# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:28:40*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/446.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/446.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_210/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_210_S291_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_210/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_210_S291_L003_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|---|---|
| Analysis date: | Mon May 29 21:28:39 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 61,151,195 |
| Mapped reads | 52,736,214 / 86.24% |
| Unmapped reads | 8,414,981 / 13.76% |
| Mapped paired reads | 52,736,214 / 86.24% |
| Mapped reads, first in pair | 26,439,113 / 43.24% |
| Mapped reads,  second in pair | 26,297,101 / 43% |
| Mapped reads, both in pair | 51,516,138 / 84.24% |
| Mapped reads, singletons | 1,220,076 / 2% |
| Read min/max/mean length | 30 / 151 / 148.2 |
| Duplicated reads (flagged) | 7,565,676 / 12.37% |
| Clipped reads | 12,553,936 / 20.53% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 2,231,620,179 / 30.78% |
| Number/percentage of C's | 1,394,139,395 / 19.23% |
| Number/percentage of T's | 2,231,662,214 / 30.78% |
| Number/percentage of G's | 1,393,770,036 / 19.22% |
| Number/percentage of N's | 26,757 / 0% |
| GC Percentage | 38.45% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 23.3287 |
| Standard Deviation | 196.0724 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.92 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 238,417.78 |
| Standard Deviation | 2,329,864.51 |
| P25/Median/P75 | 315 / 416 / 542 |

## 2.6. Mismatches and indels

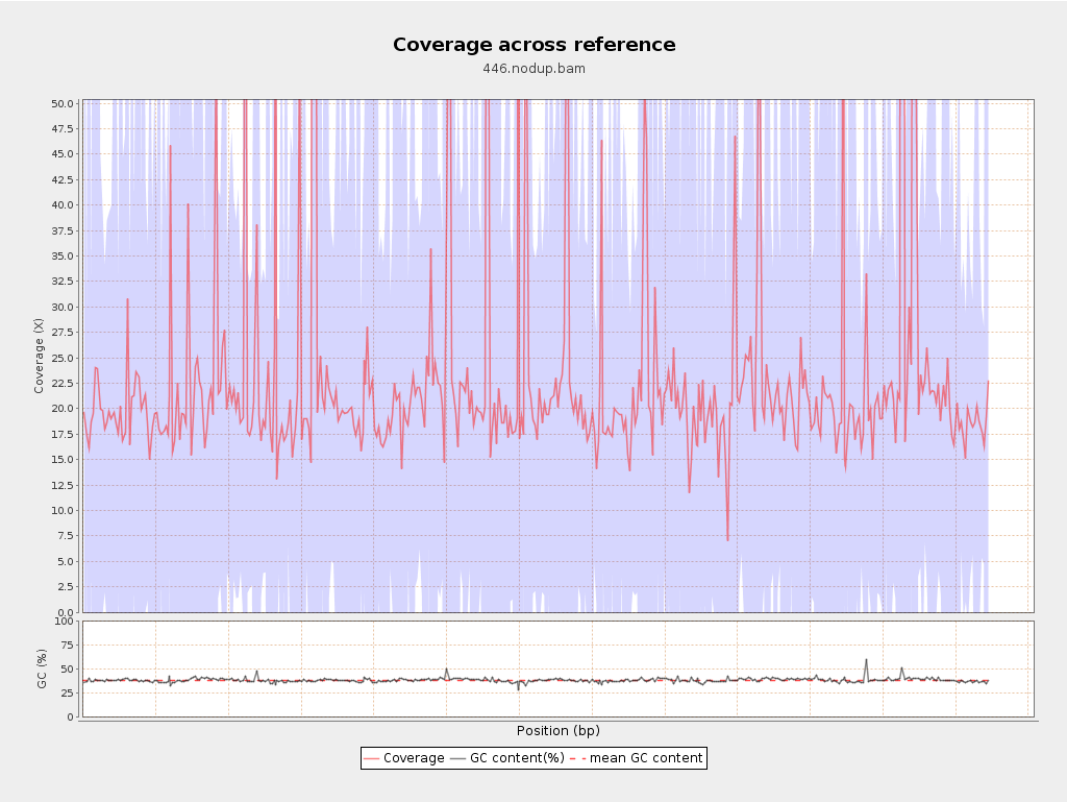
| | |
|---|---|
| General error rate | 2.35% |
| Mismatches | 156,510,572 |
| Insertions | 5,011,622 |
| Mapped reads with at least one insertion | 8.52% |
| Deletions | 5,076,702 |
| Mapped reads with at least one deletion | 8.54% |
| Homopolymer indels | 56.63% |

## 2.7. Chromosome stats

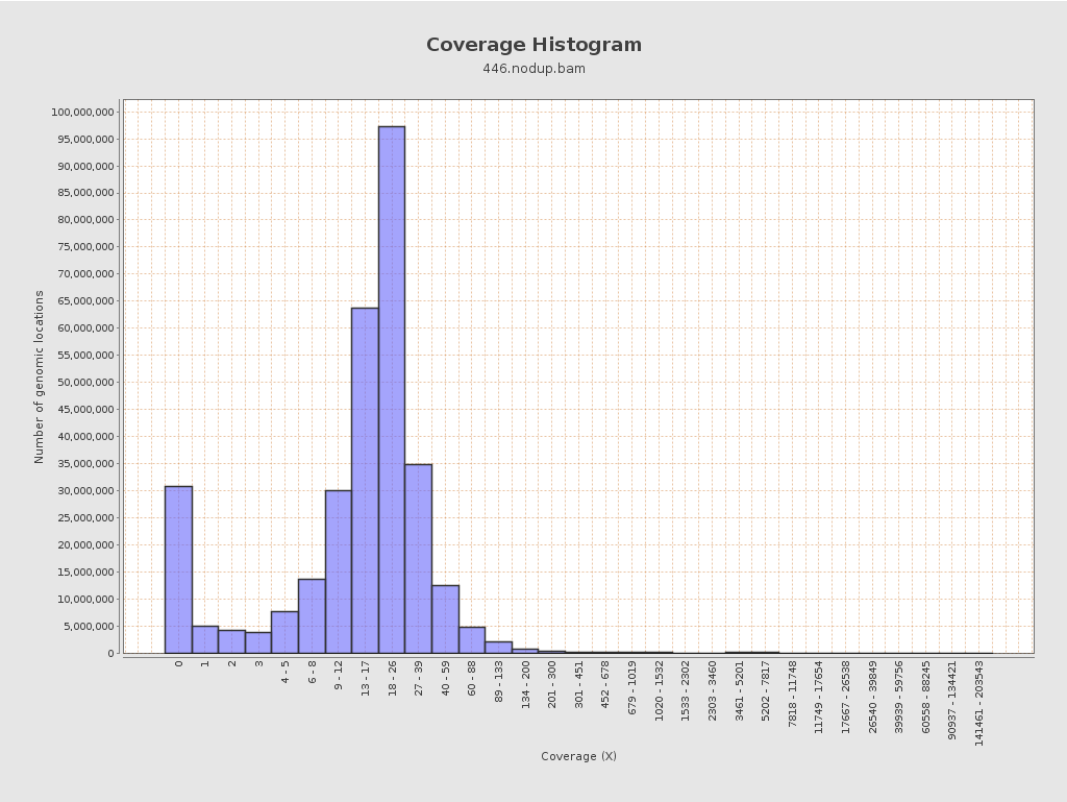
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 581973916 | 19.579 | 73.9565 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 872099995 | 23.8291 | 213.0671 |
| LT669790.1 | 30422129 | 780480505 | 25.655 | 212.7939 |
| LT669791.1 | 52758100 | 1196535129 | 22.6796 | 193.955 |
| LT669792.1 | 28376109 | 660493667 | 23.2764 | 188.2259 |
| LT669793.1 | 33388210 | 715709145 | 21.436 | 102.6007 |
| LT669794.1 | 50579949 | 1131885766 | 22.3782 | 182.1396 |
| LT669795.1 | 49795044 | 1331038805 | 26.7303 | 274.7337 |

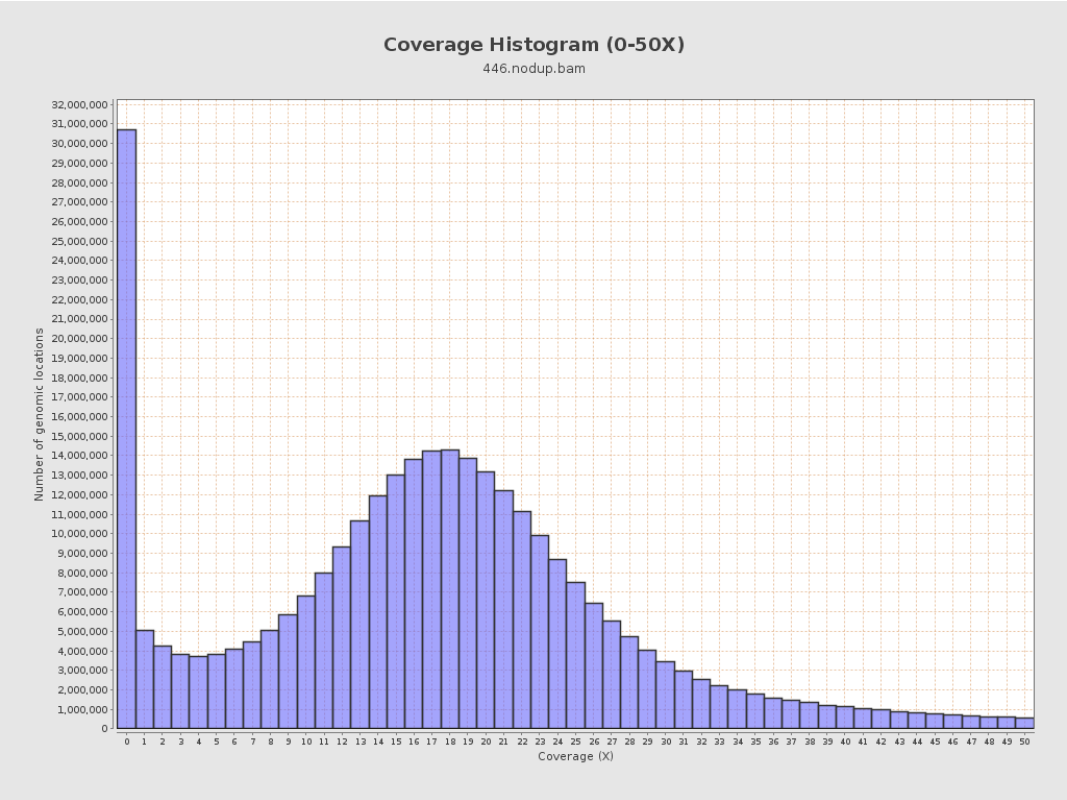
# 3. Results : Coverage across reference



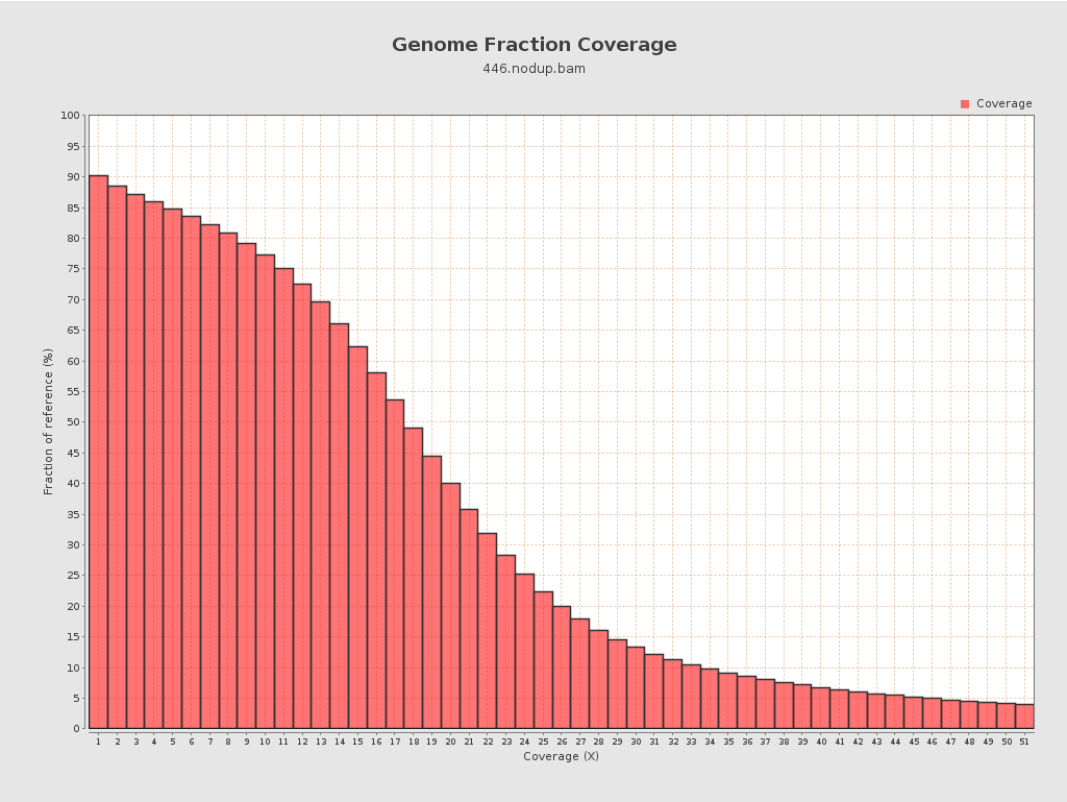
# 4. Results : Coverage Histogram



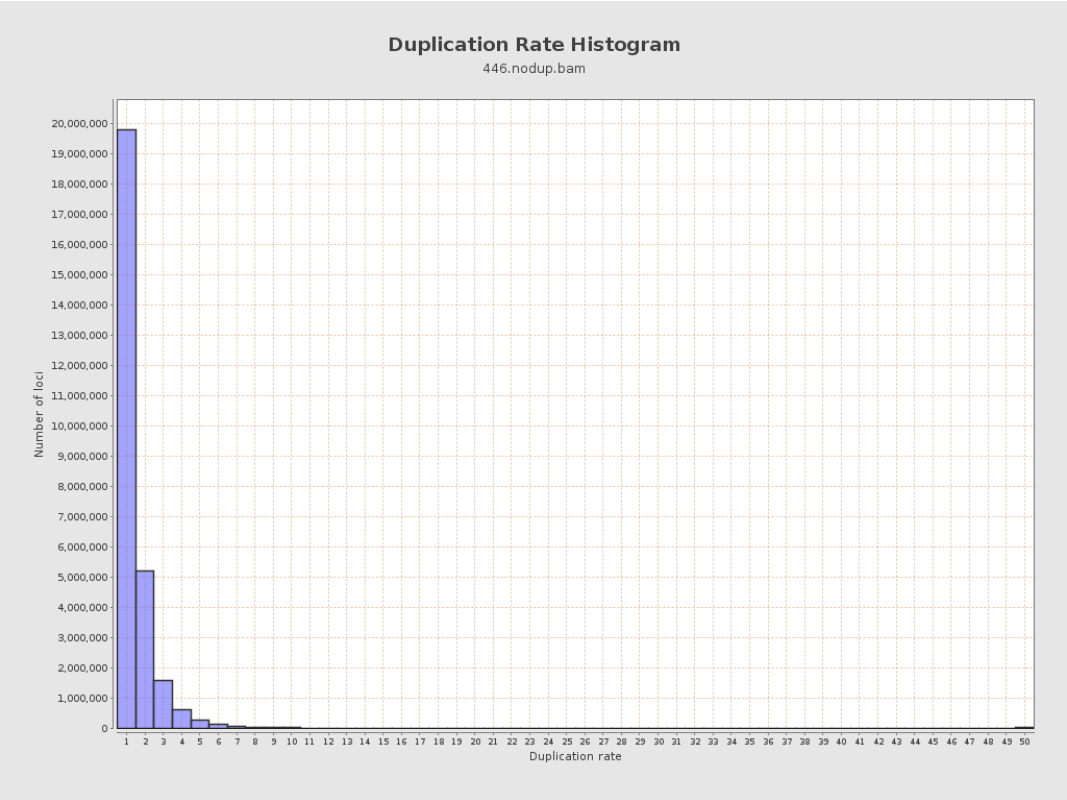
# 5. Results : Coverage Histogram (0-50X)



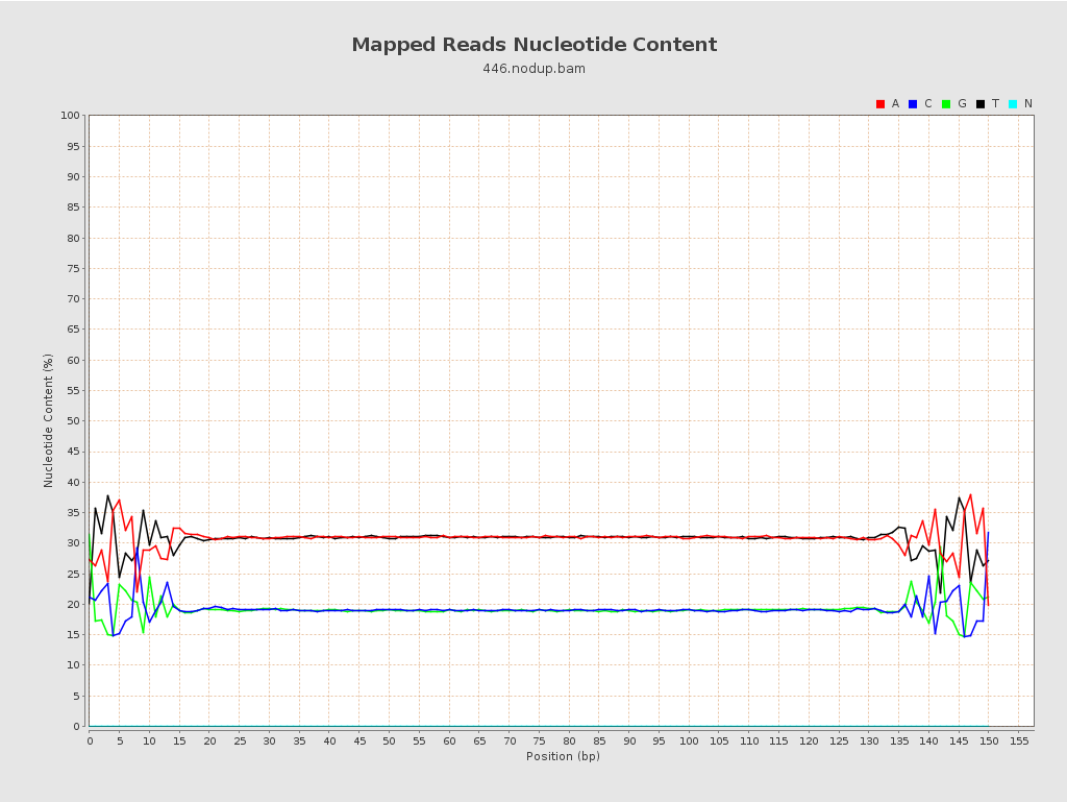
# 6. Results : Genome Fraction Coverage



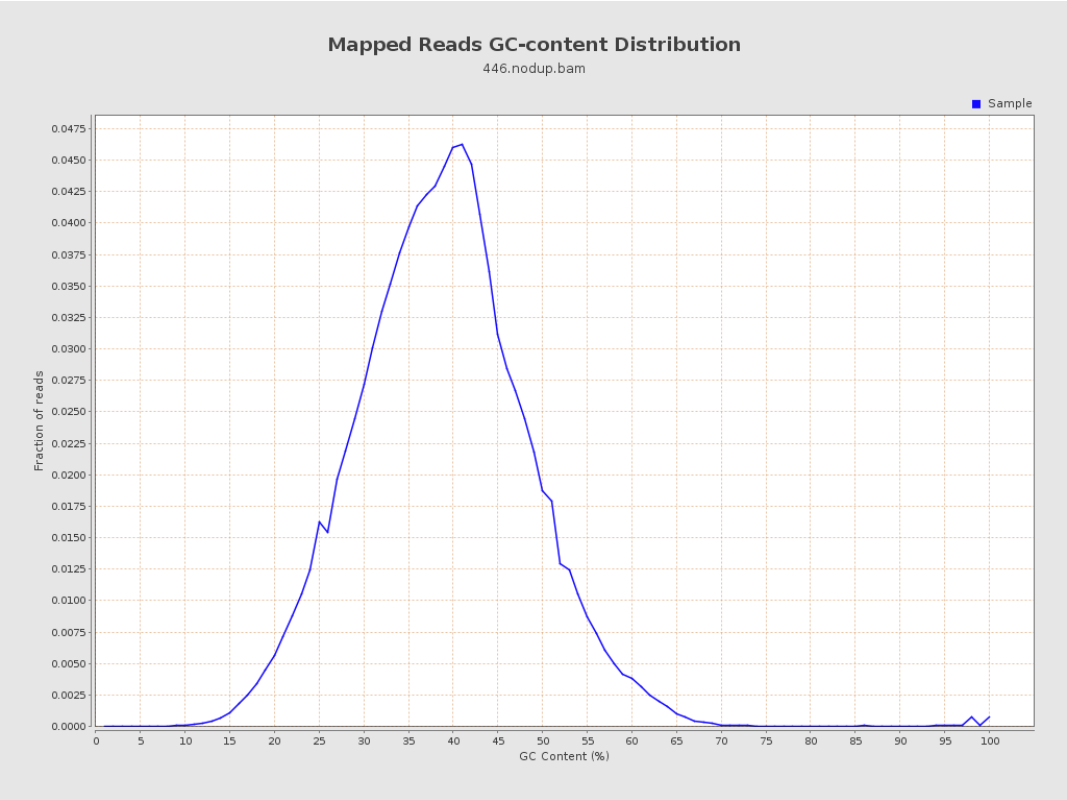
# 7. Results : Duplication Rate Histogram



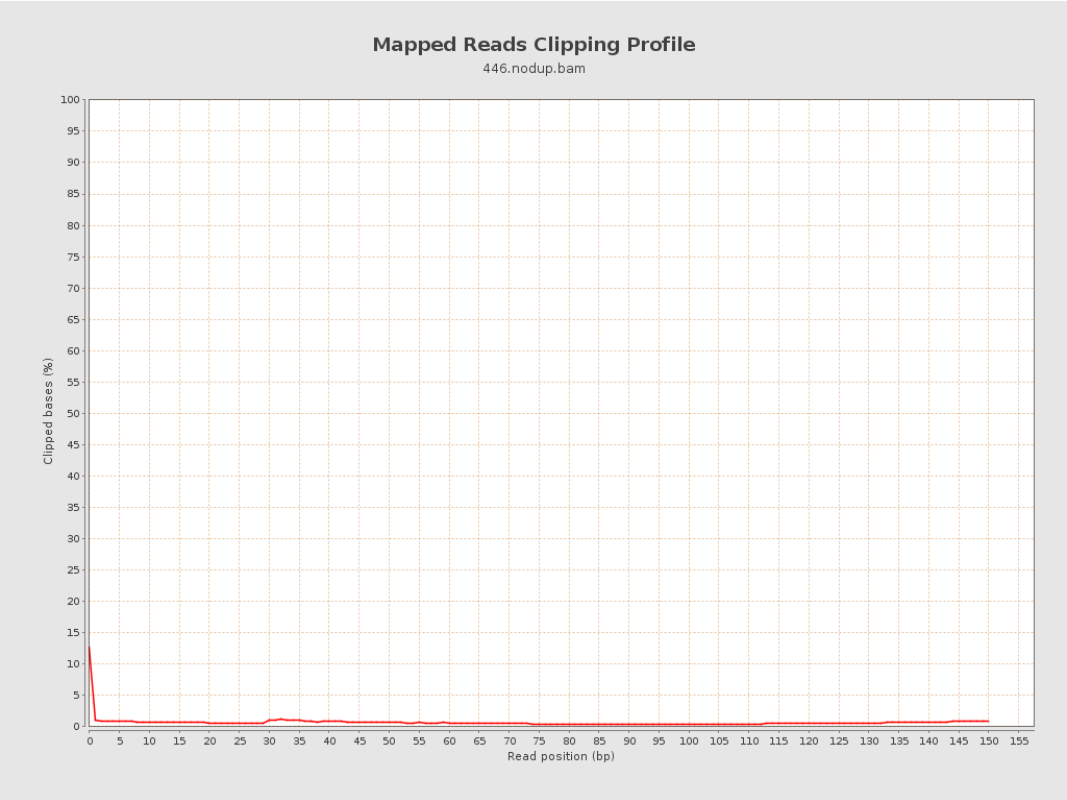
# 8. Results : Mapped Reads Nucleotide Content



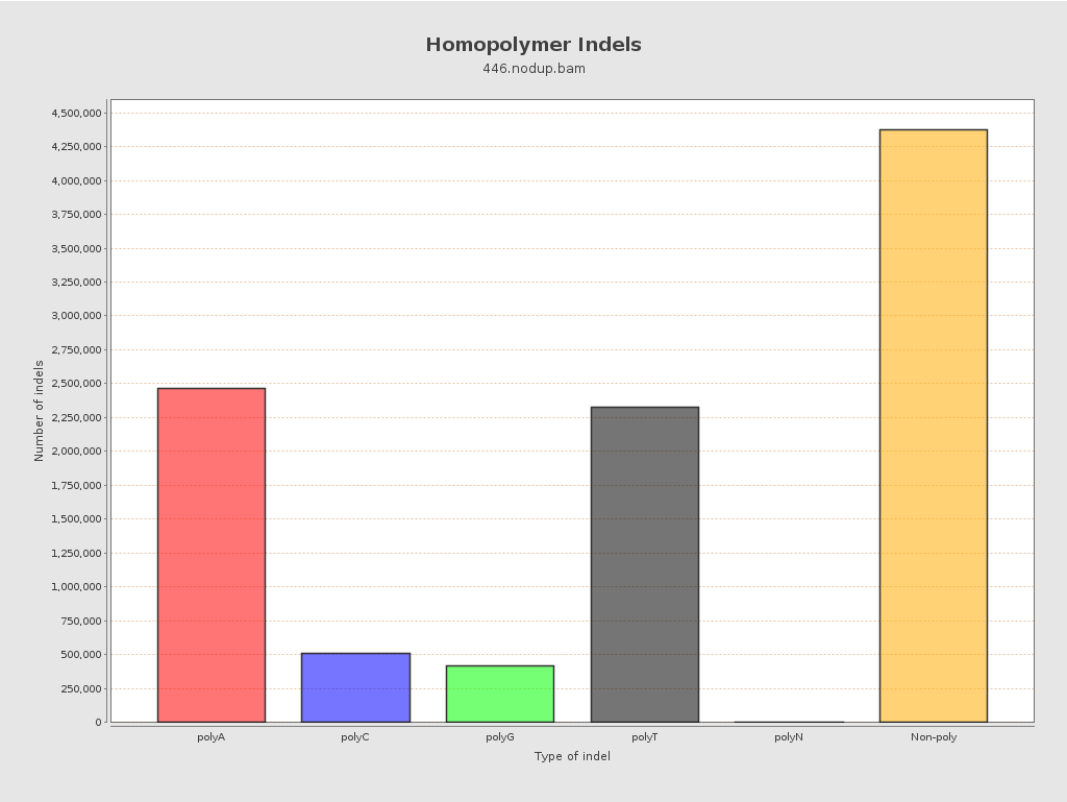
# 9. Results : Mapped Reads GC-content Distribution



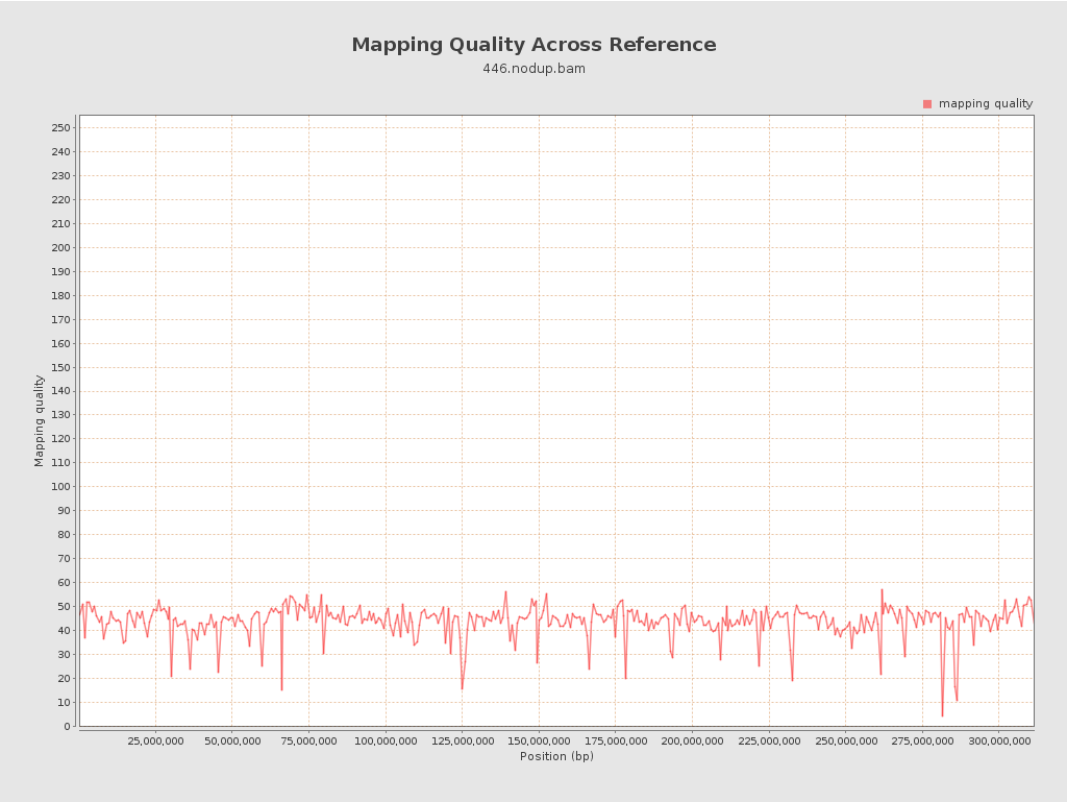
# 10. Results : Mapped Reads Clipping Profile



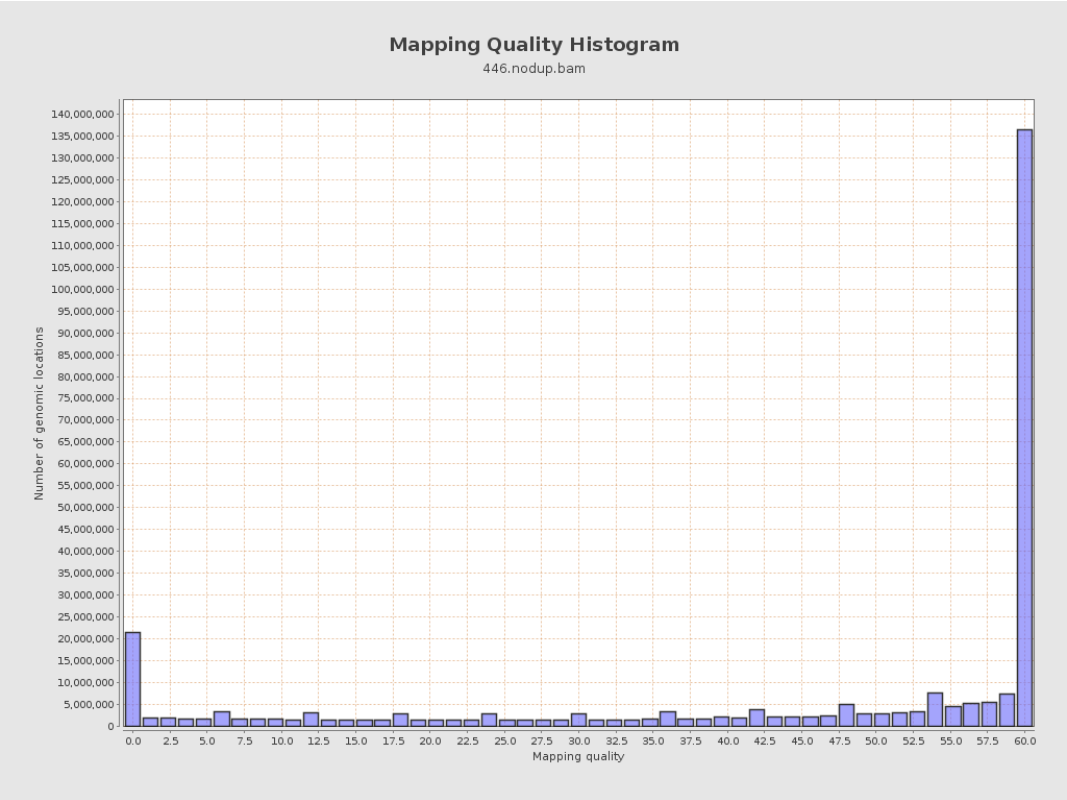
# 11. Results : Homopolymer Indels



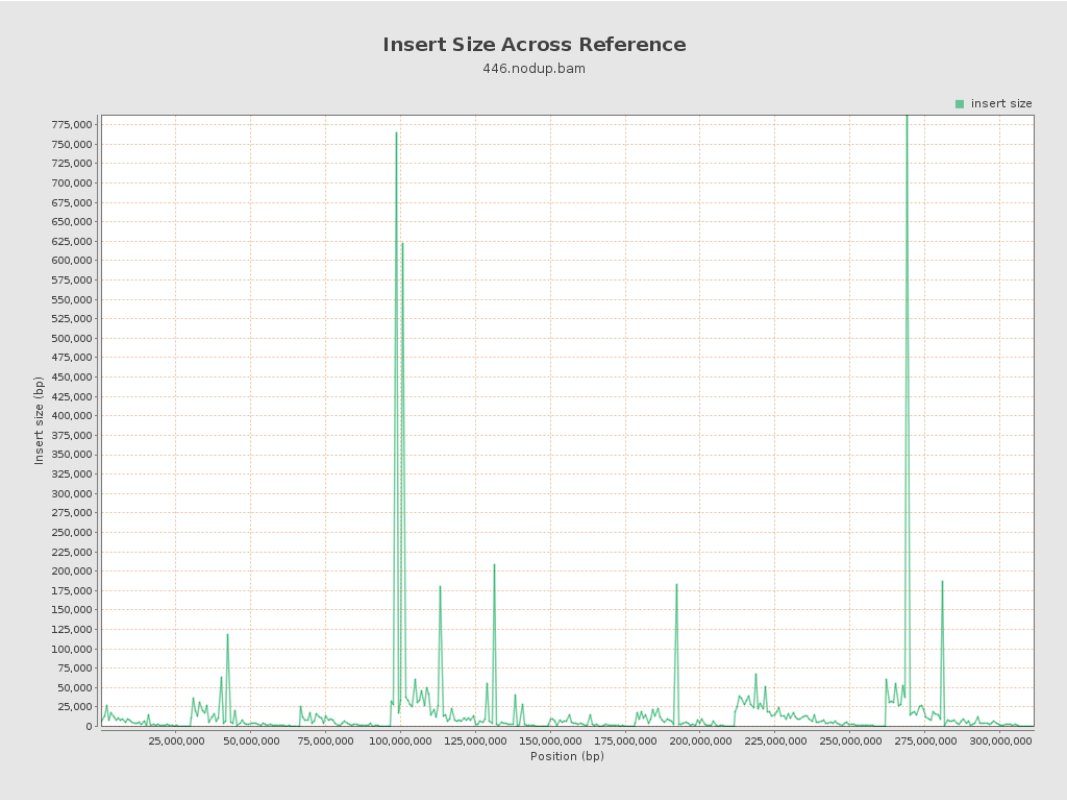
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram