

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:28:18*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/145
3
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1453 .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_534/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_534_S101_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_534/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_534_S101_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:28:17 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	63,942,858
Mapped reads	60,424,253 / 94.5%
Unmapped reads	3,518,605 / 5.5%
Mapped paired reads	60,424,253 / 94.5%
Mapped reads, first in pair	30,312,621 / 47.41%
Mapped reads, second in pair	30,111,632 / 47.09%
Mapped reads, both in pair	59,214,818 / 92.61%
Mapped reads, singletons	1,209,435 / 1.89%
Read min/max/mean length	30 / 151 / 148.05
Duplicated reads (flagged)	8,300,795 / 12.98%
Clipped reads	14,198,563 / 22.21%

### 2.2. ACGT Content

Number/percentage of A's	2,580,606,829 / 30.9%
Number/percentage of C's	1,596,873,532 / 19.12%
Number/percentage of T's	2,582,896,348 / 30.92%
Number/percentage of G's	1,592,445,344 / 19.06%
Number/percentage of N's	59,220 / 0%
GC Percentage	38.18%

### 2.3. Coverage

Mean	26.8713
Standard Deviation	196.7213

## 2.4. Mapping Quality

Mean Mapping Quality	44
----------------------	----

## 2.5. Insert size

Mean	225,380.51
Standard Deviation	2,254,470.03
P25/Median/P75	316 / 415 / 538

## 2.6. Mismatches and indels

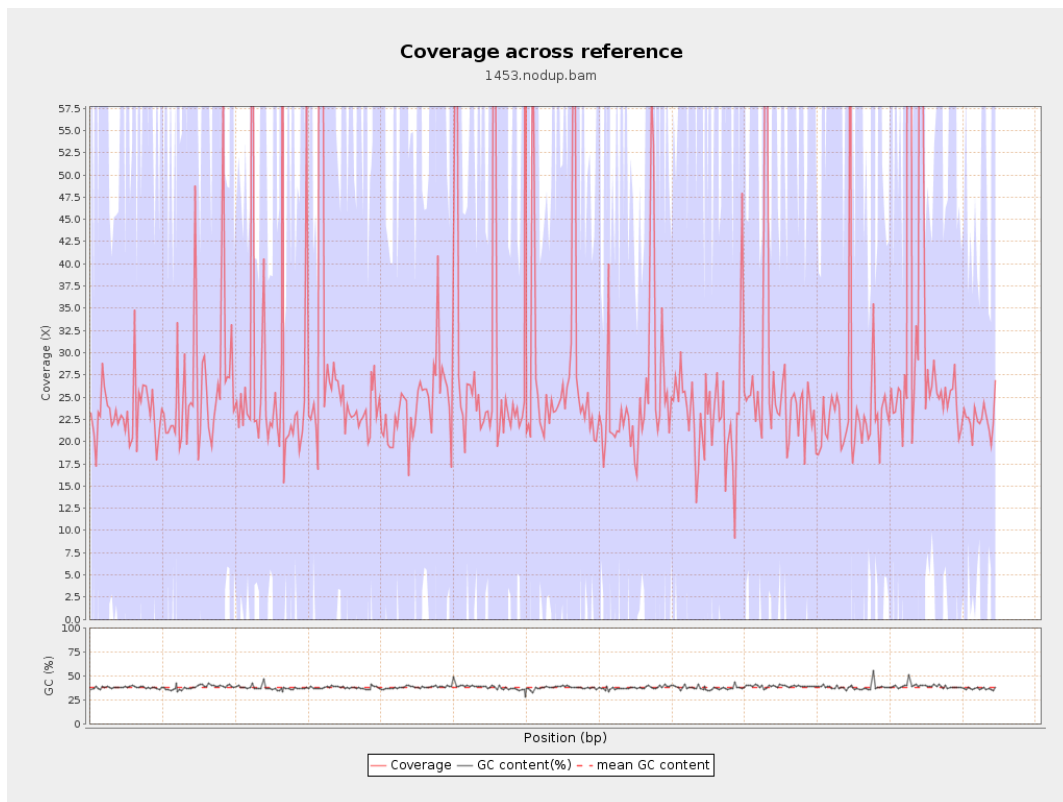
General error rate	2.5%
Mismatches	193,119,127
Insertions	5,592,182
Mapped reads with at least one insertion	8.32%
Deletions	5,698,246
Mapped reads with at least one deletion	8.35%
Homopolymer indels	55.99%

## 2.7. Chromosome stats

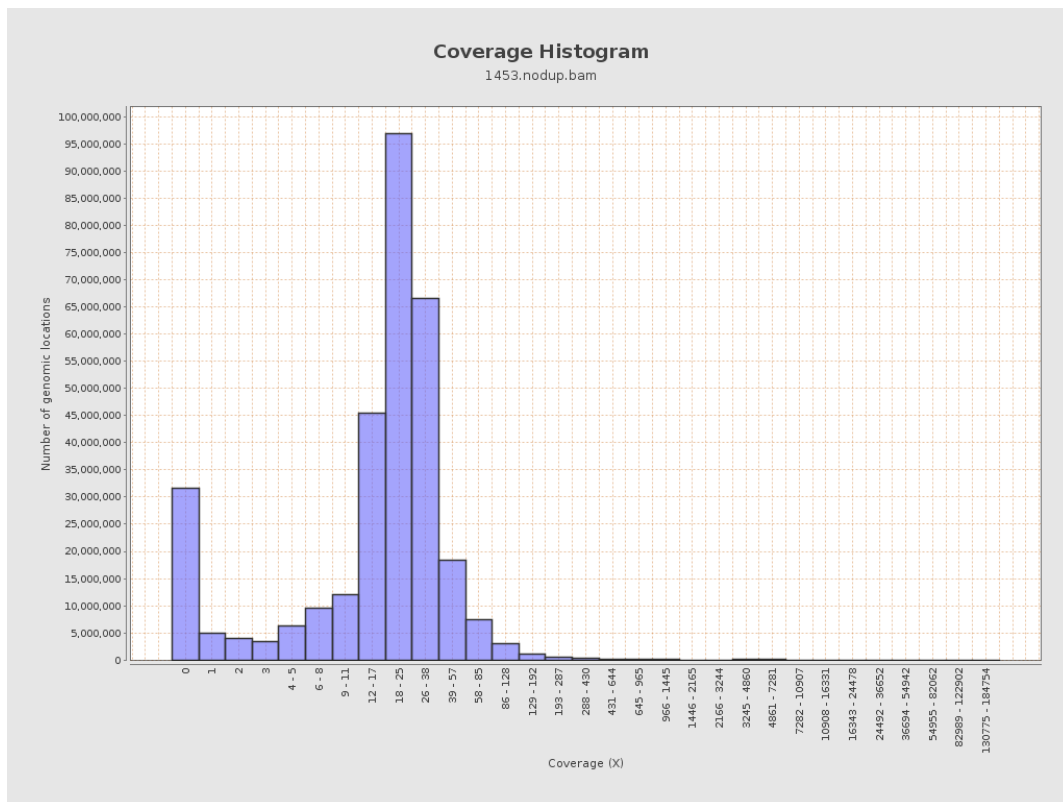
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	684341332	23.0229	77.3201

LT669789.1	36598175	997728935	27.2617	218.1708
LT669790.1	30422129	892857515	29.3489	198.8374
LT669791.1	52758100	1378206610	26.1231	189.5994
LT669792.1	28376109	764437855	26.9395	198.3193
LT669793.1	33388210	823355577	24.6601	103.6682
LT669794.1	50579949	1293217723	25.5678	186.9431
LT669795.1	49795044	1540084147	30.9285	276.1393

### 3. Results : Coverage across reference

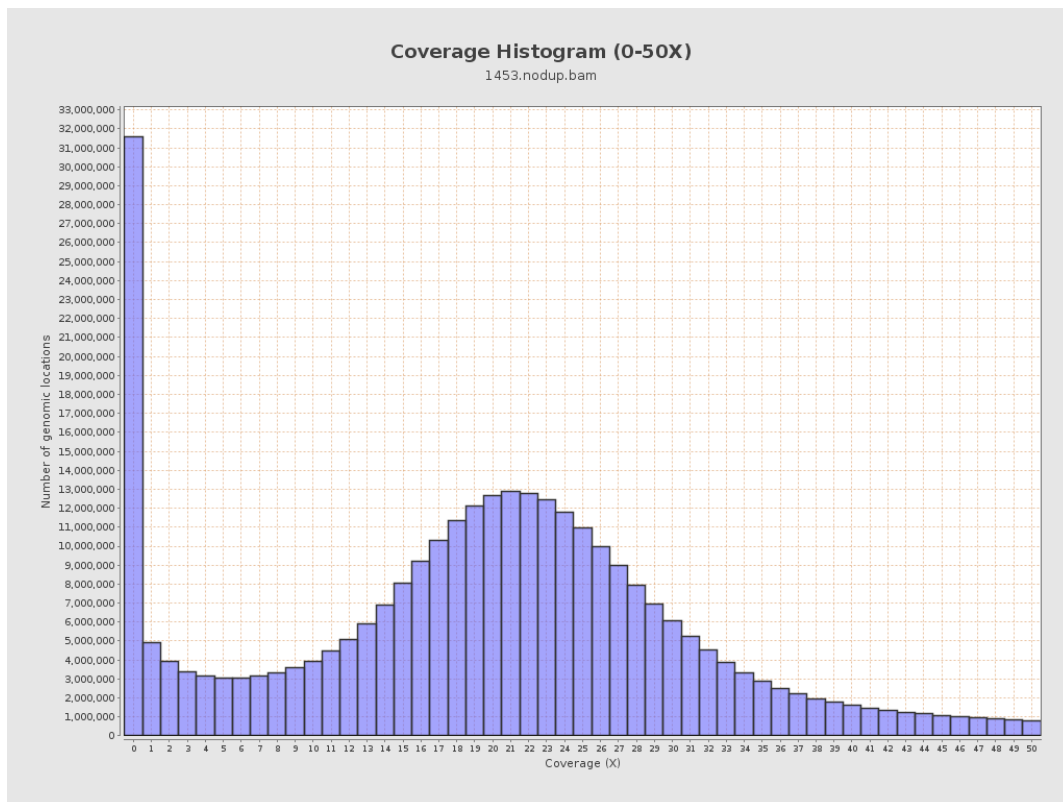


## 4. Results : Coverage Histogram

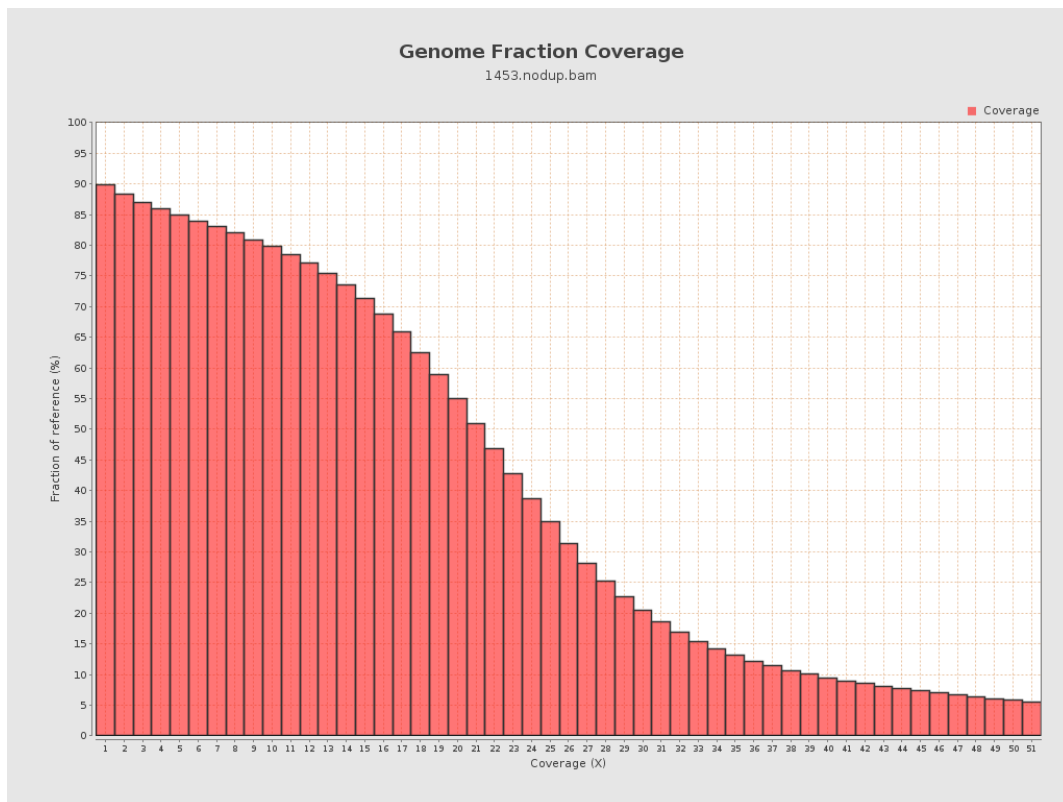




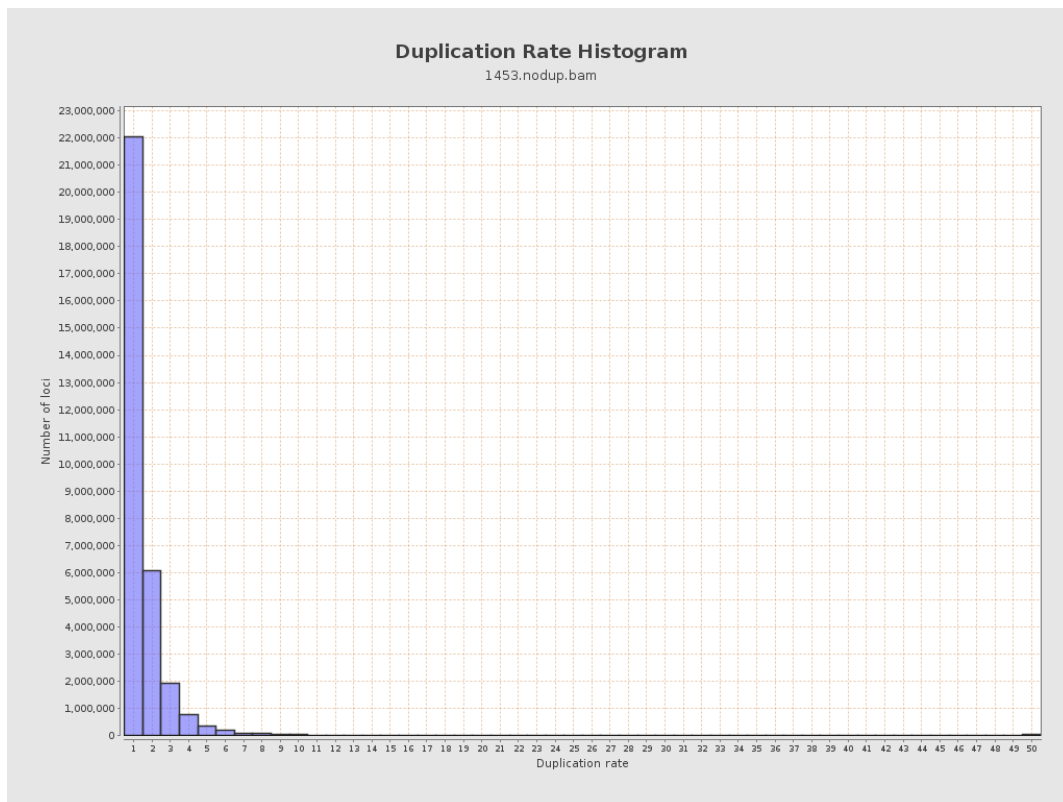
## 5. Results : Coverage Histogram (0-50X)



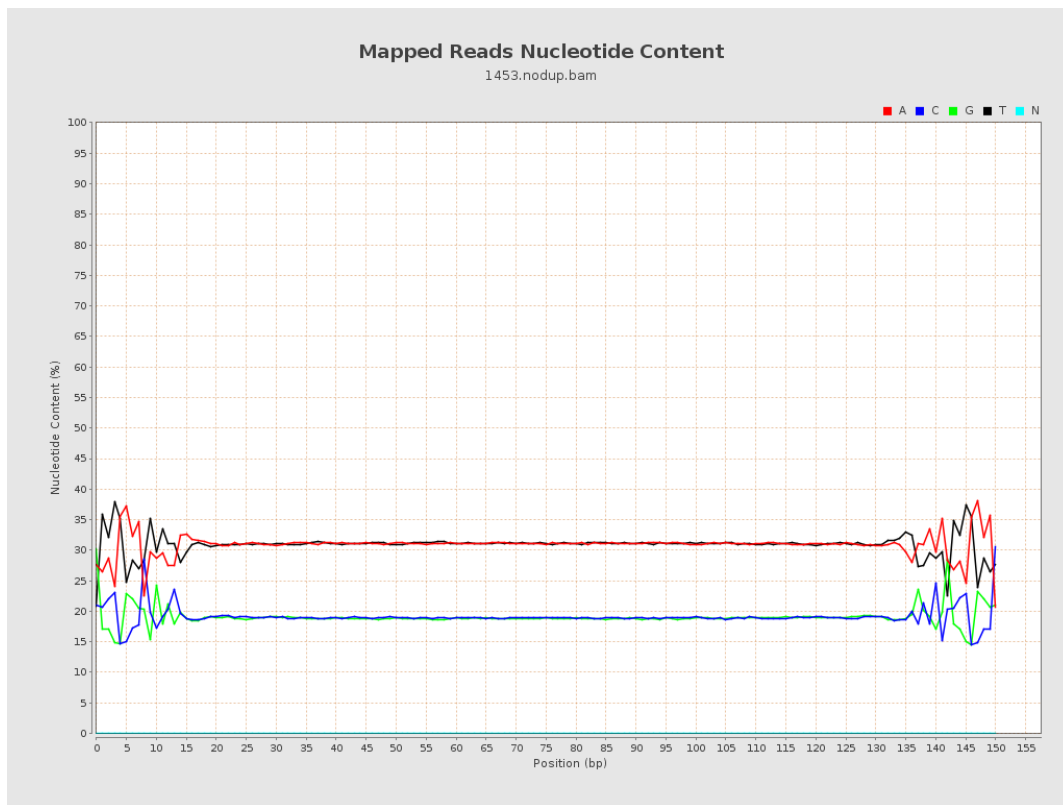
## 6. Results : Genome Fraction Coverage



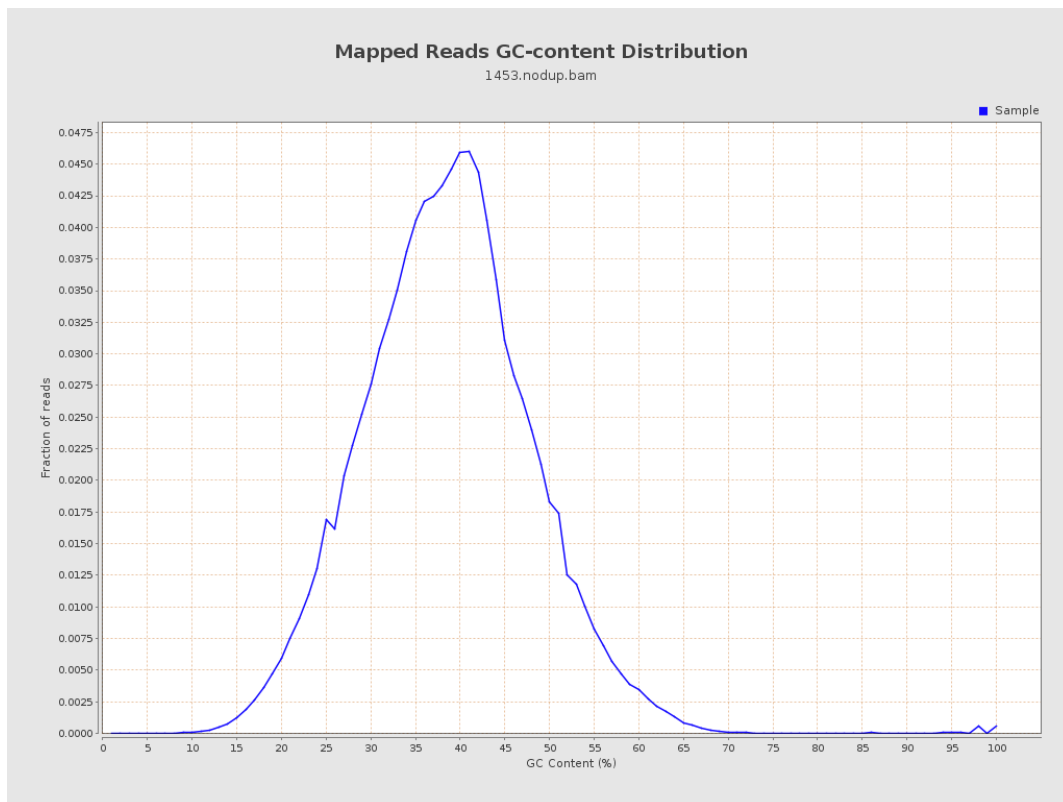
## 7. Results : Duplication Rate Histogram



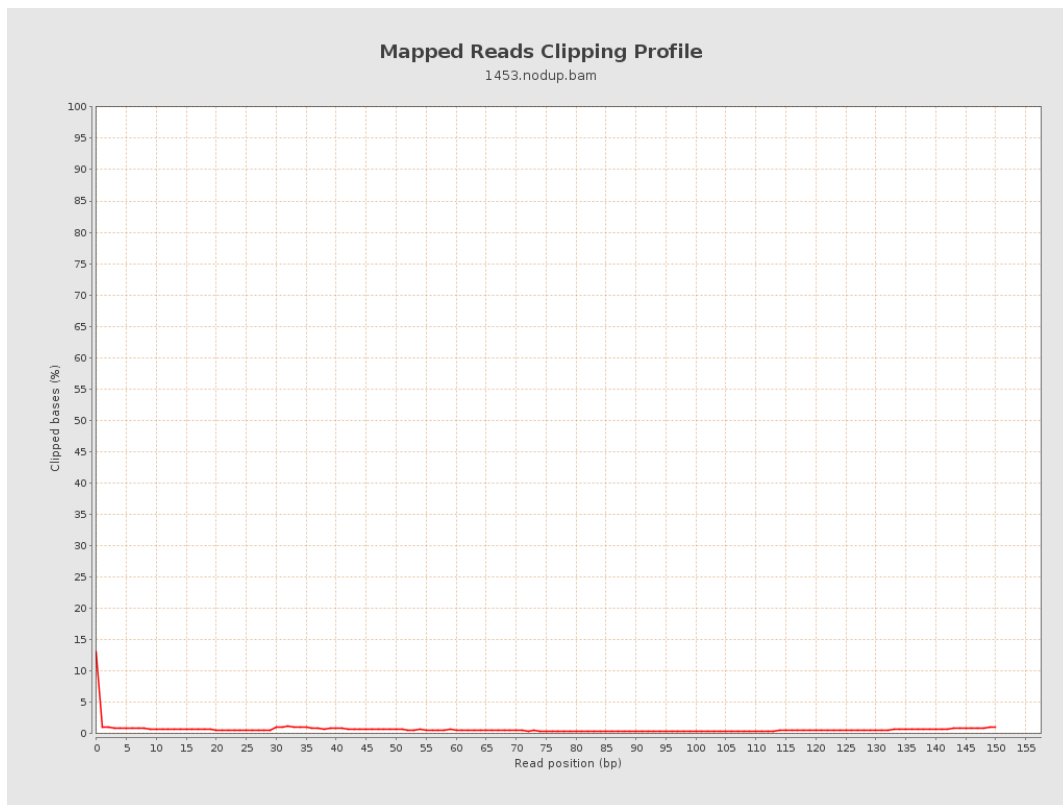
## 8. Results : Mapped Reads Nucleotide Content



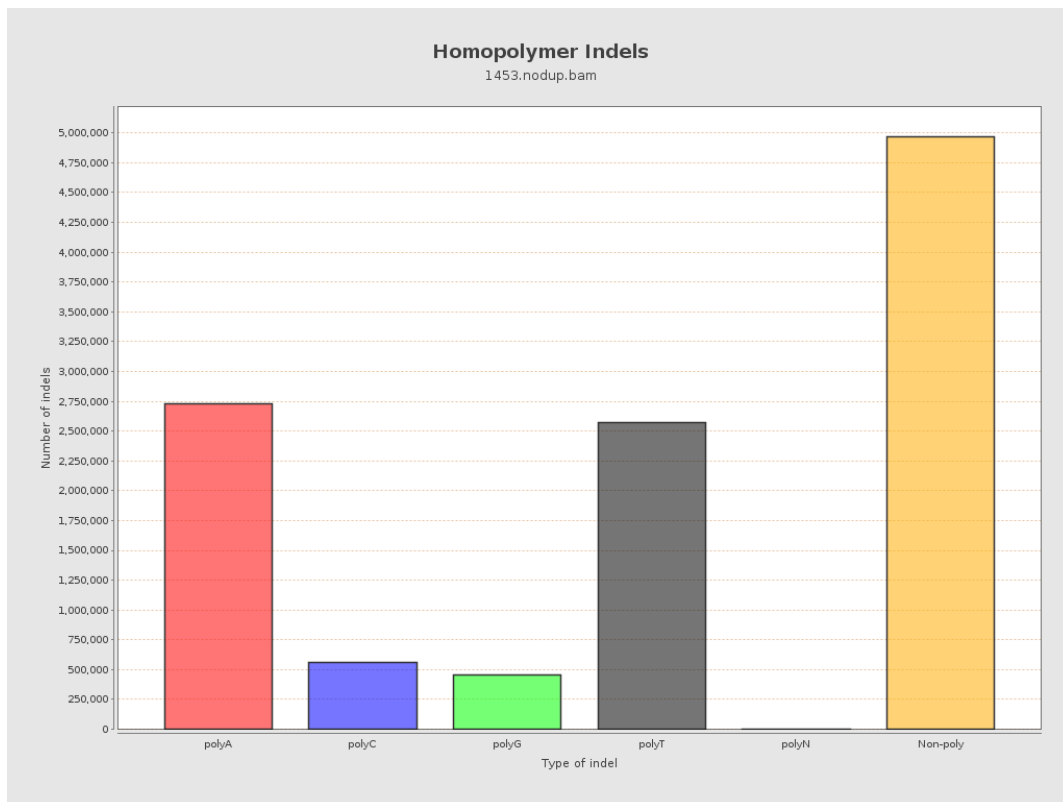
## 9. Results : Mapped Reads GC-content Distribution



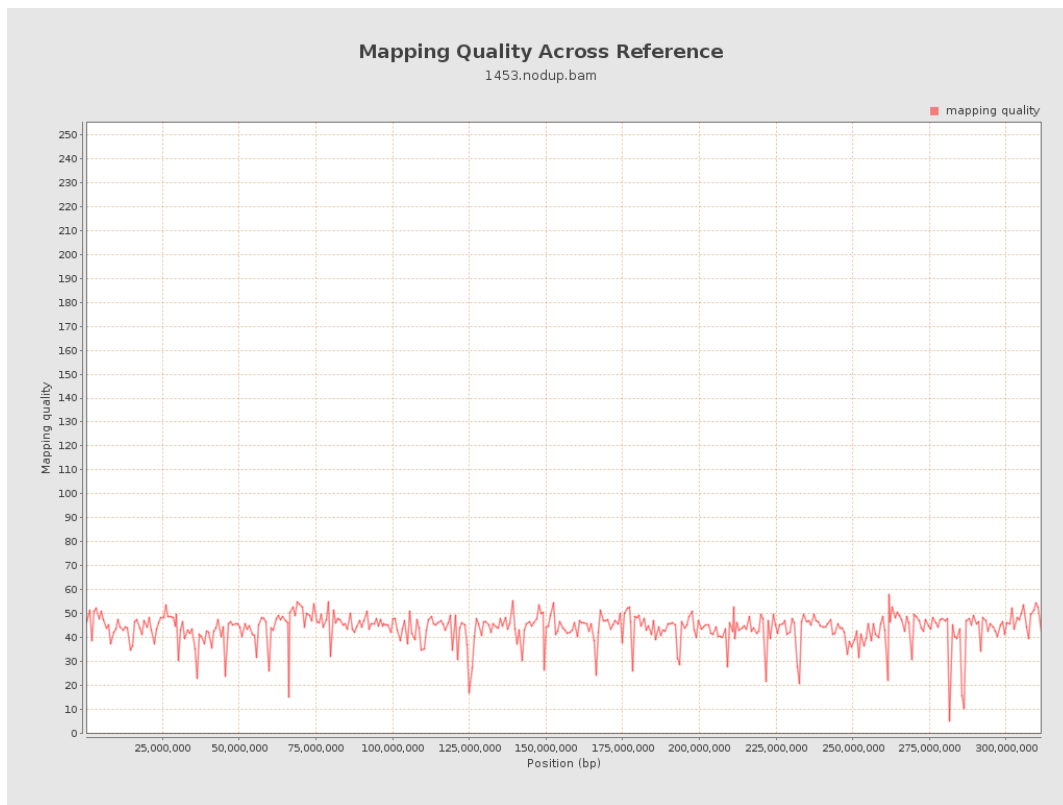
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

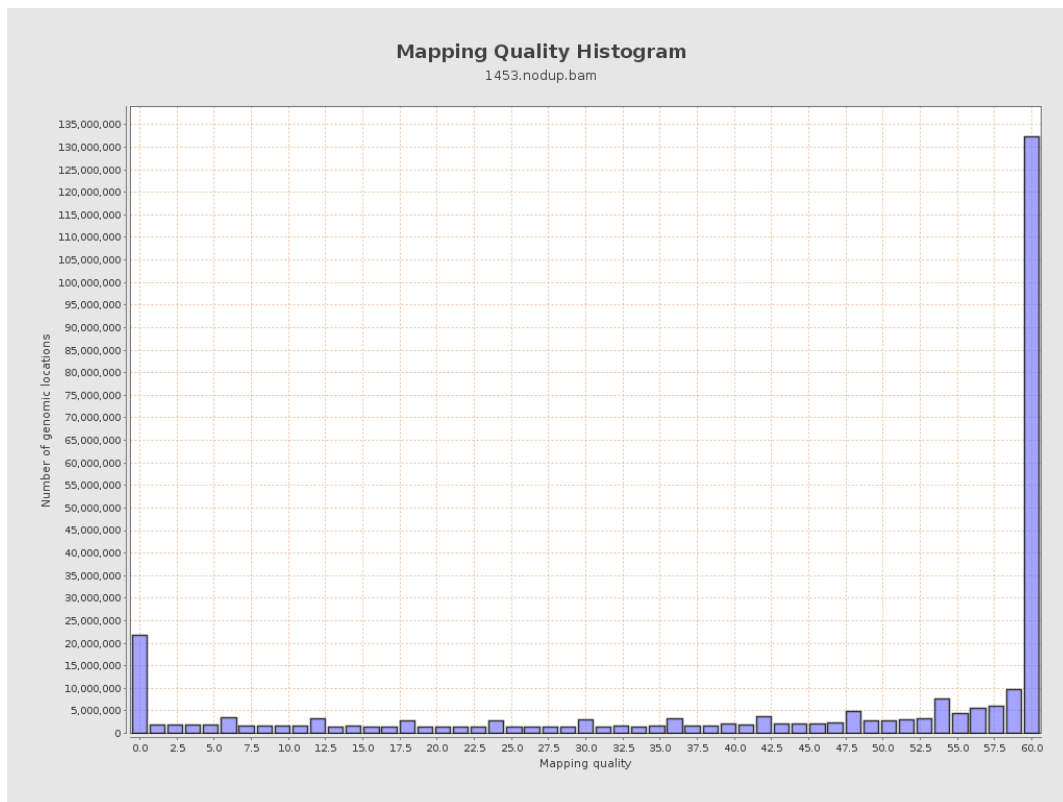


## 12. Results : Mapping Quality Across Reference

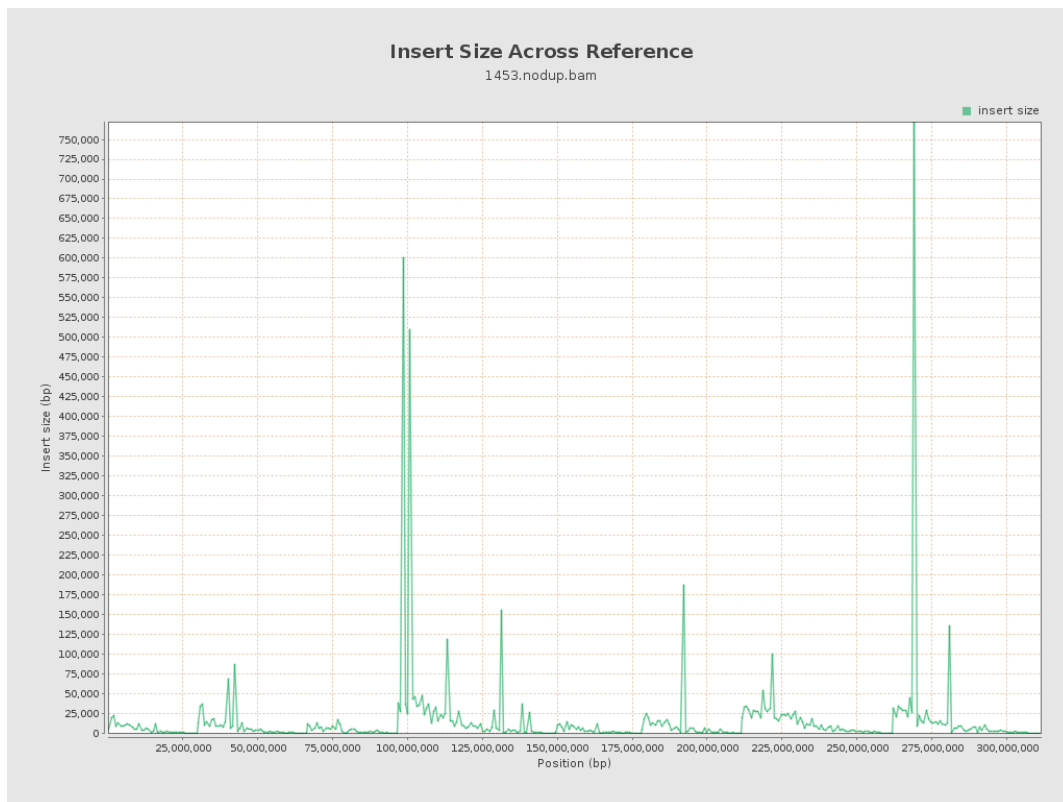




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

