# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:25:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1483
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1483 .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_107/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_107_S197_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_107/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_107_S197_L002_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| | |

| | |
|---|---|
| Number of windows: | 400 |
| Analysis date: | Mon May 29 21:25:52 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 50,793,157 |
| Mapped reads | 46,837,794 / 92.21% |
| Unmapped reads | 3,955,363 / 7.79% |
| Mapped paired reads | 46,837,794 / 92.21% |
| Mapped reads, first in pair | 23,459,304 / 46.19% |
| Mapped reads,  second in pair | 23,378,490 / 46.03% |
| Mapped reads, both in pair | 45,538,345 / 89.65% |
| Mapped reads, singletons | 1,299,449 / 2.56% |
| Read min/max/mean length | 30 / 151 / 148.06 |
| Duplicated reads (flagged) | 8,250,008 / 16.24% |
| Clipped reads | 10,789,600 / 21.24% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,998,395,214 / 30.99% |
| Number/percentage of C's | 1,224,572,408 / 18.99% |
| Number/percentage of T's | 2,001,697,270 / 31.04% |
| Number/percentage of G's | 1,223,829,926 / 18.98% |
| Number/percentage of N's | 27,682 / 0% |
| GC Percentage | 37.97% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 20.7468 |
| Standard Deviation | 170.3844 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.52 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 255,652.3 |
| Standard Deviation | 2,442,900.9 |
| P25/Median/P75 | 329 / 429 / 557 |

## 2.6. Mismatches and indels

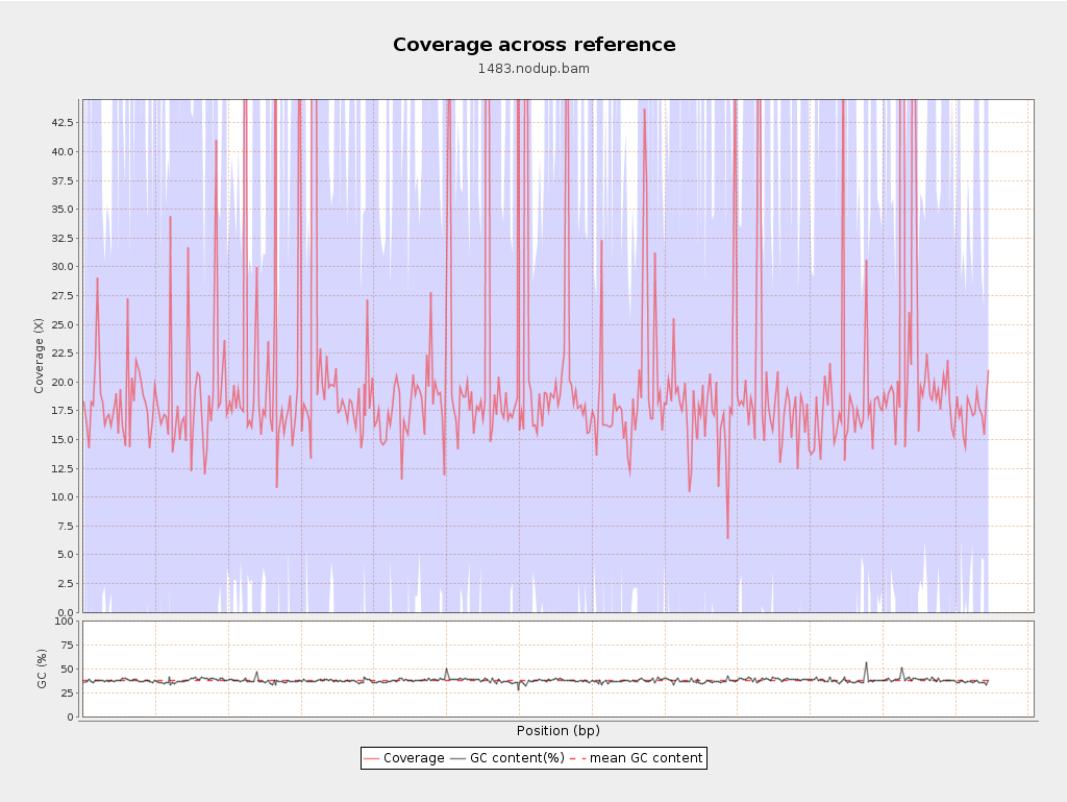
| | |
|---|---|
| General error rate | 2.3% |
| Mismatches | 135,216,452 |
| Insertions | 4,618,826 |
| Mapped reads with at least one insertion | 8.8% |
| Deletions | 4,511,716 |
| Mapped reads with at least one deletion | 8.51% |
| Homopolymer indels | 57.08% |

## 2.7. Chromosome stats

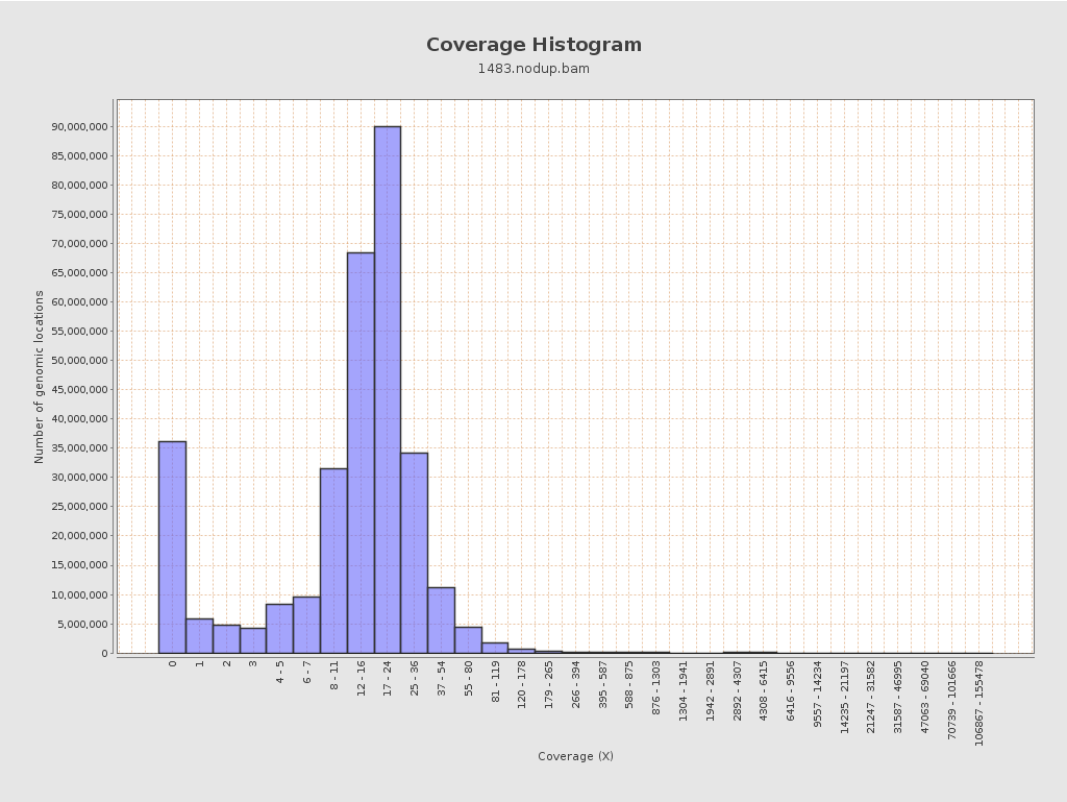
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 541574015 | 18.2199 | 73.4355 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 753320986 | 20.5836 | 185.1249 |
| LT669790.1 | 30422129 | 753802471 | 24.7781 | 233.6084 |
| LT669791.1 | 52758100 | 1061728520 | 20.1245 | 185.5611 |
| LT669792.1 | 28376109 | 604140024 | 21.2904 | 166.0053 |
| LT669793.1 | 33388210 | 633055479 | 18.9604 | 90.0033 |
| LT669794.1 | 50579949 | 962045348 | 19.0203 | 140.3046 |
| LT669795.1 | 49795044 | 1155921338 | 23.2136 | 205.6744 |

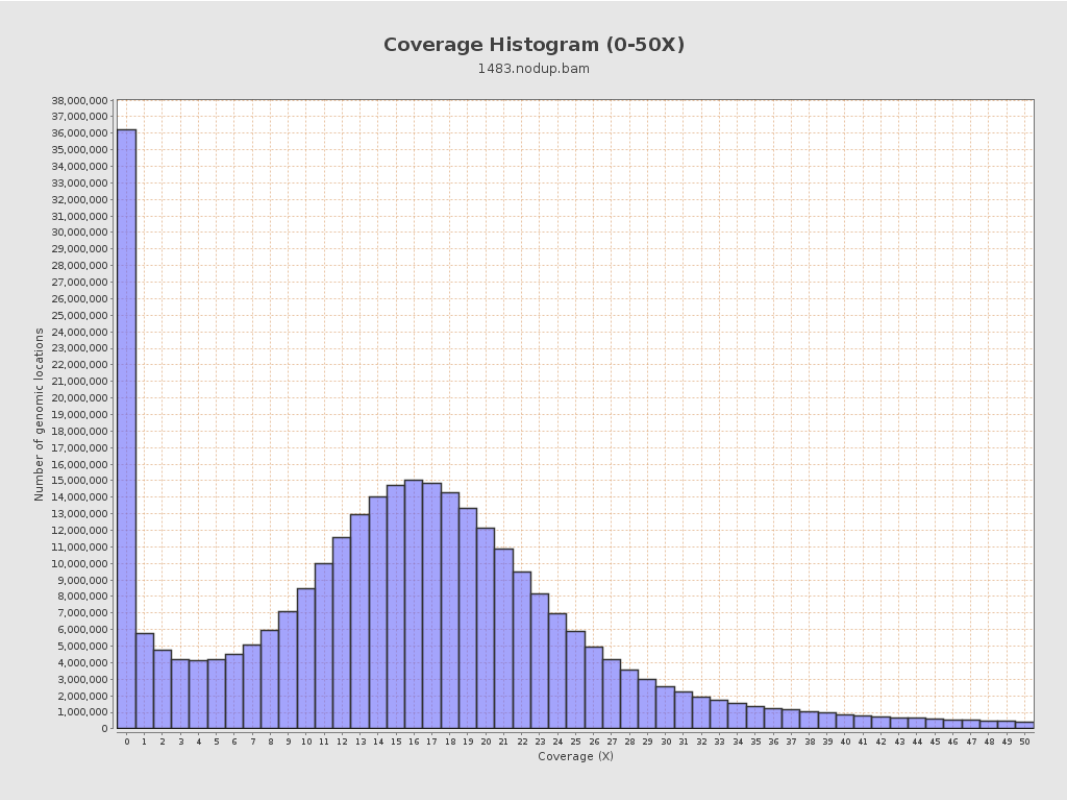
# 3. Results : Coverage across reference



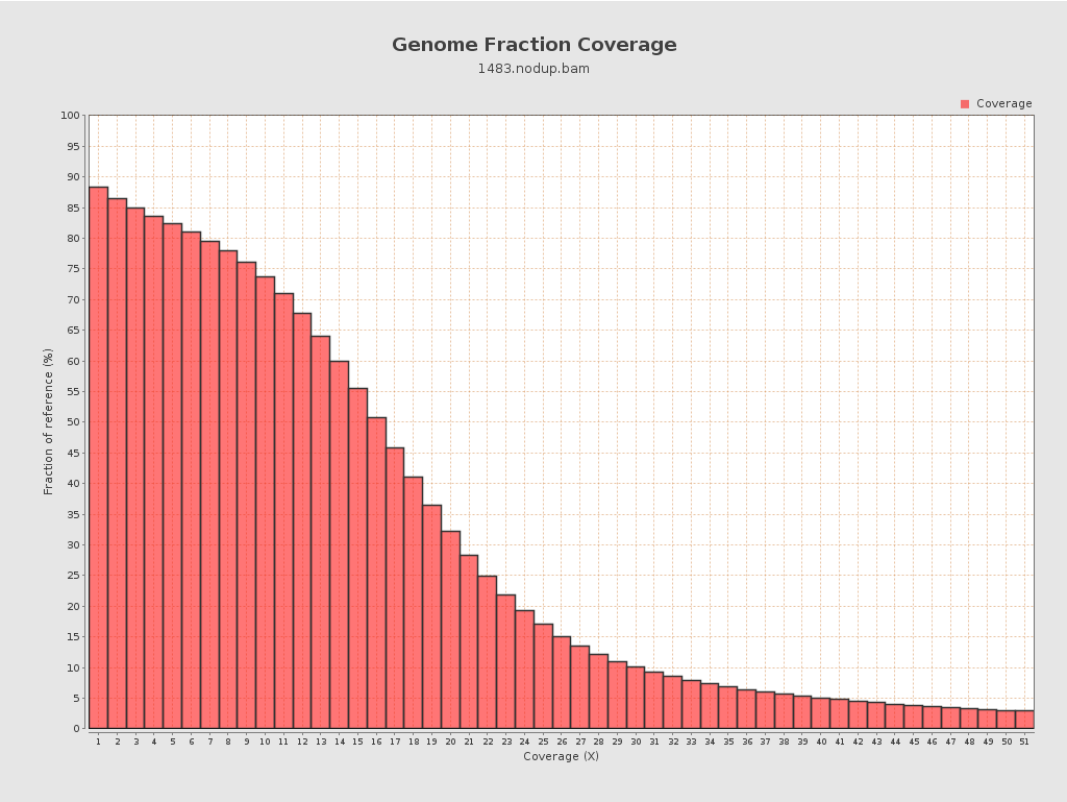
# 4. Results : Coverage Histogram



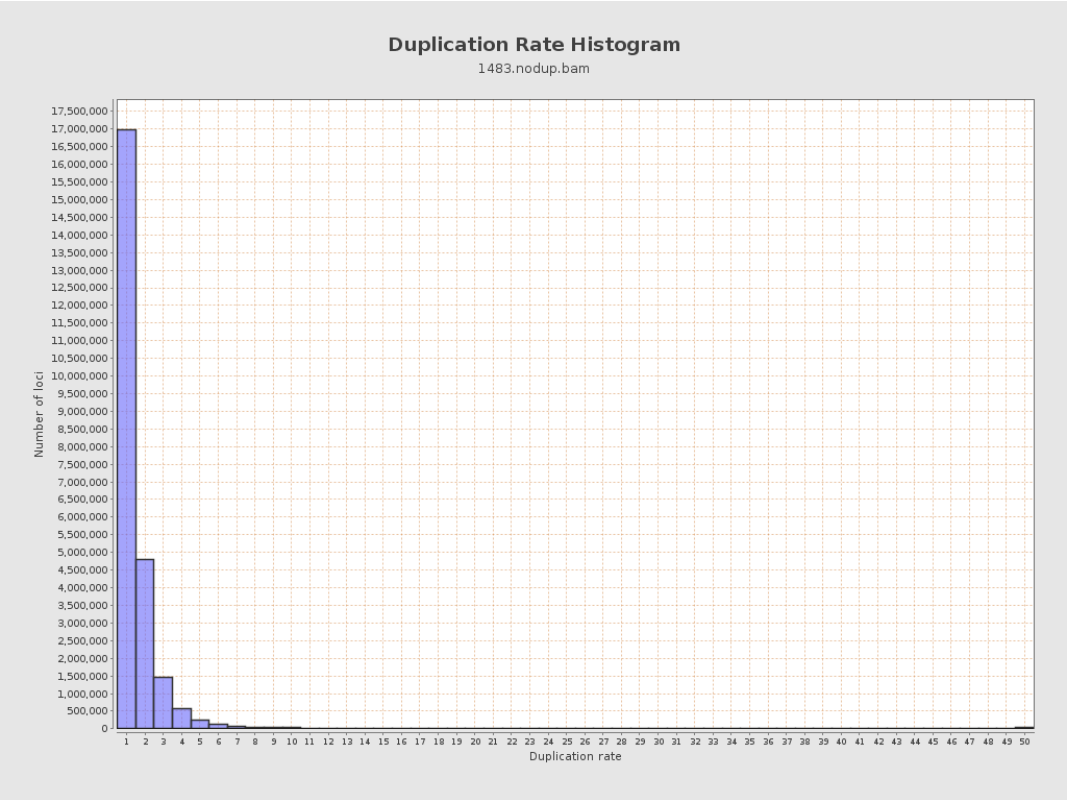
# 5. Results : Coverage Histogram (0-50X)



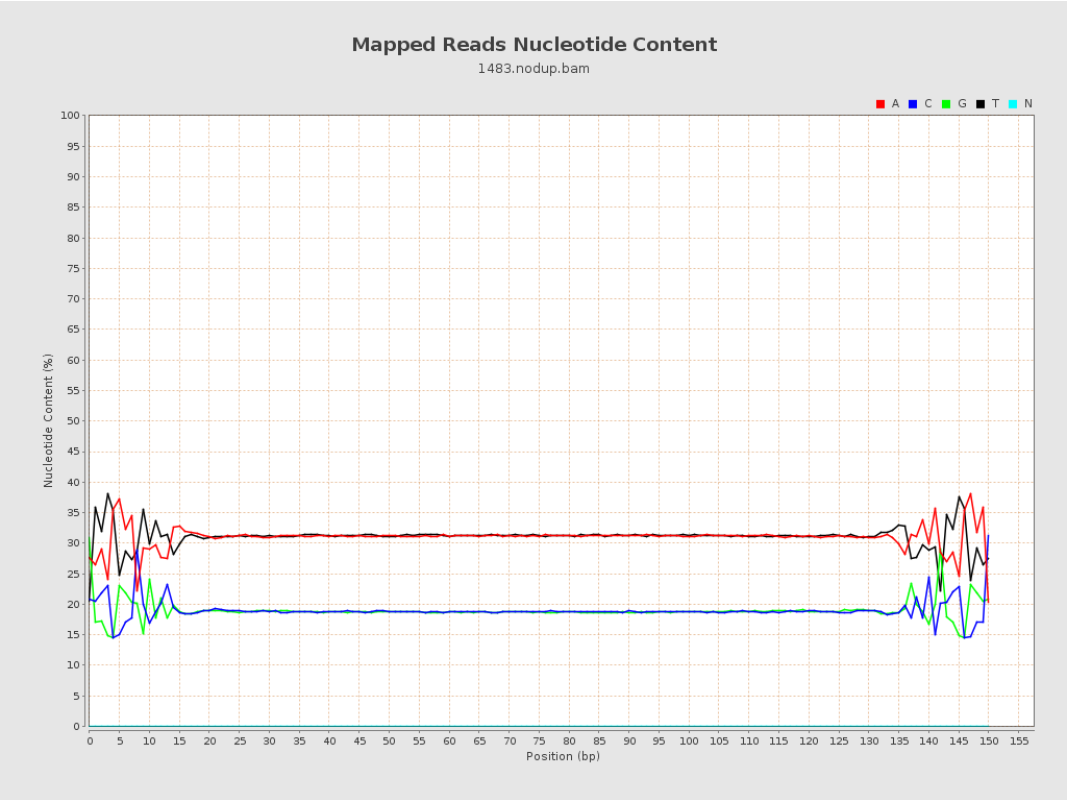
# 6. Results : Genome Fraction Coverage



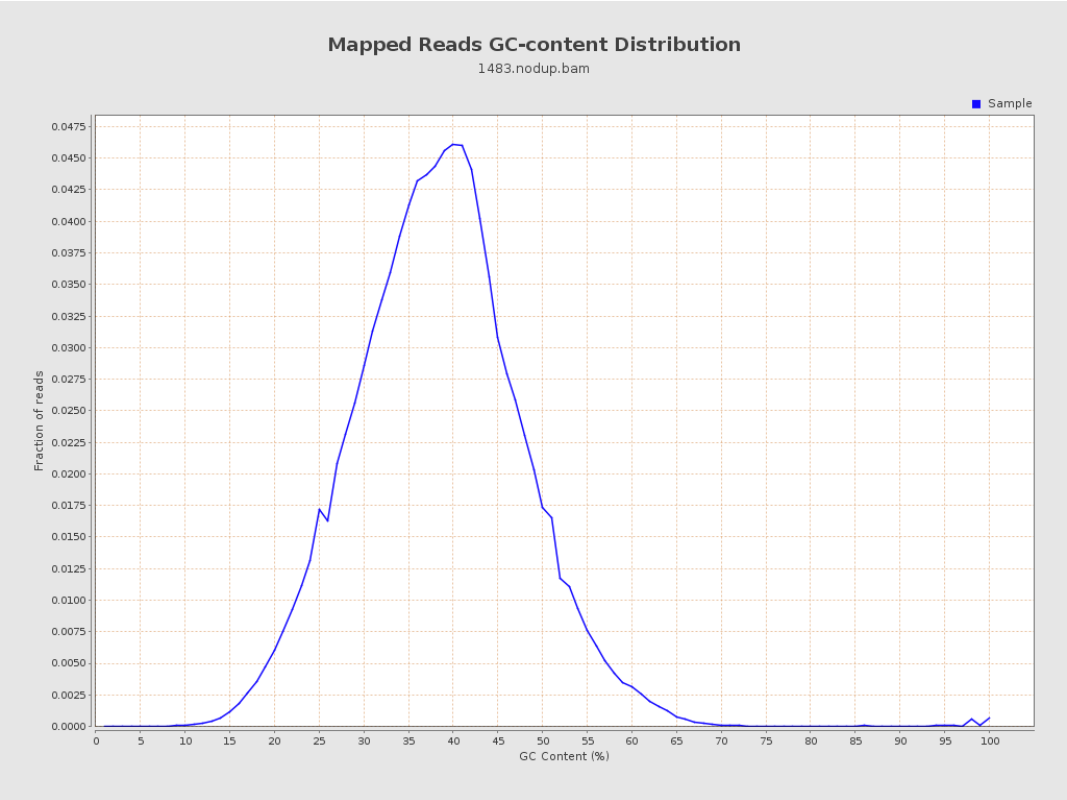
# 7. Results : Duplication Rate Histogram



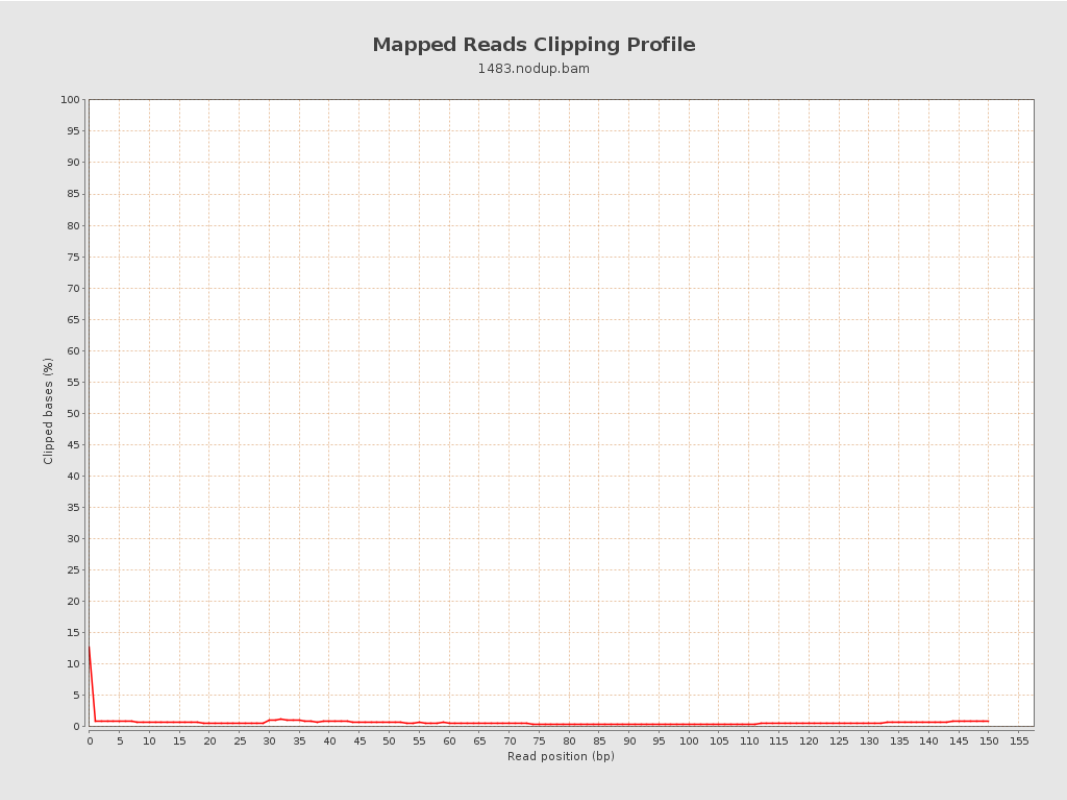
# 8. Results : Mapped Reads Nucleotide Content



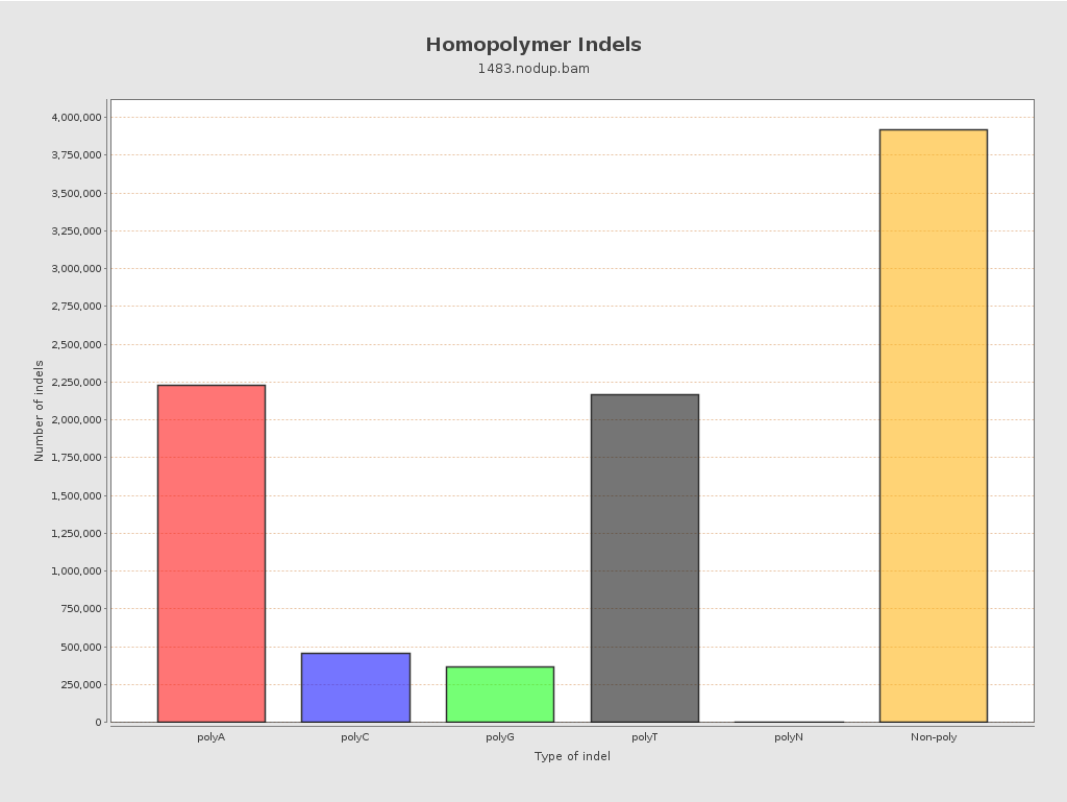
# 9. Results : Mapped Reads GC-content Distribution



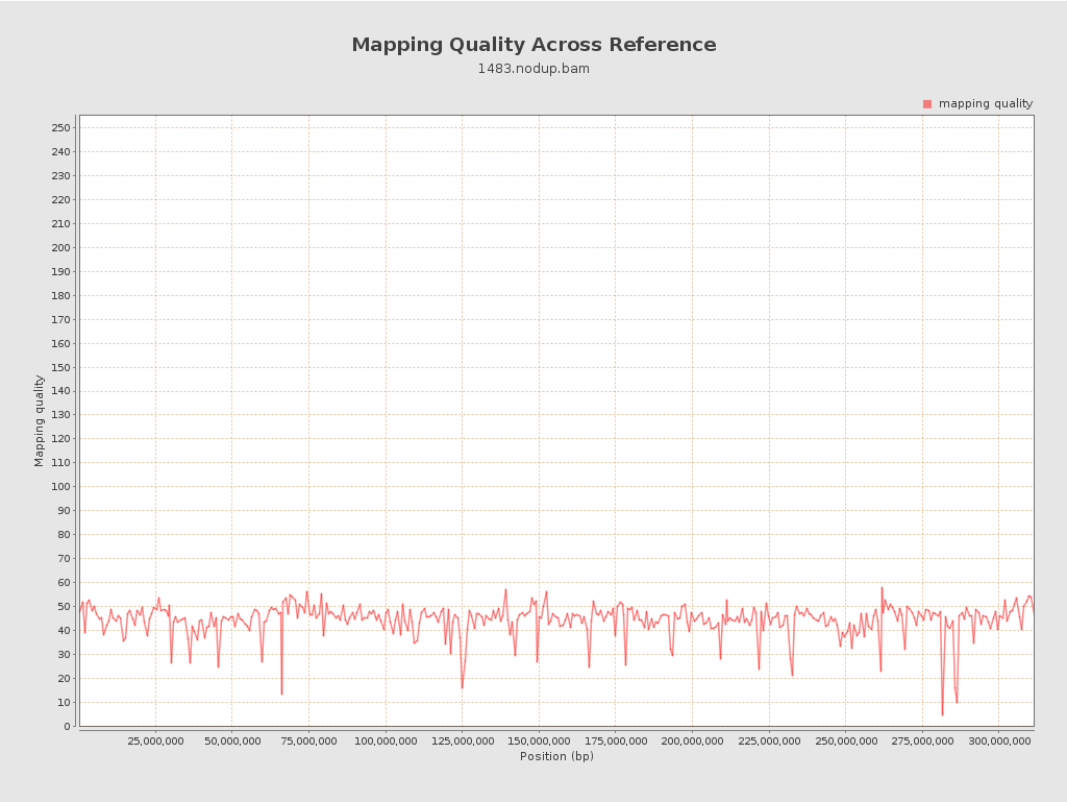
# 10. Results : Mapped Reads Clipping Profile



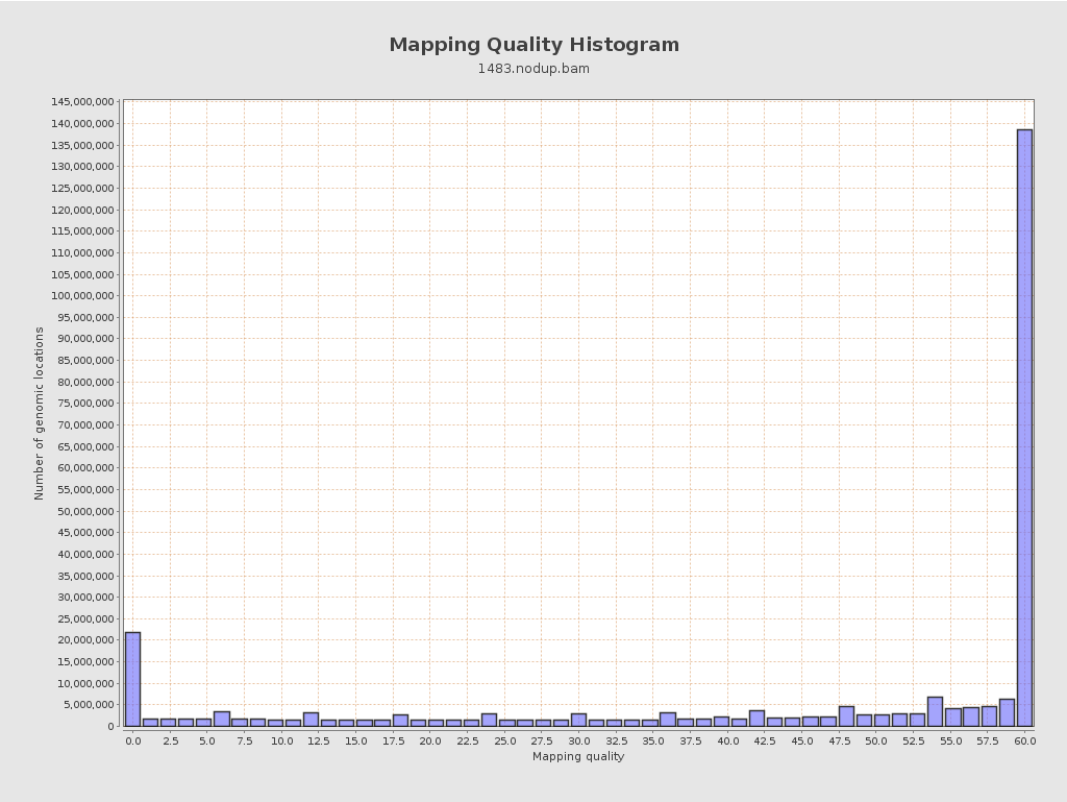
# 11. Results : Homopolymer Indels



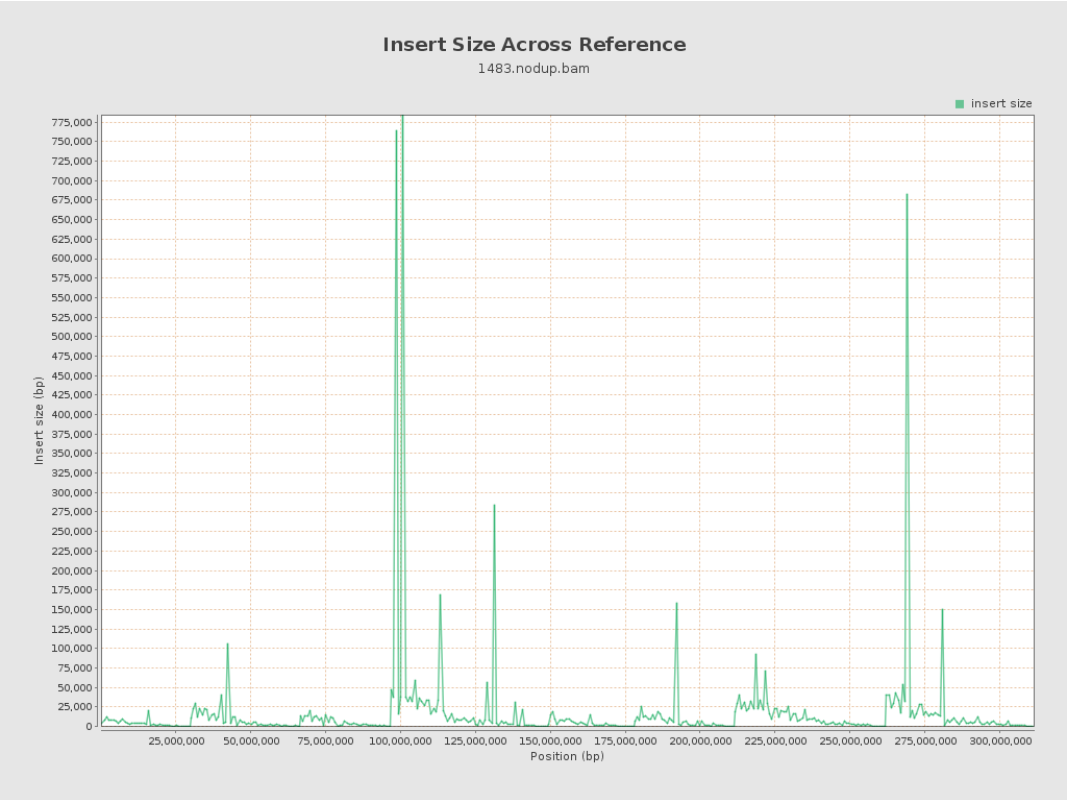
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram