

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:36:35*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/137
3
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1373 .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_457/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_457_S432_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_457/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_457_S432_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:36:34 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	77,058,592
Mapped reads	73,035,130 / 94.78%
Unmapped reads	4,023,462 / 5.22%
Mapped paired reads	73,035,130 / 94.78%
Mapped reads, first in pair	36,549,324 / 47.43%
Mapped reads, second in pair	36,485,806 / 47.35%
Mapped reads, both in pair	71,695,329 / 93.04%
Mapped reads, singletons	1,339,801 / 1.74%
Read min/max/mean length	30 / 151 / 148.07
Duplicated reads (flagged)	11,469,899 / 14.88%
Clipped reads	15,812,101 / 20.52%

### 2.2. ACGT Content

Number/percentage of A's	3,130,281,711 / 30.79%
Number/percentage of C's	1,955,285,929 / 19.23%
Number/percentage of T's	3,135,801,950 / 30.84%
Number/percentage of G's	1,946,379,429 / 19.14%
Number/percentage of N's	34,205 / 0%
GC Percentage	38.37%

### 2.3. Coverage

Mean	32.7126
Standard Deviation	242.5756

## 2.4. Mapping Quality

Mean Mapping Quality	43.86
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## 2.5. Insert size

Mean	233,489.25
Standard Deviation	2,278,986.22
P25/Median/P75	340 / 445 / 584

## 2.6. Mismatches and indels

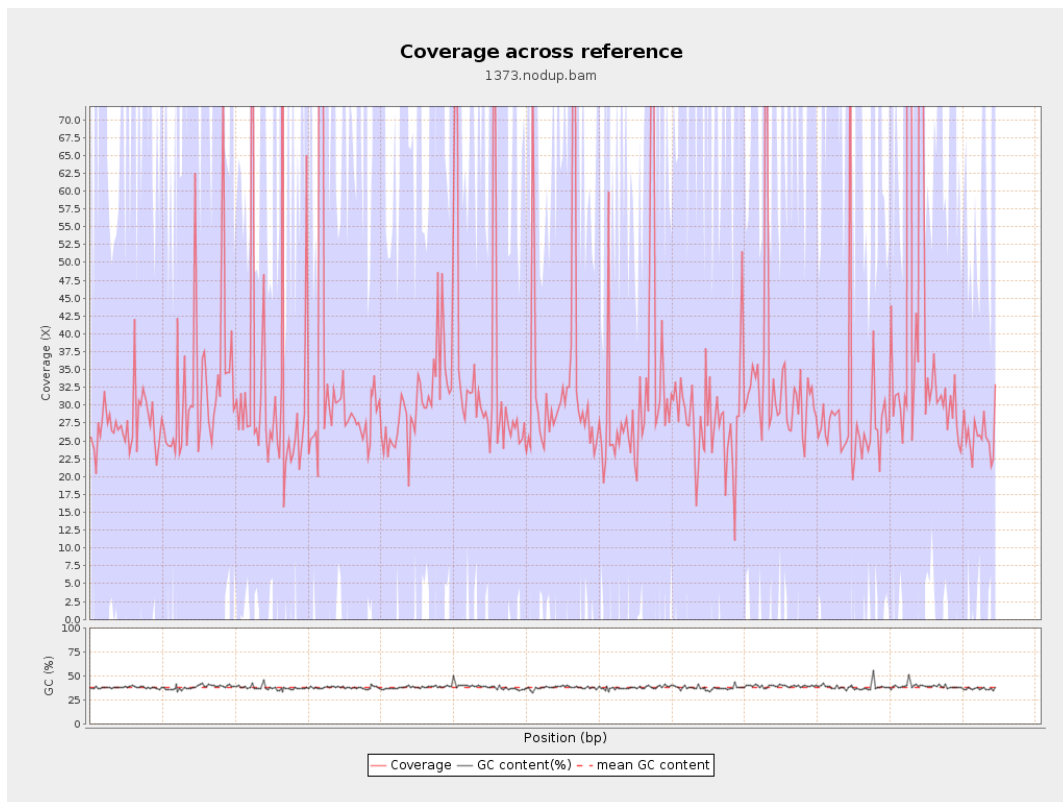
General error rate	2.28%
Mismatches	213,392,203
Insertions	6,782,773
Mapped reads with at least one insertion	8.36%
Deletions	7,042,953
Mapped reads with at least one deletion	8.57%
Homopolymer indels	56.45%

## 2.7. Chromosome stats

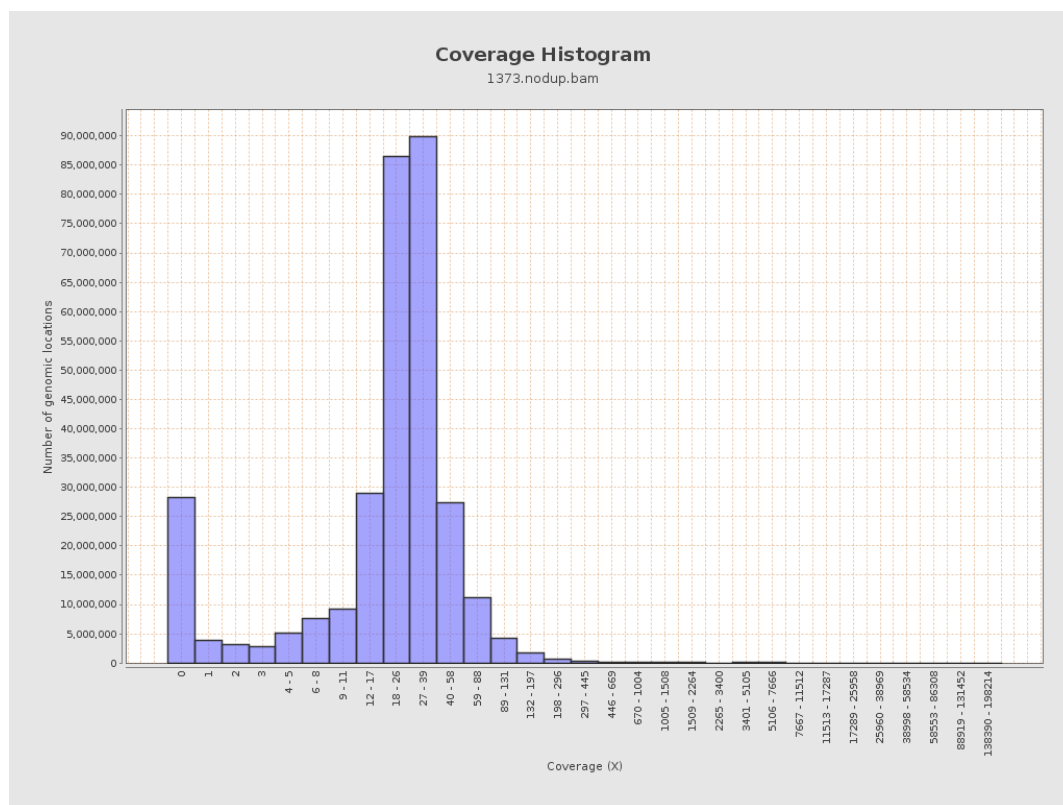
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	801986621	26.9808	69.9537

LT669789.1	36598175	1237984063	33.8264	270.7444
LT669790.1	30422129	1025153907	33.6976	226.4161
LT669791.1	52758100	1696837447	32.1626	200.395
LT669792.1	28376109	897979777	31.6456	255.9534
LT669793.1	33388210	1029309603	30.8285	178.2163
LT669794.1	50579949	1583769288	31.3122	214.3412
LT669795.1	49795044	1921601473	38.5902	363.6592

### 3. Results : Coverage across reference

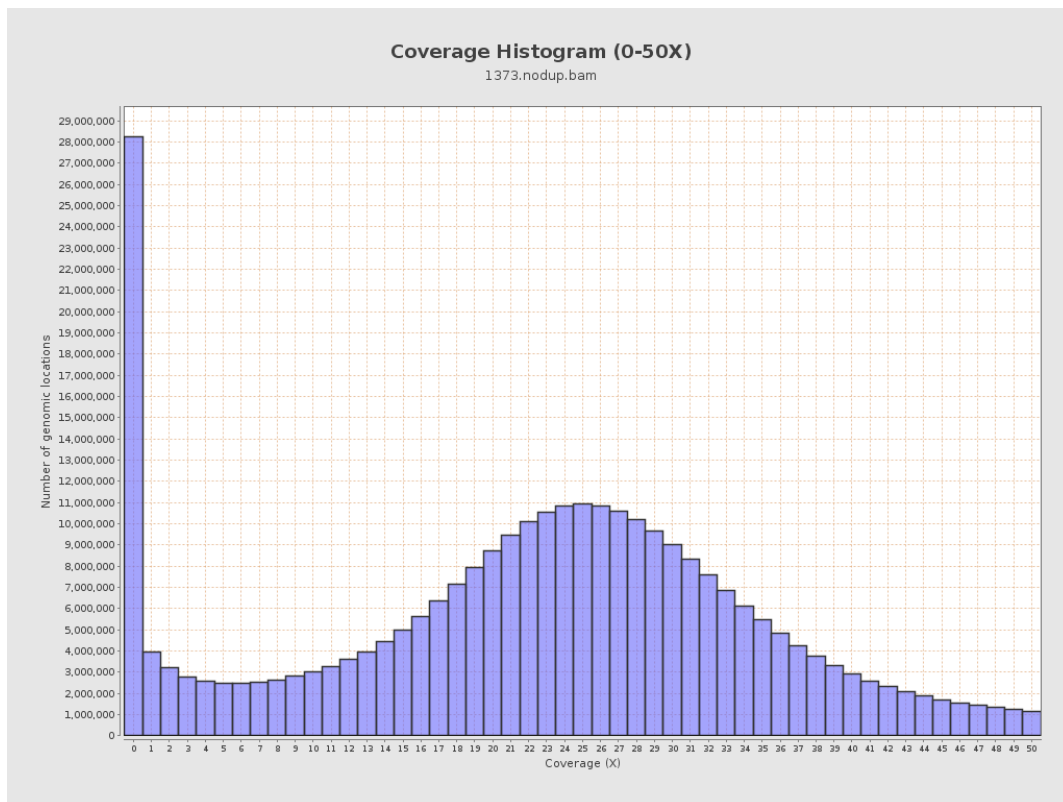


## 4. Results : Coverage Histogram

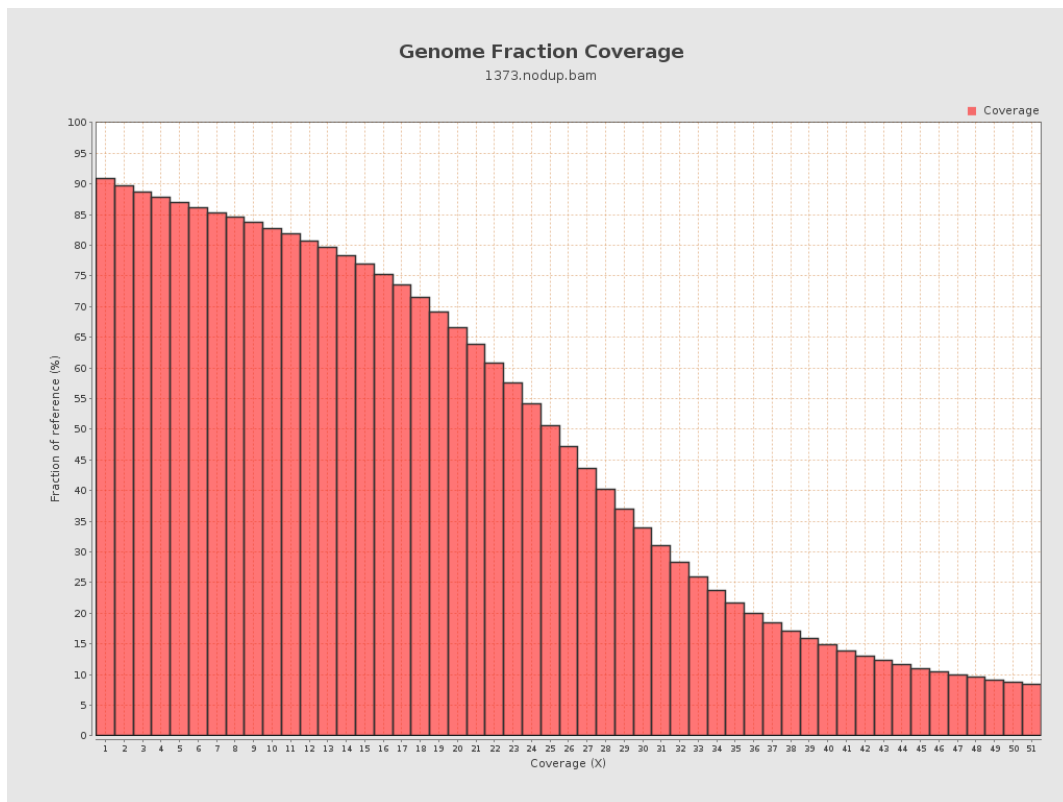




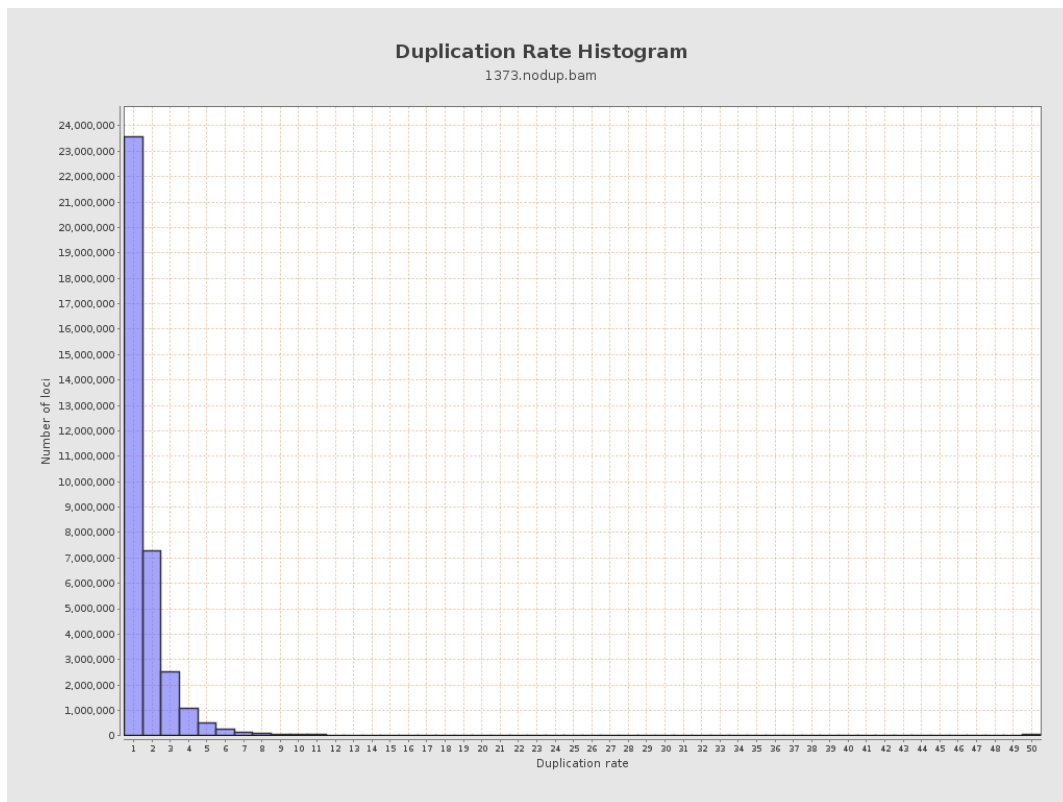
## 5. Results : Coverage Histogram (0-50X)



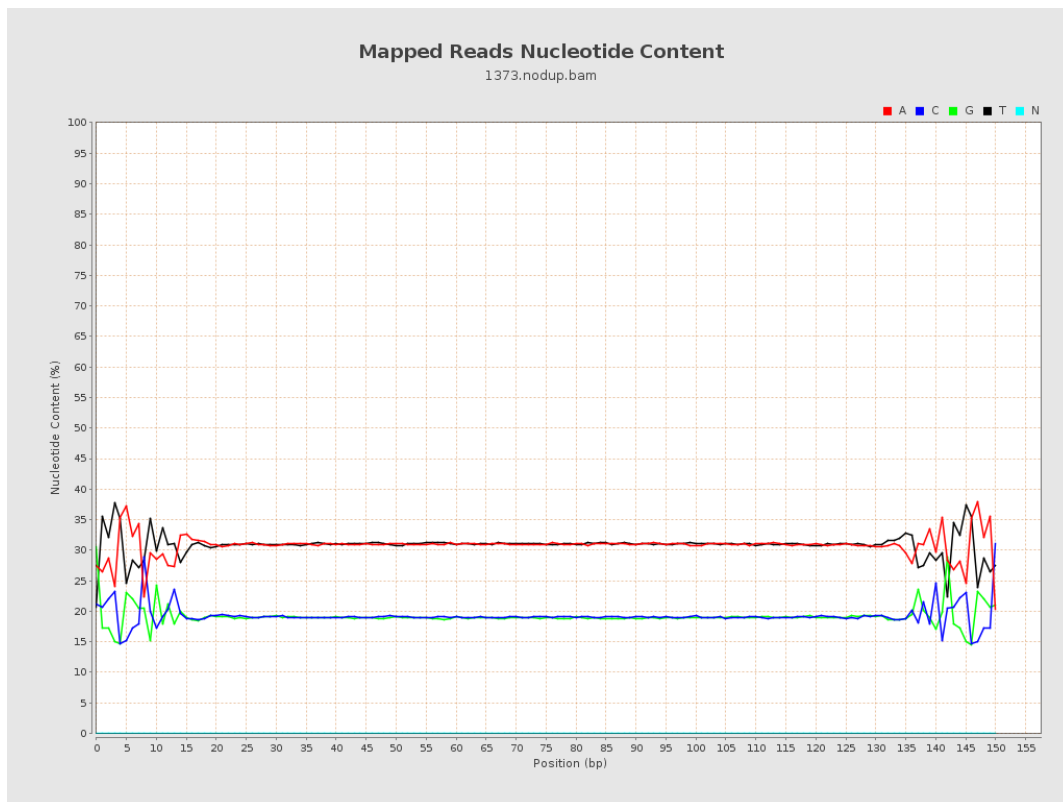
## 6. Results : Genome Fraction Coverage



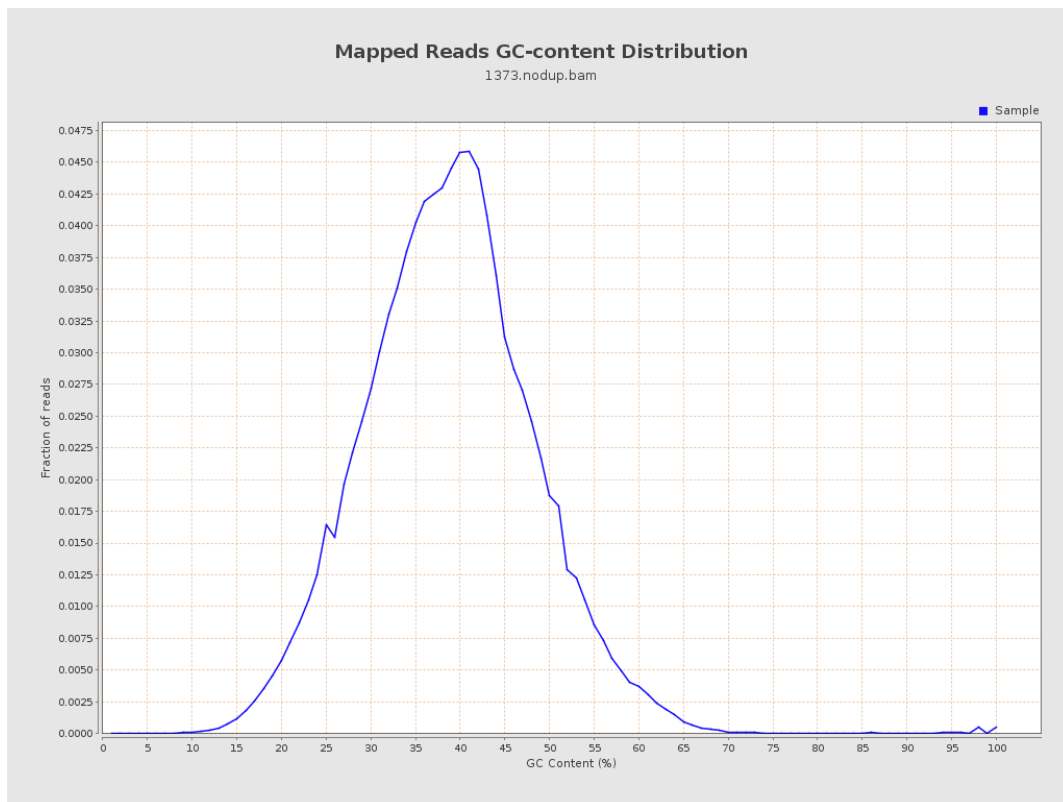
## 7. Results : Duplication Rate Histogram



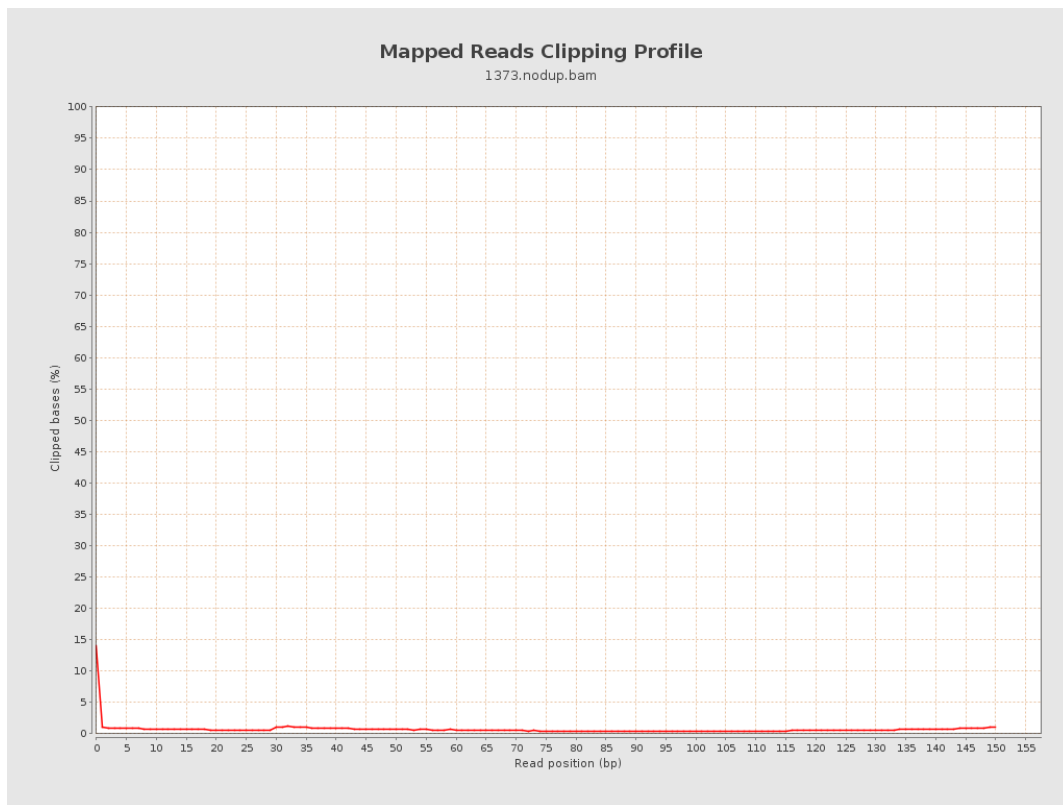
## 8. Results : Mapped Reads Nucleotide Content



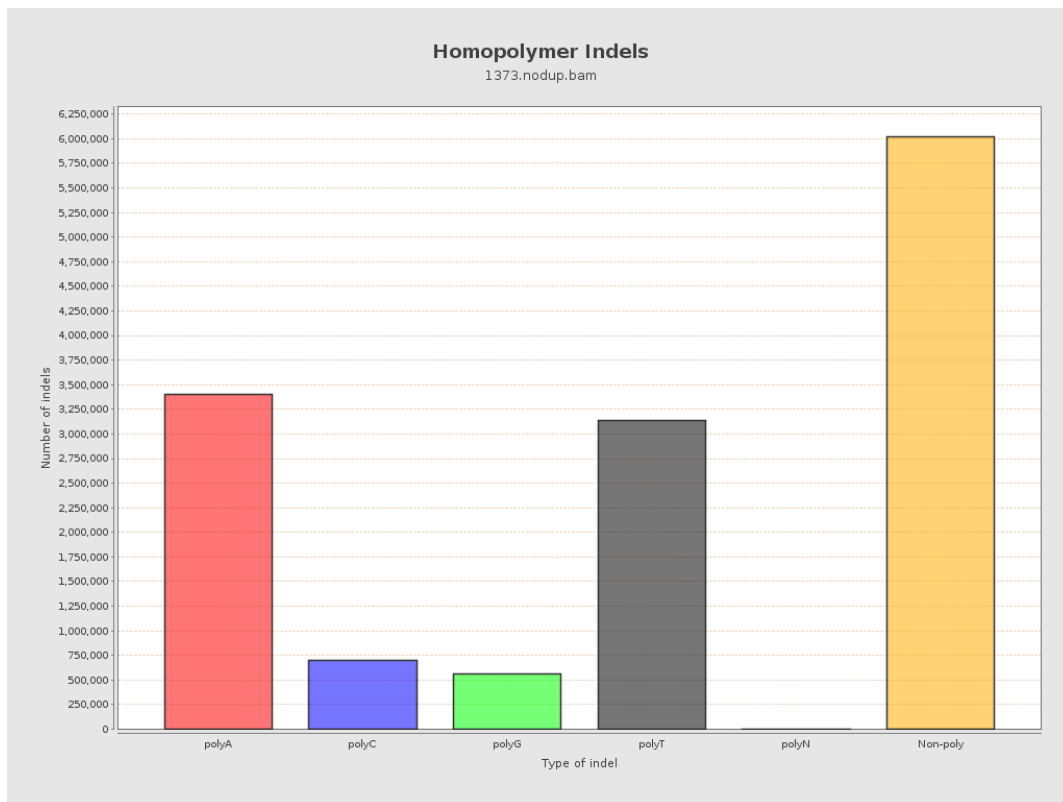
## 9. Results : Mapped Reads GC-content Distribution



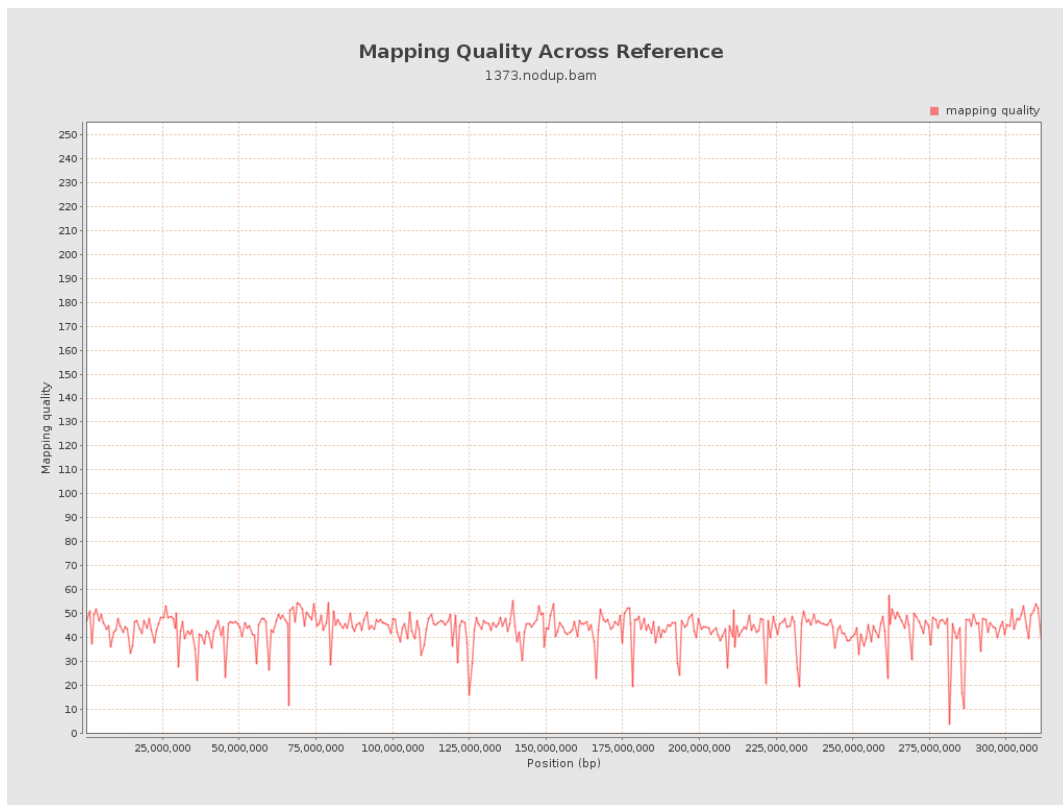
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

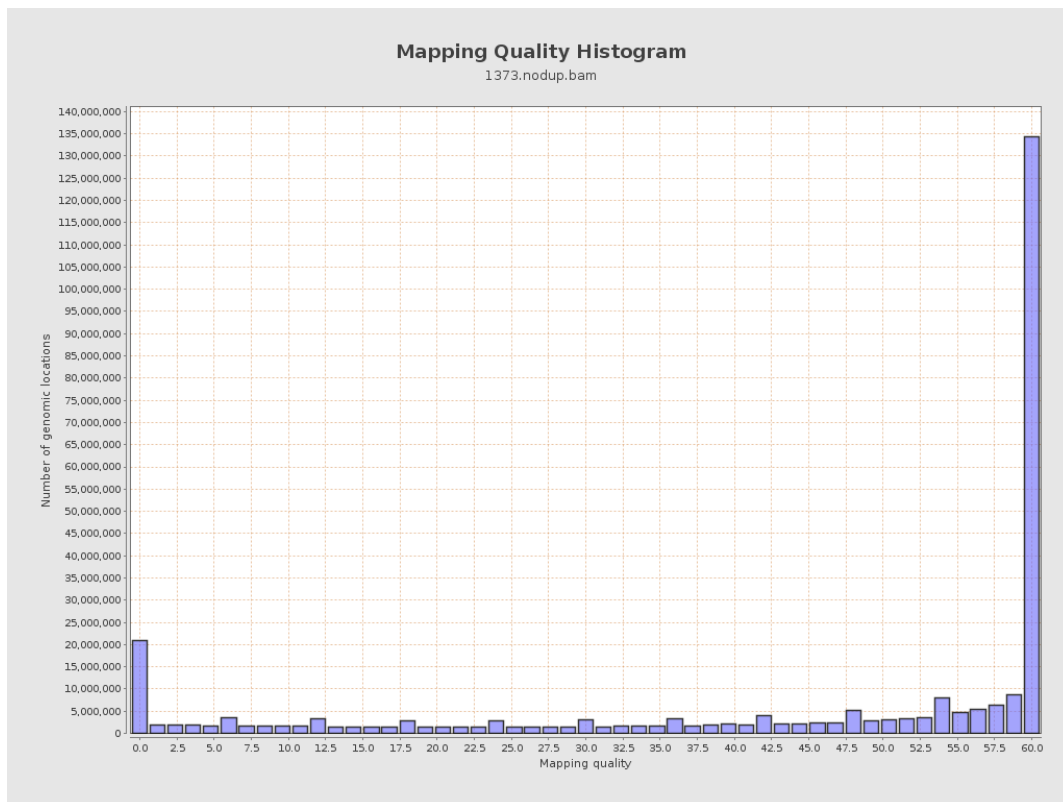


## 12. Results : Mapping Quality Across Reference

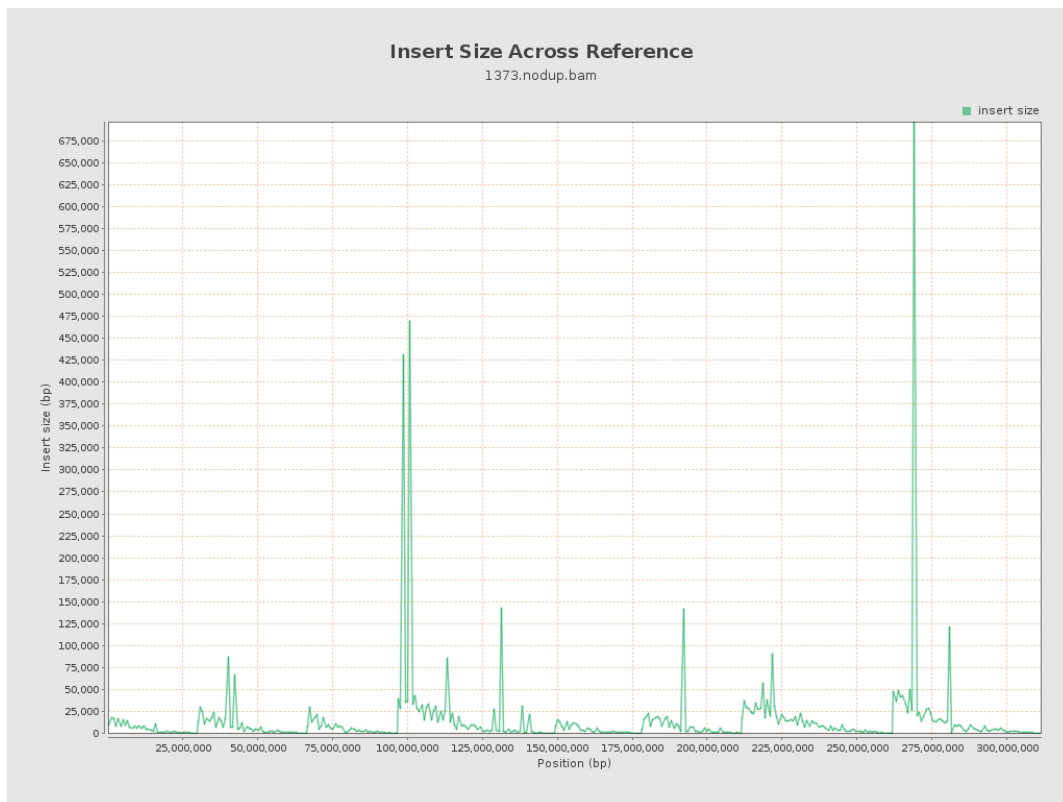




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

