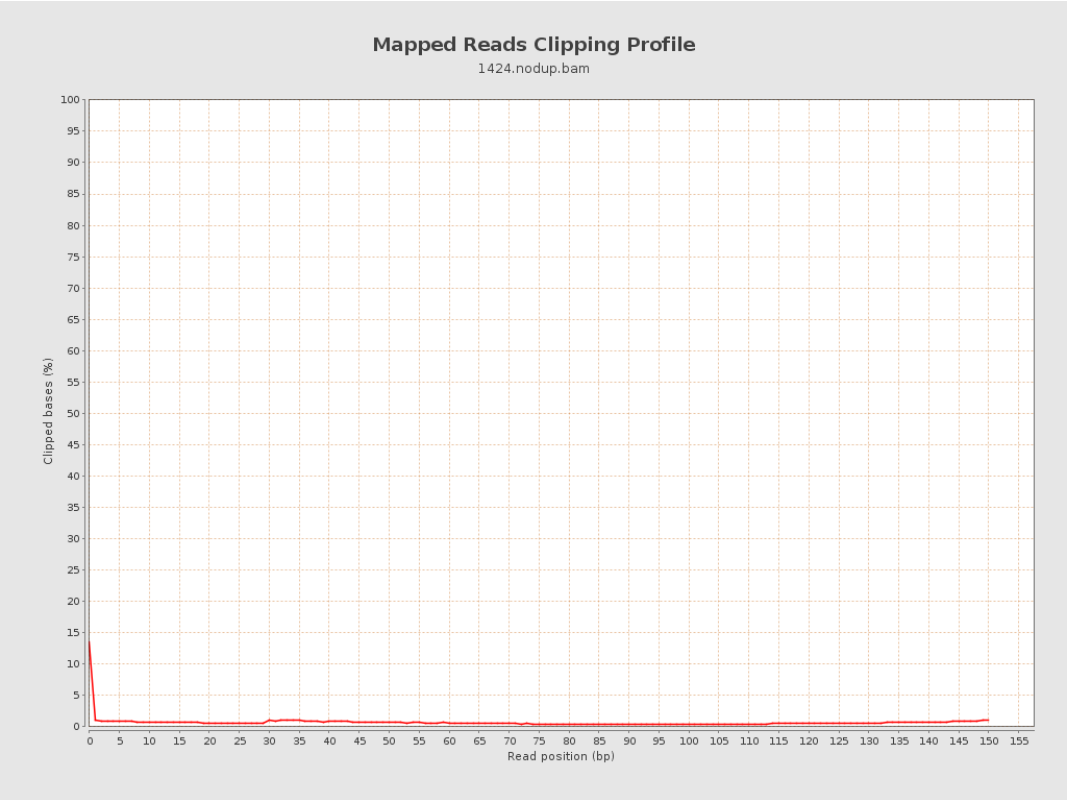
# 8. Results : Mapped Reads Nucleotide Content



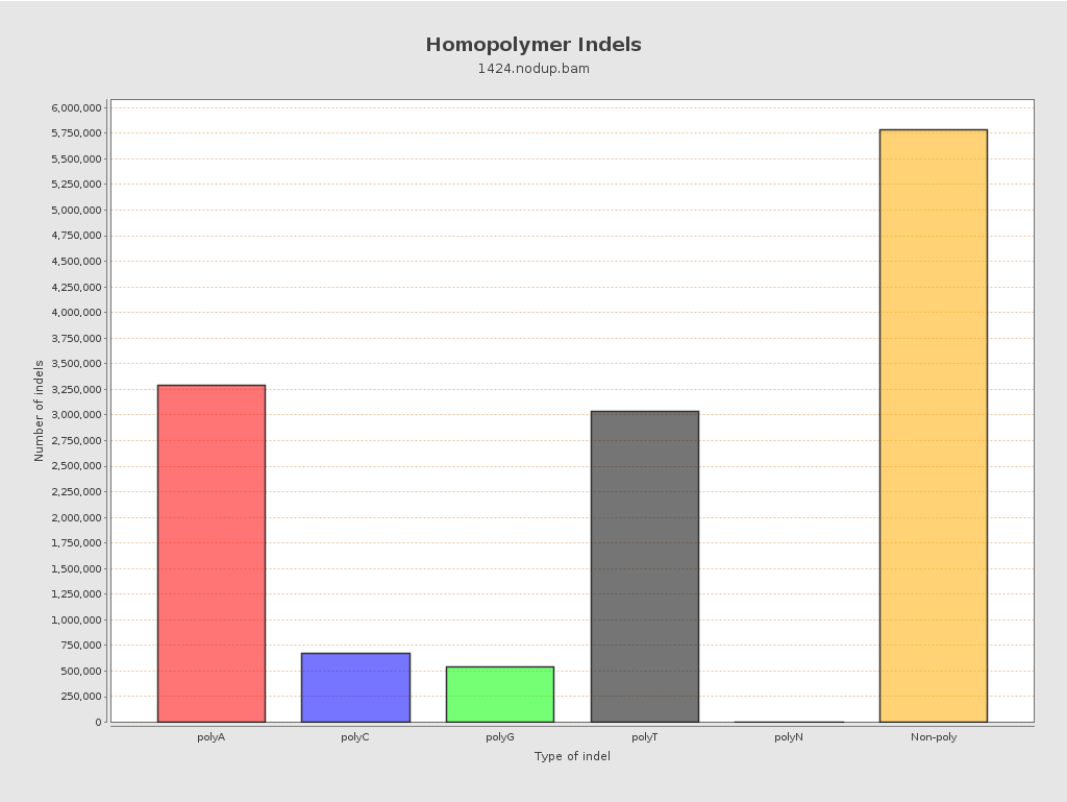
# 9. Results : Mapped Reads GC-content Distribution



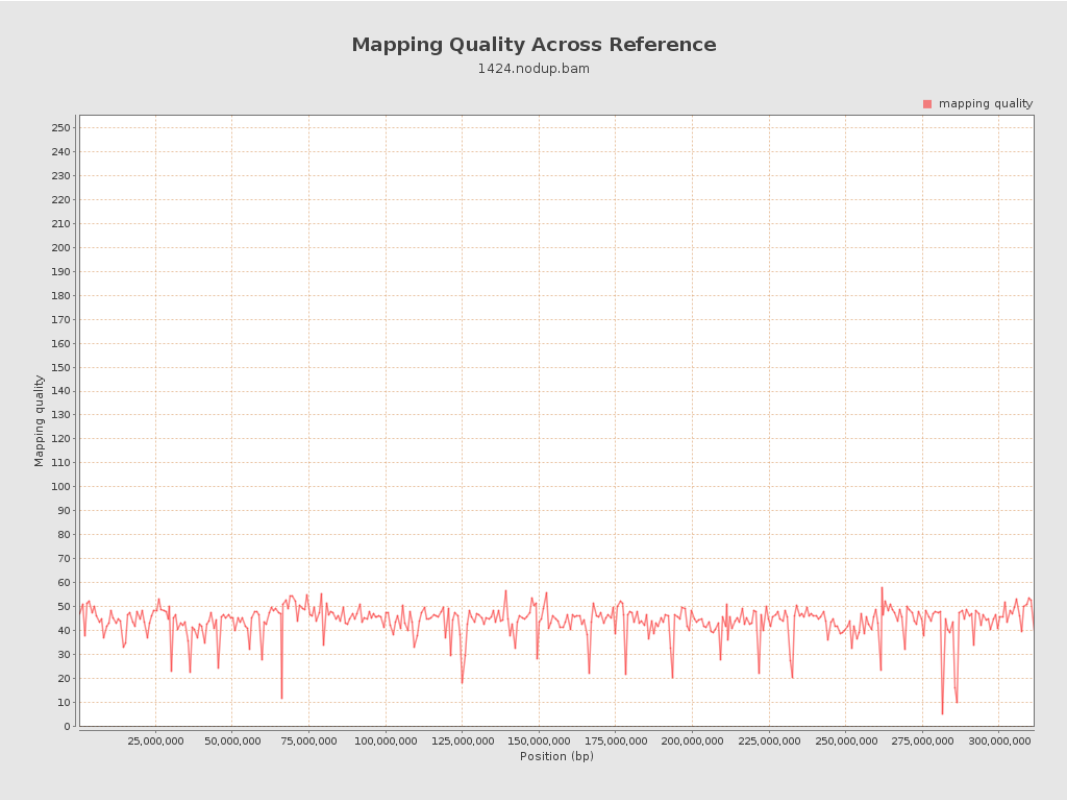
# 10. Results : Mapped Reads Clipping Profile



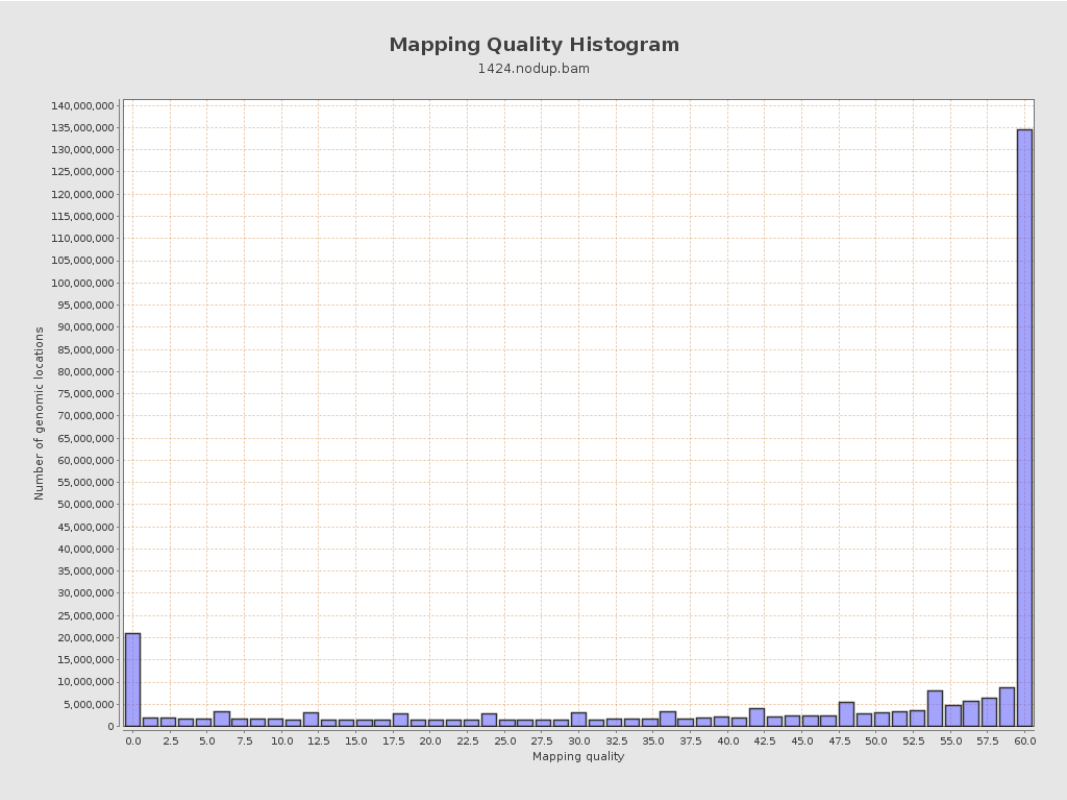
# 11. Results : Homopolymer Indels



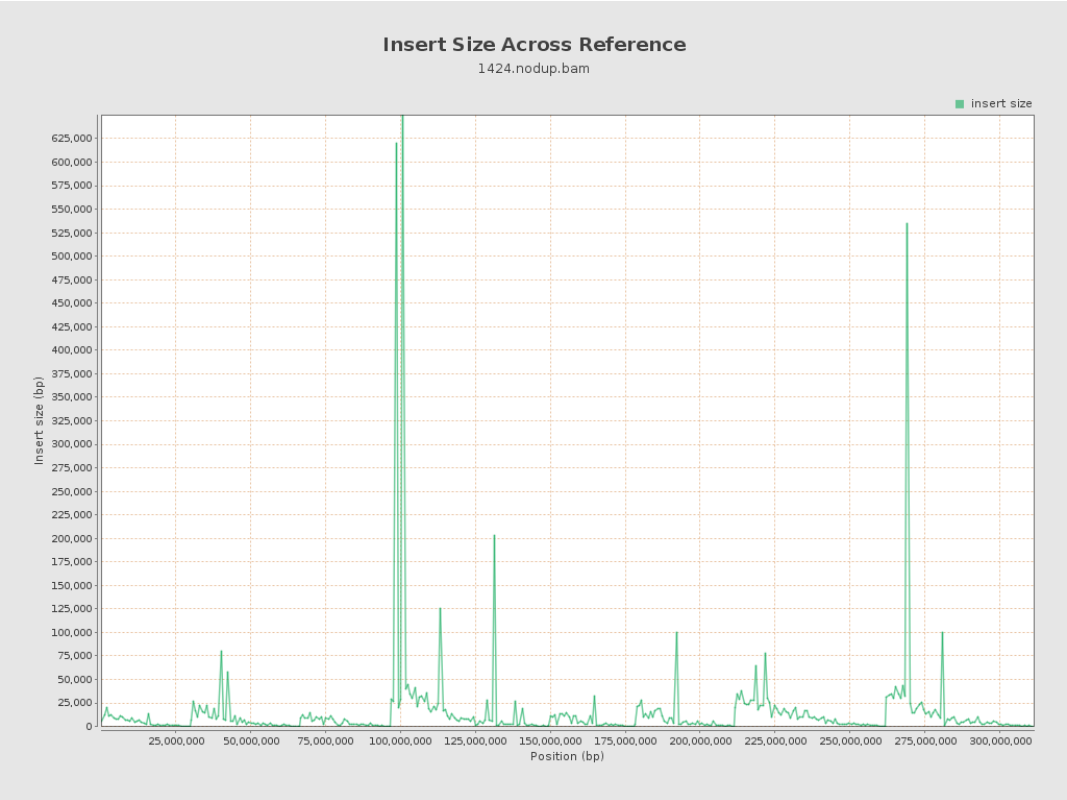
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram