

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:31:55*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/138
1
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1381.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_418/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_418_S393_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_418/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_418_S393_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:31:54 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	66,691,602
Mapped reads	61,983,630 / 92.94%
Unmapped reads	4,707,972 / 7.06%
Mapped paired reads	61,983,630 / 92.94%
Mapped reads, first in pair	31,051,248 / 46.56%
Mapped reads, second in pair	30,932,382 / 46.38%
Mapped reads, both in pair	60,415,618 / 90.59%
Mapped reads, singletons	1,568,012 / 2.35%
Read min/max/mean length	30 / 151 / 148.07
Duplicated reads (flagged)	11,207,492 / 16.8%
Clipped reads	14,255,894 / 21.38%

### 2.2. ACGT Content

Number/percentage of A's	2,625,568,336 / 30.66%
Number/percentage of C's	1,658,944,879 / 19.37%
Number/percentage of T's	2,629,625,999 / 30.71%
Number/percentage of G's	1,648,504,154 / 19.25%
Number/percentage of N's	29,580 / 0%
GC Percentage	38.63%

### 2.3. Coverage

Mean	27.5454
Standard Deviation	267.63

## 2.4. Mapping Quality

Mean Mapping Quality	43.31
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## 2.5. Insert size

Mean	252,482.66
Standard Deviation	2,380,307.73
P25/Median/P75	353 / 460 / 599

## 2.6. Mismatches and indels

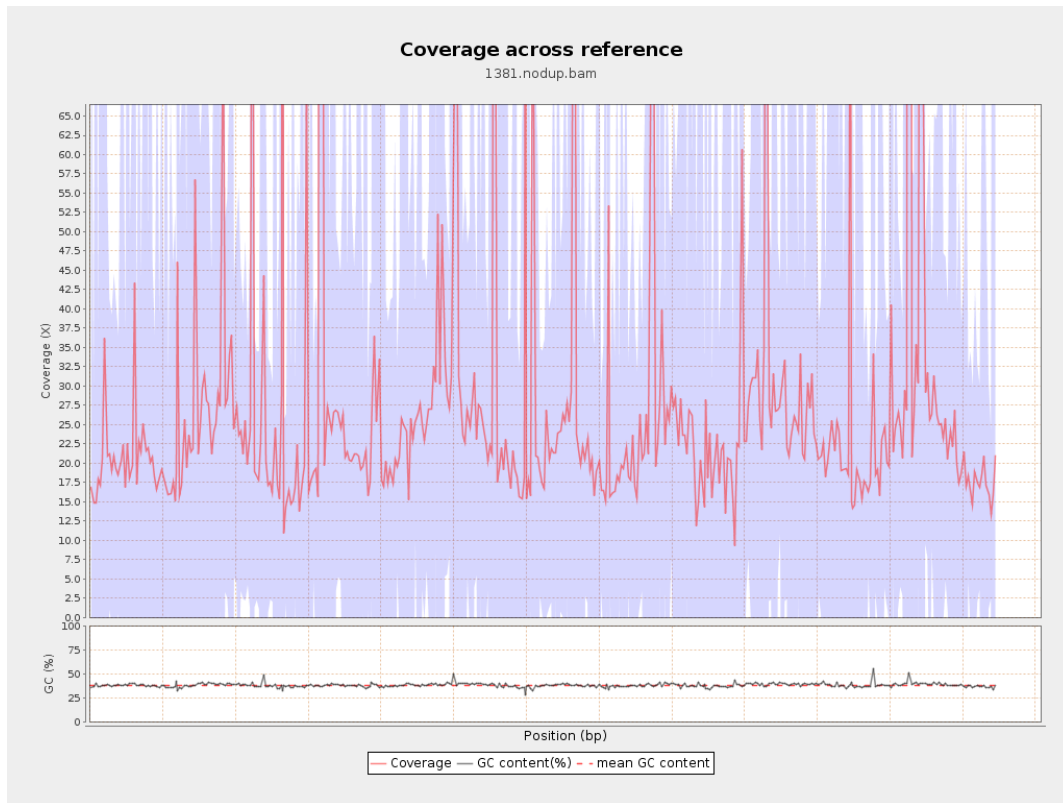
General error rate	2.39%
Mismatches	188,678,566
Insertions	5,949,104
Mapped reads with at least one insertion	8.63%
Deletions	5,889,556
Mapped reads with at least one deletion	8.43%
Homopolymer indels	56.1%

## 2.7. Chromosome stats

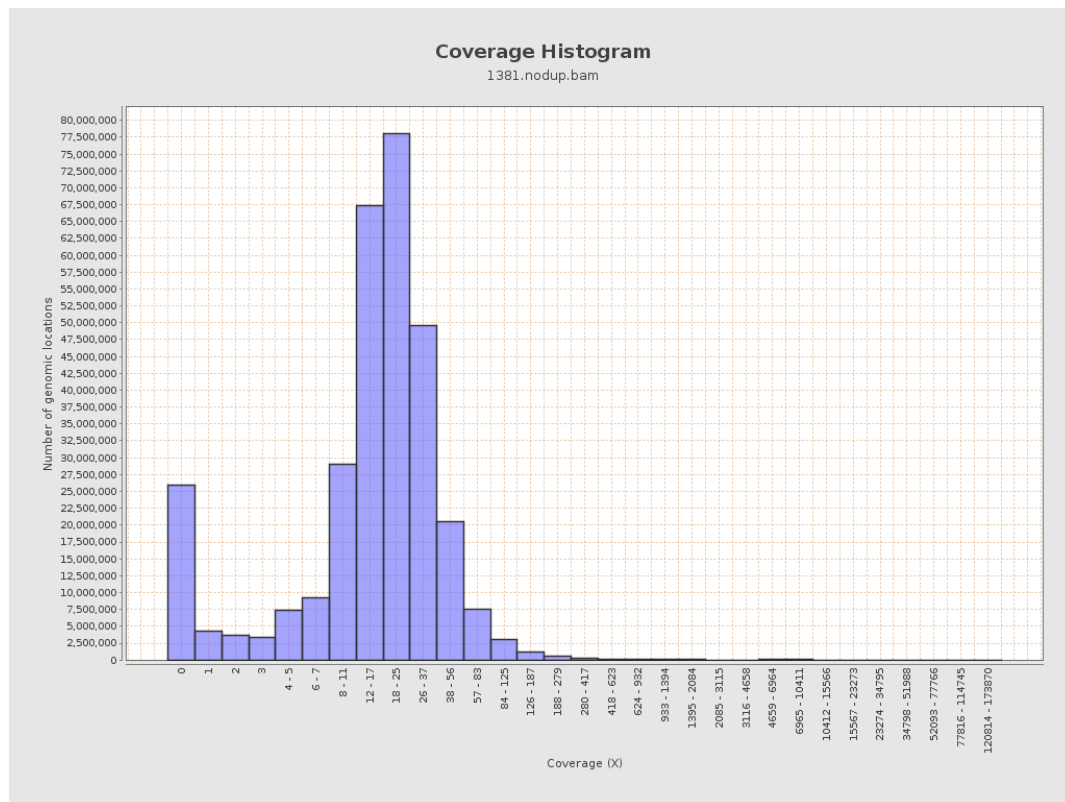
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	597808363	20.1117	81.4623

LT669789.1	36598175	1052315210	28.7532	299.2793
LT669790.1	30422129	881395427	28.9722	285.4788
LT669791.1	52758100	1474349563	27.9455	250.308
LT669792.1	28376109	743666288	26.2075	315.5752
LT669793.1	33388210	848356737	25.4089	194.066
LT669794.1	50579949	1361988562	26.9274	245.0137
LT669795.1	49795044	1624436474	32.6225	345.3371

### 3. Results : Coverage across reference

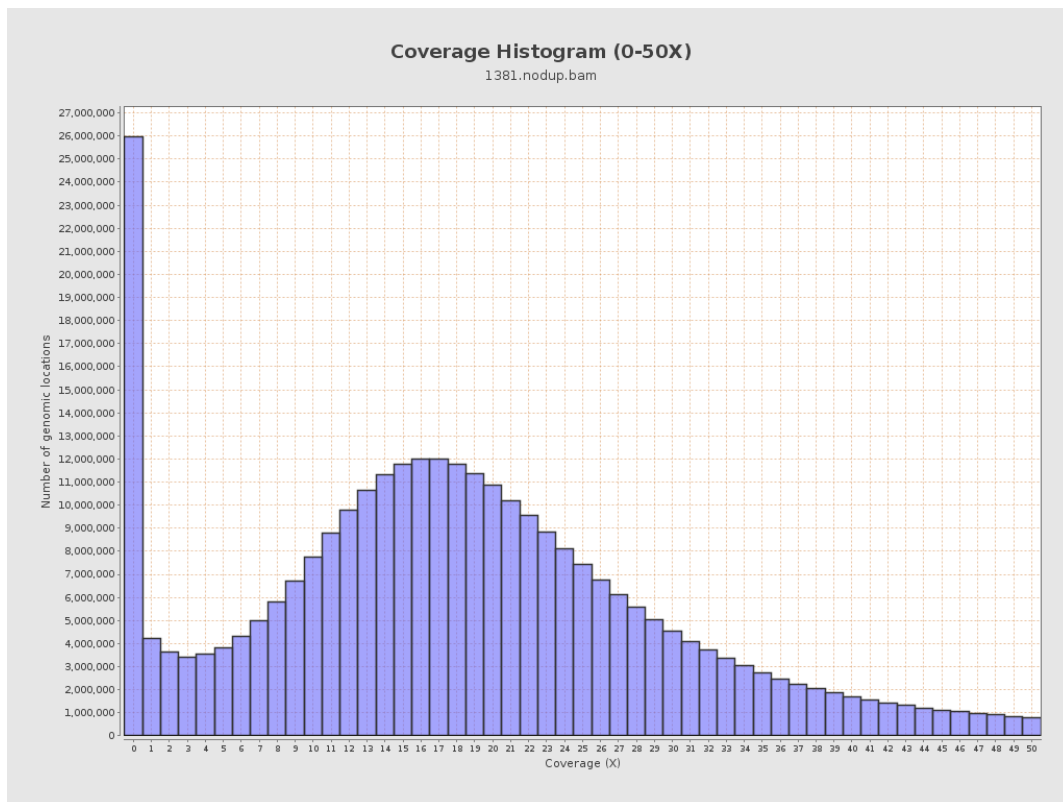


## 4. Results : Coverage Histogram

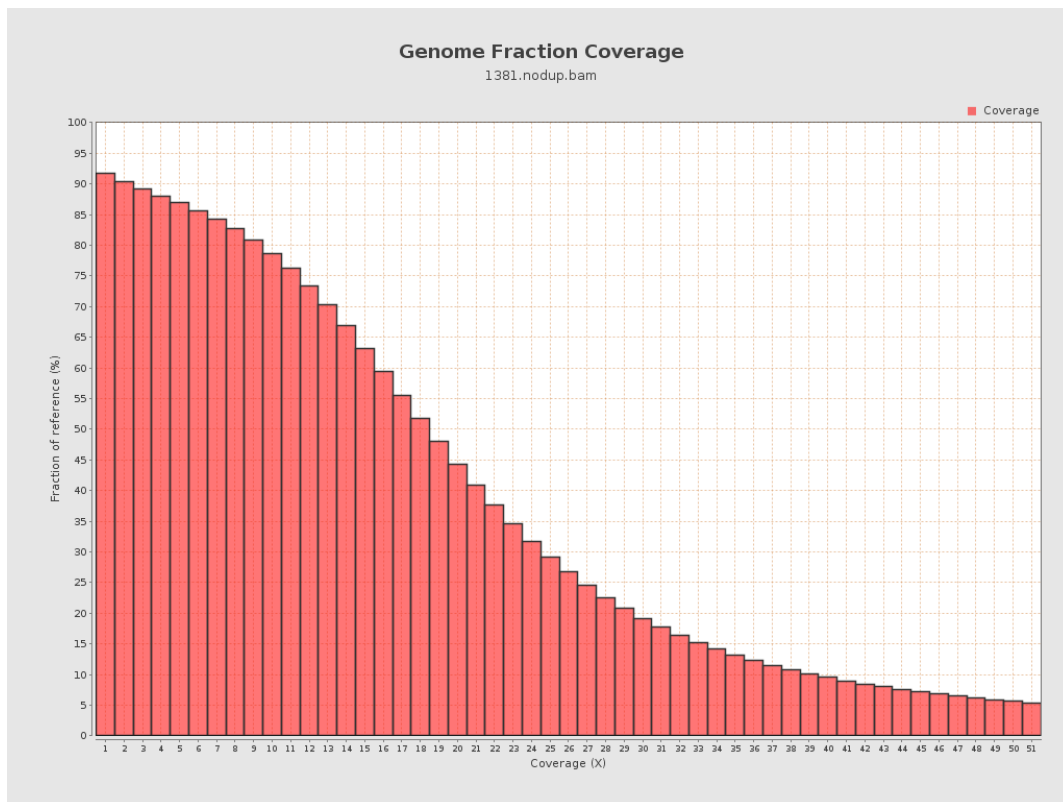




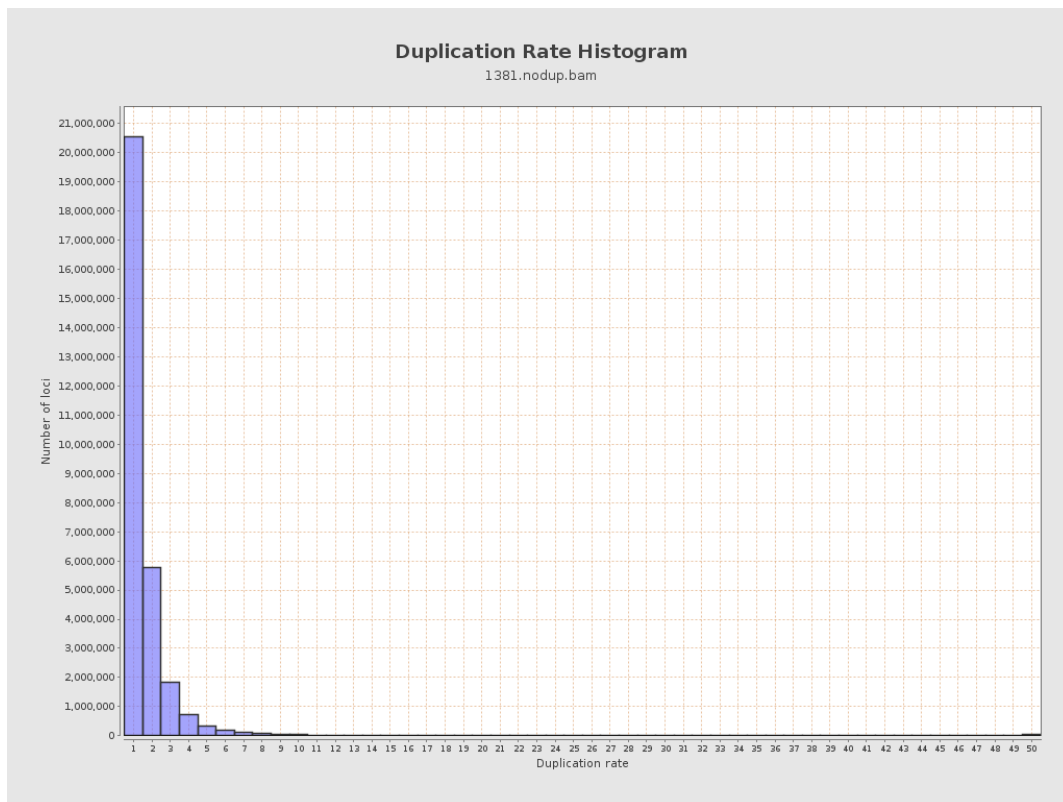
## 5. Results : Coverage Histogram (0-50X)



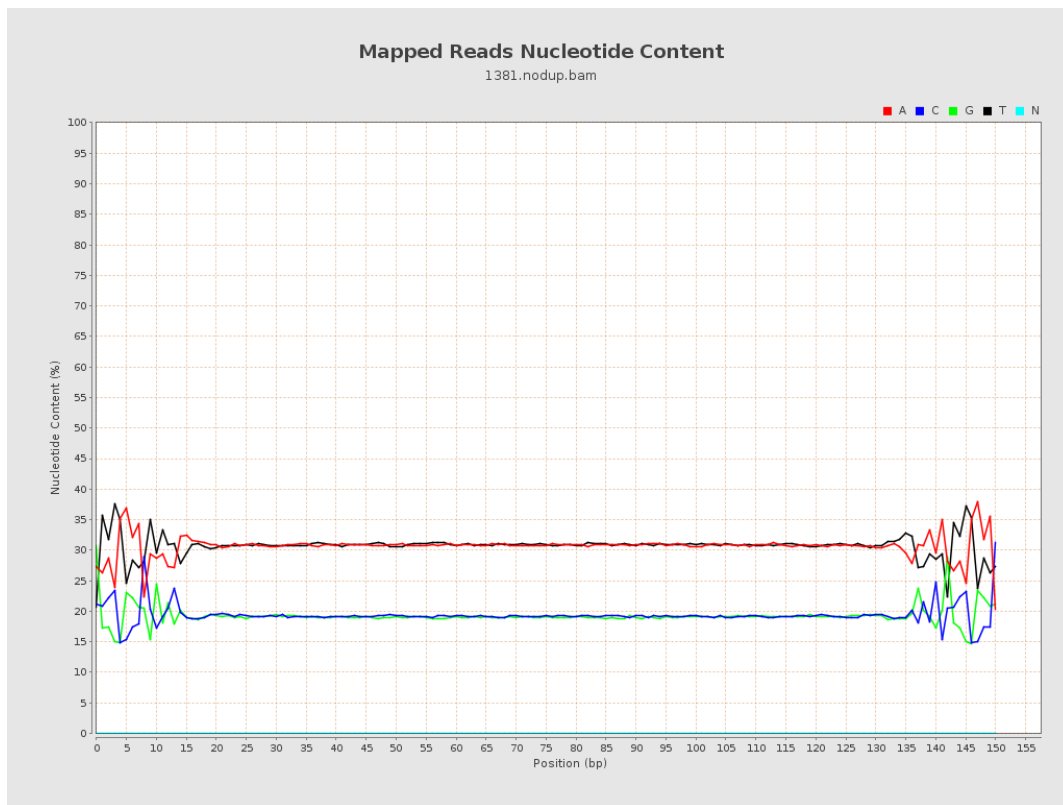
## 6. Results : Genome Fraction Coverage



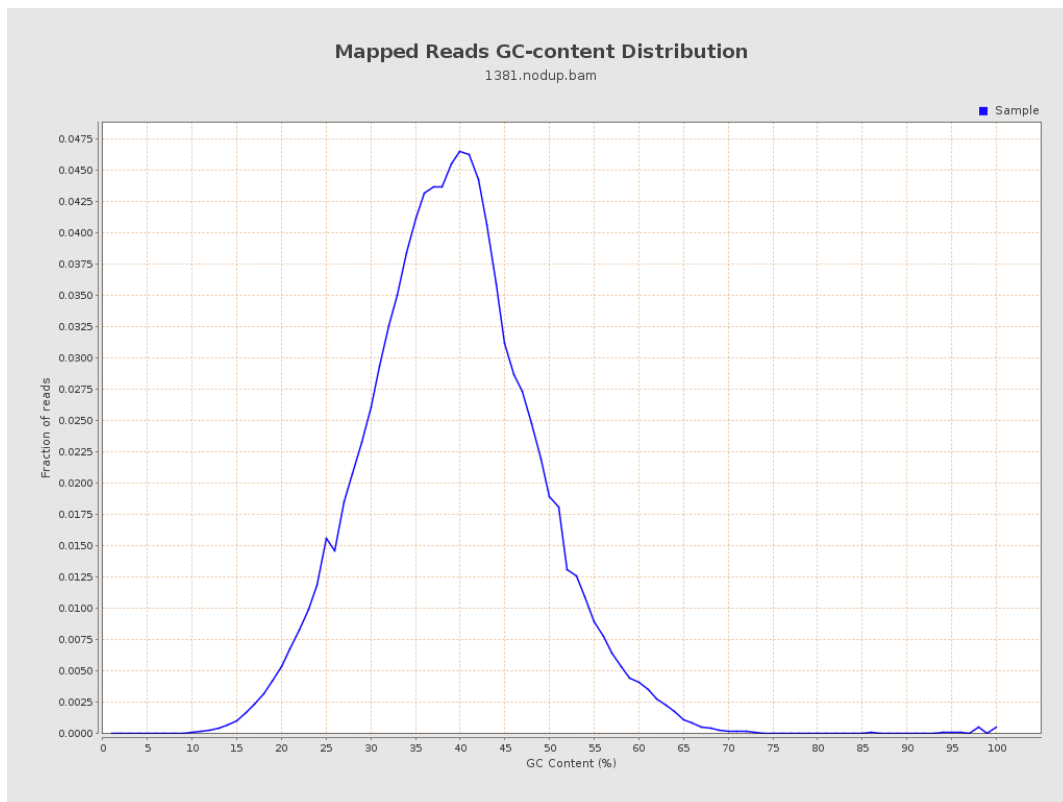
## 7. Results : Duplication Rate Histogram



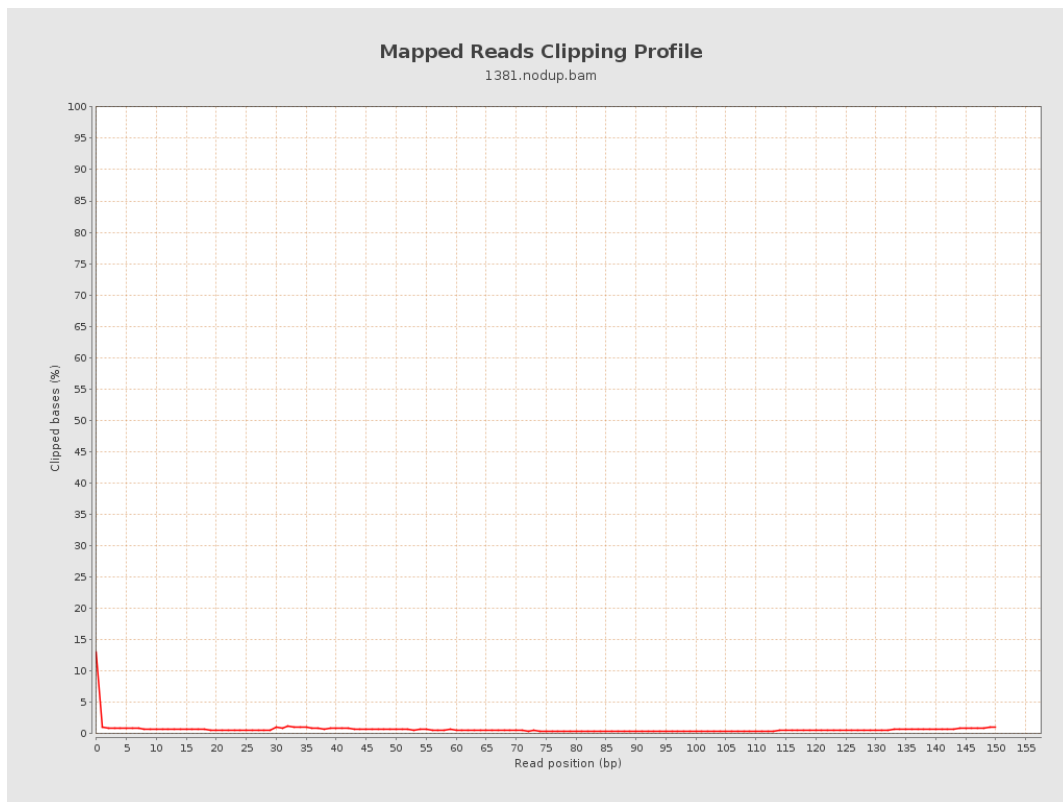
## 8. Results : Mapped Reads Nucleotide Content



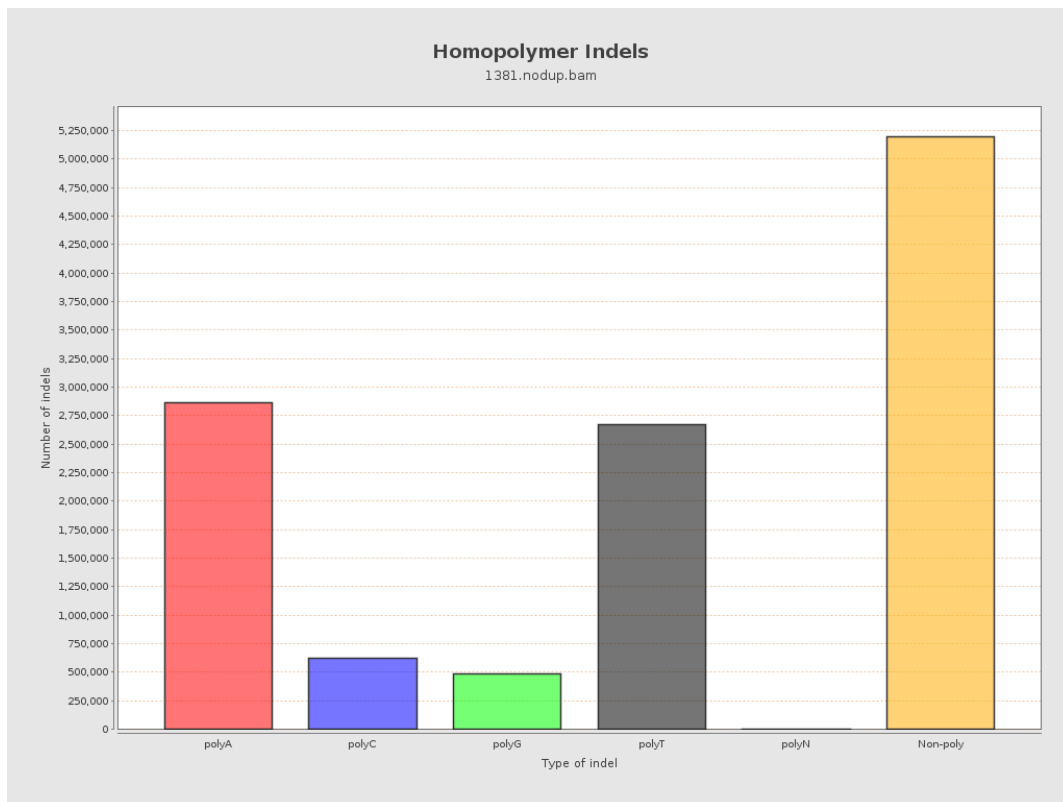
## 9. Results : Mapped Reads GC-content Distribution



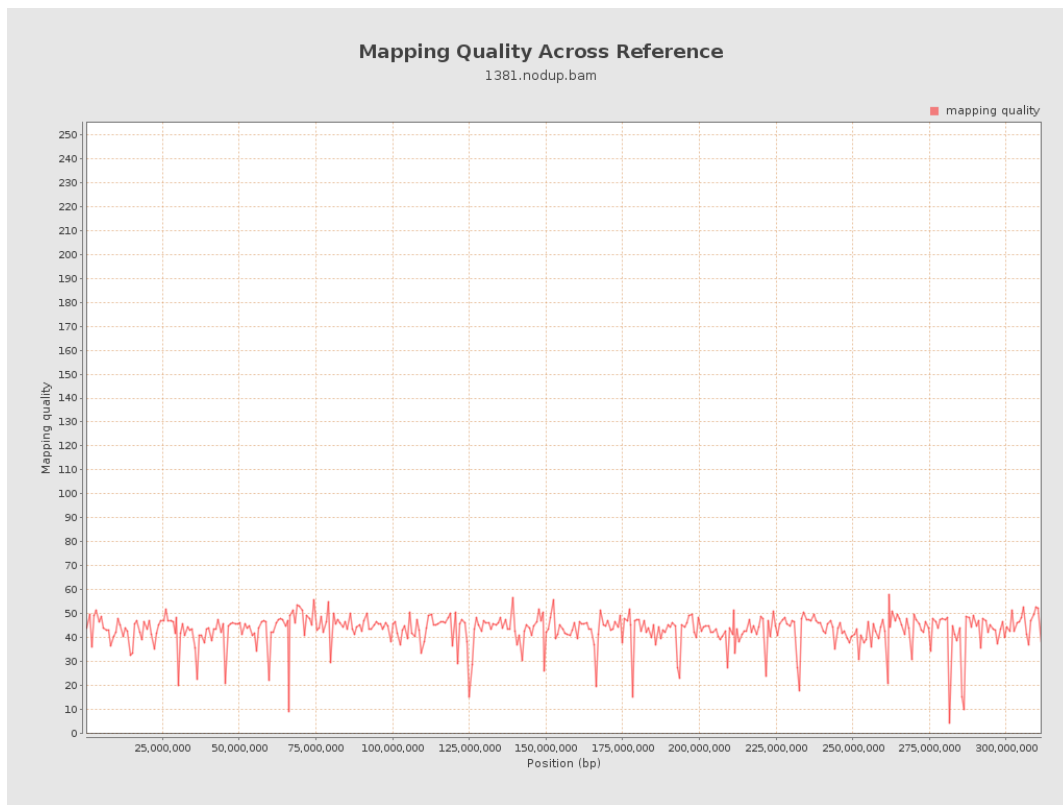
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

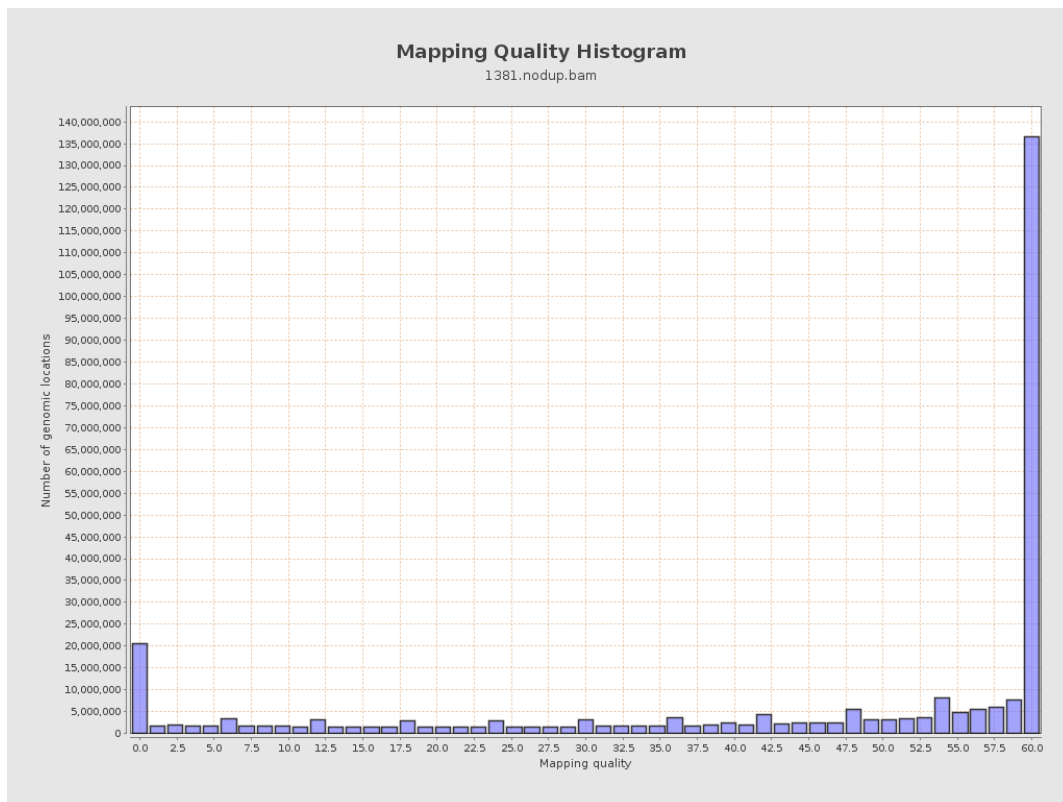


## 12. Results : Mapping Quality Across Reference

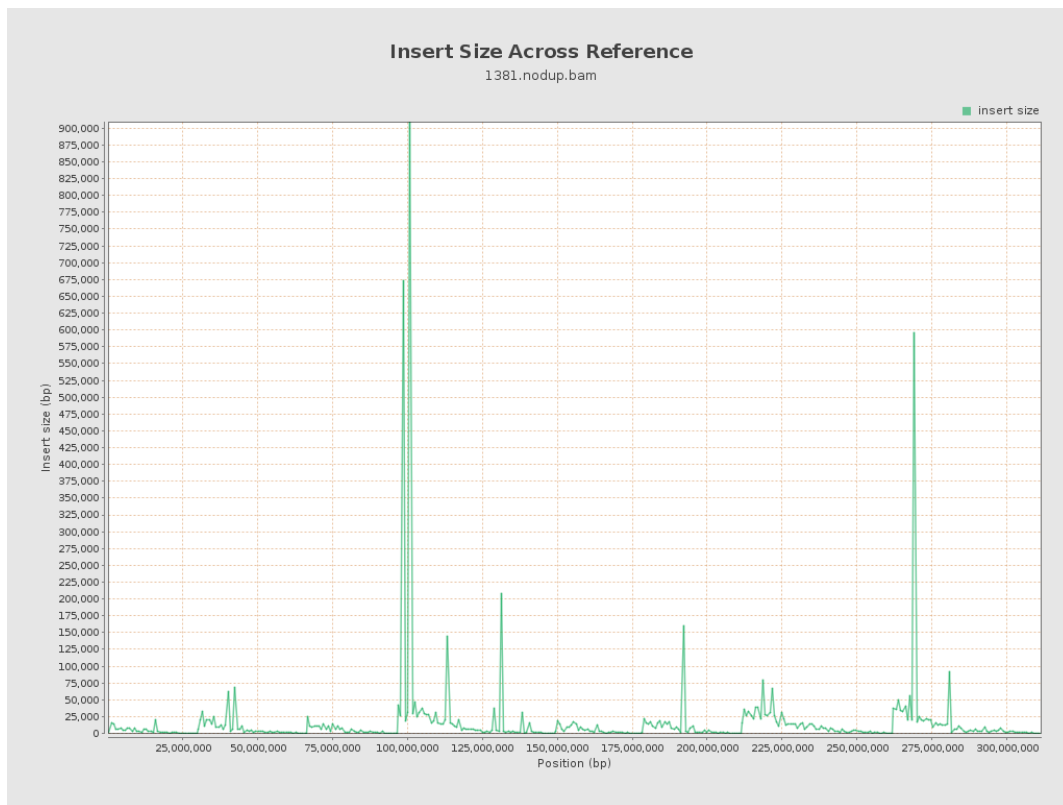




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

