

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:49:54*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/397
L
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 397L .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\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_589/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_589_S156_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_589/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_589_S156_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:49:54 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	115,494,144
Mapped reads	106,446,698 / 92.17%
Unmapped reads	9,047,446 / 7.83%
Mapped paired reads	106,446,698 / 92.17%
Mapped reads, first in pair	53,360,369 / 46.2%
Mapped reads, second in pair	53,086,329 / 45.96%
Mapped reads, both in pair	103,448,861 / 89.57%
Mapped reads, singletons	2,997,837 / 2.6%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	19,599,049 / 16.97%
Clipped reads	24,812,944 / 21.48%

### 2.2. ACGT Content

Number/percentage of A's	4,526,713,777 / 30.86%
Number/percentage of C's	2,807,717,046 / 19.14%
Number/percentage of T's	4,532,815,267 / 30.9%
Number/percentage of G's	2,800,903,489 / 19.1%
Number/percentage of N's	79,515 / 0%
GC Percentage	38.24%

### 2.3. Coverage

Mean	47.1881
Standard Deviation	414.9356

## 2.4. Mapping Quality

Mean Mapping Quality	44.28
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## 2.5. Insert size

Mean	245,209.23
Standard Deviation	2,375,386.42
P25/Median/P75	330 / 431 / 562

## 2.6. Mismatches and indels

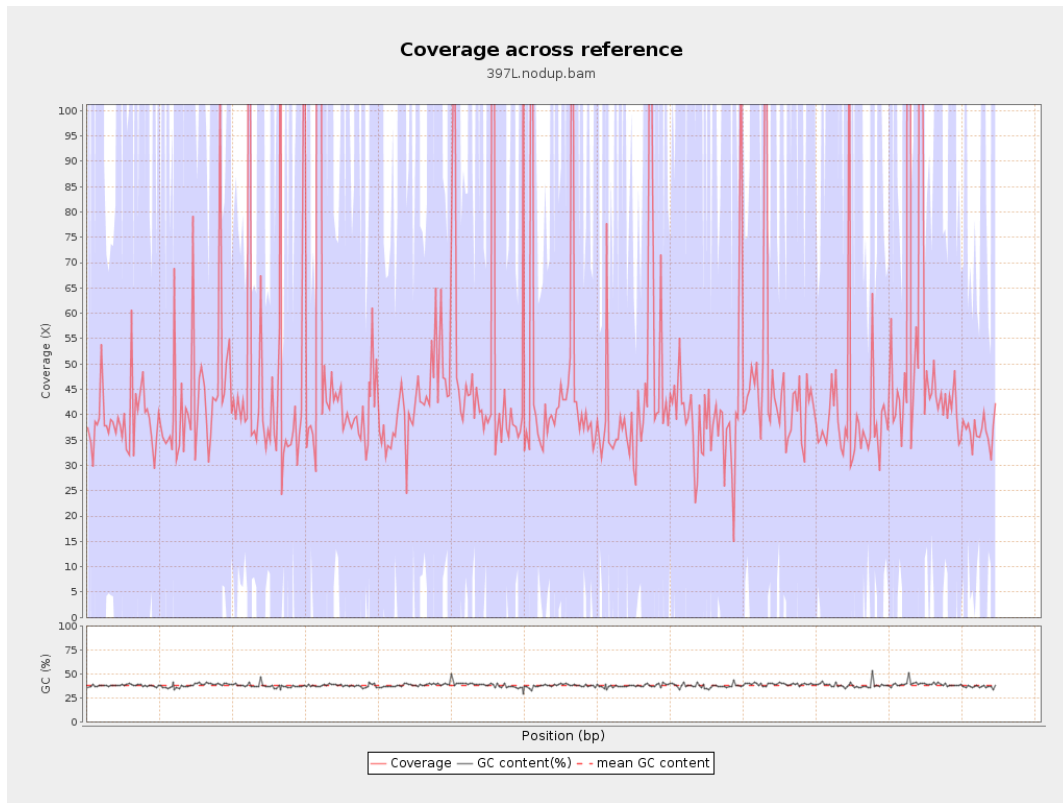
General error rate	2.44%
Mismatches	329,132,593
Insertions	10,350,297
Mapped reads with at least one insertion	8.69%
Deletions	10,053,431
Mapped reads with at least one deletion	8.38%
Homopolymer indels	56.92%

## 2.7. Chromosome stats

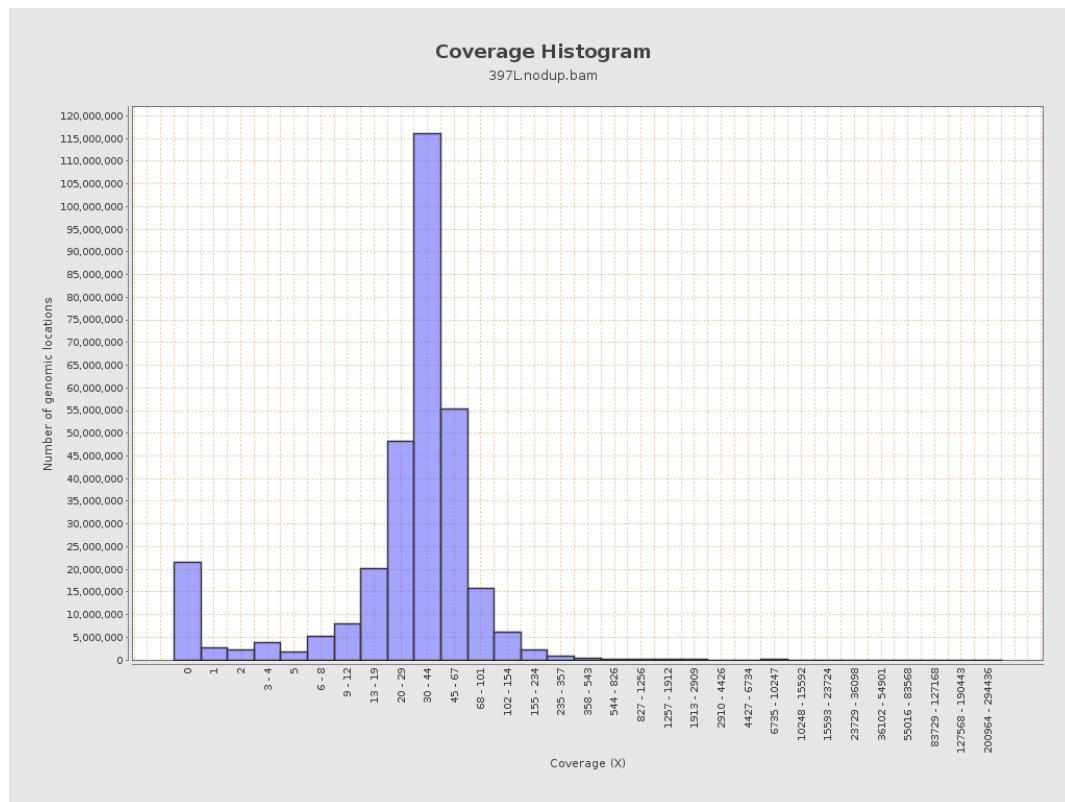
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	1142890350	38.4496	151.7217

LT669789.1	36598175	1735083558	47.409	436.9025
LT669790.1	30422129	1690153489	55.5567	566.8744
LT669791.1	52758100	2465455926	46.7313	425.979
LT669792.1	28376109	1337565427	47.137	447.6615
LT669793.1	33388210	1436209893	43.0155	269.8291
LT669794.1	50579949	2232615561	44.1403	342.5458
LT669795.1	49795044	2665835002	53.5362	502.5555

### 3. Results : Coverage across reference

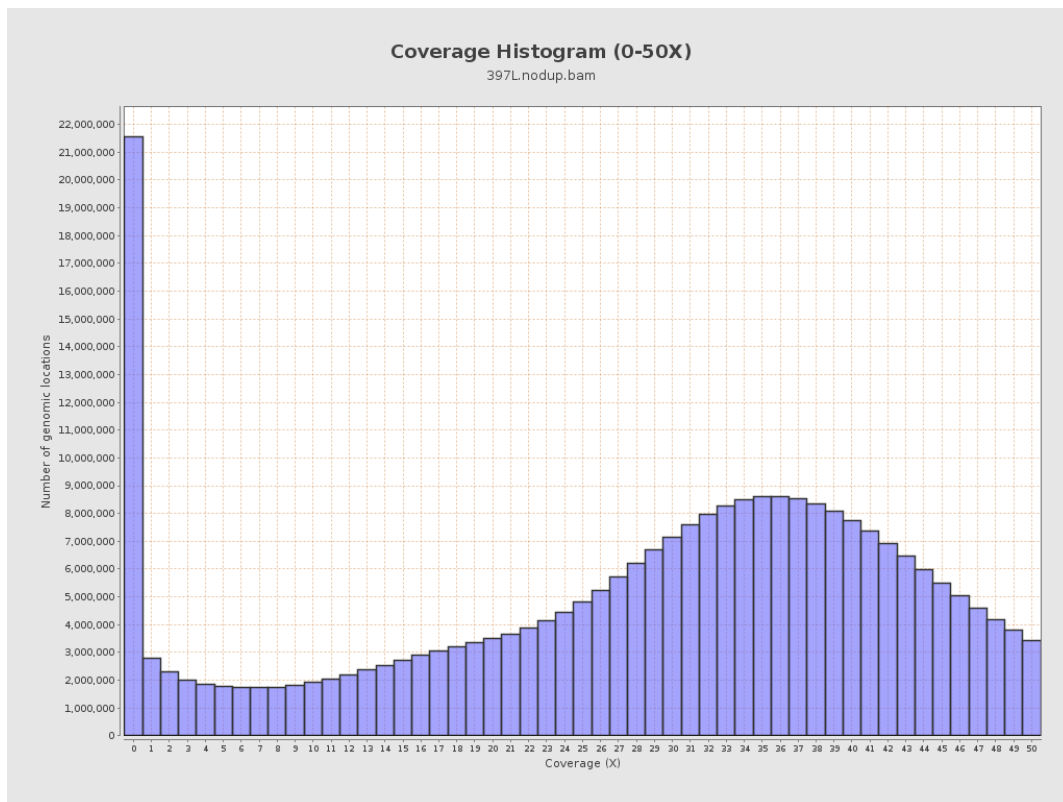


## 4. Results : Coverage Histogram

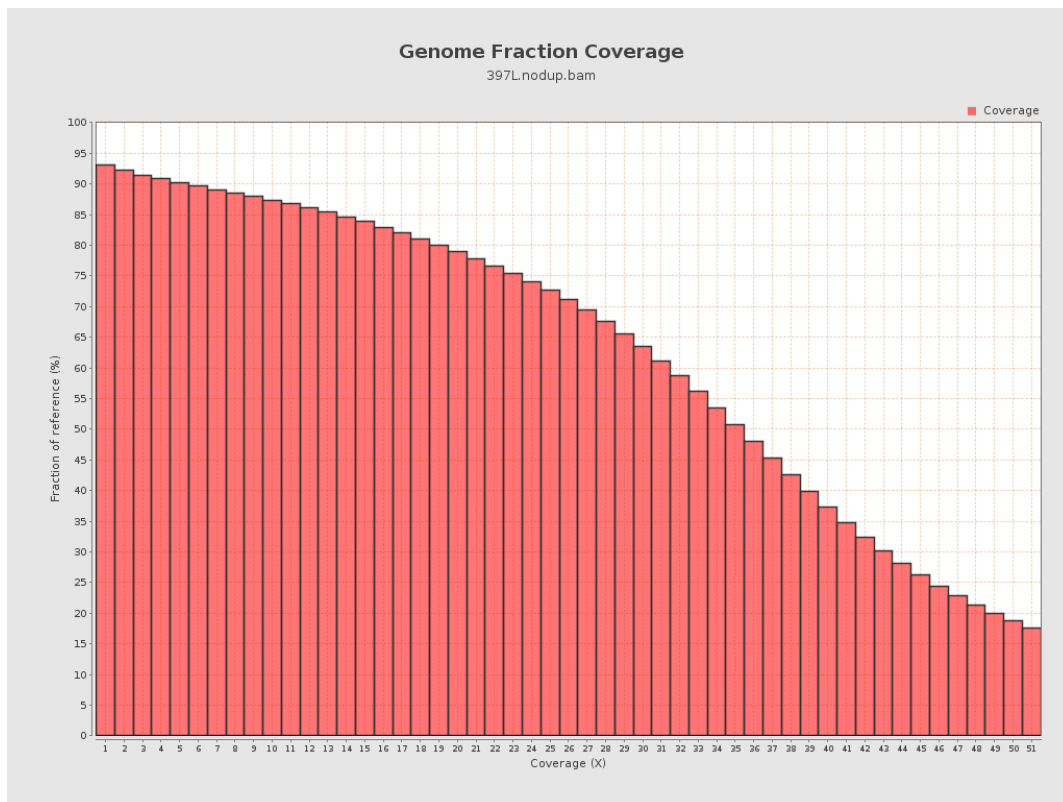




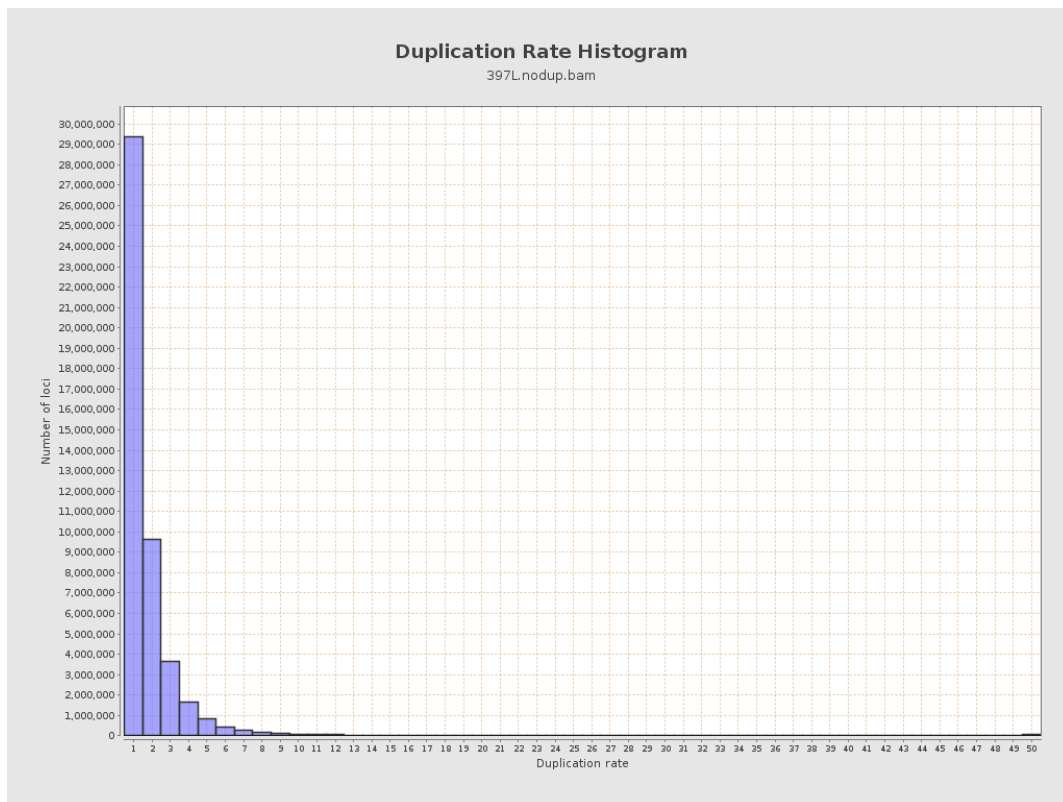
## 5. Results : Coverage Histogram (0-50X)



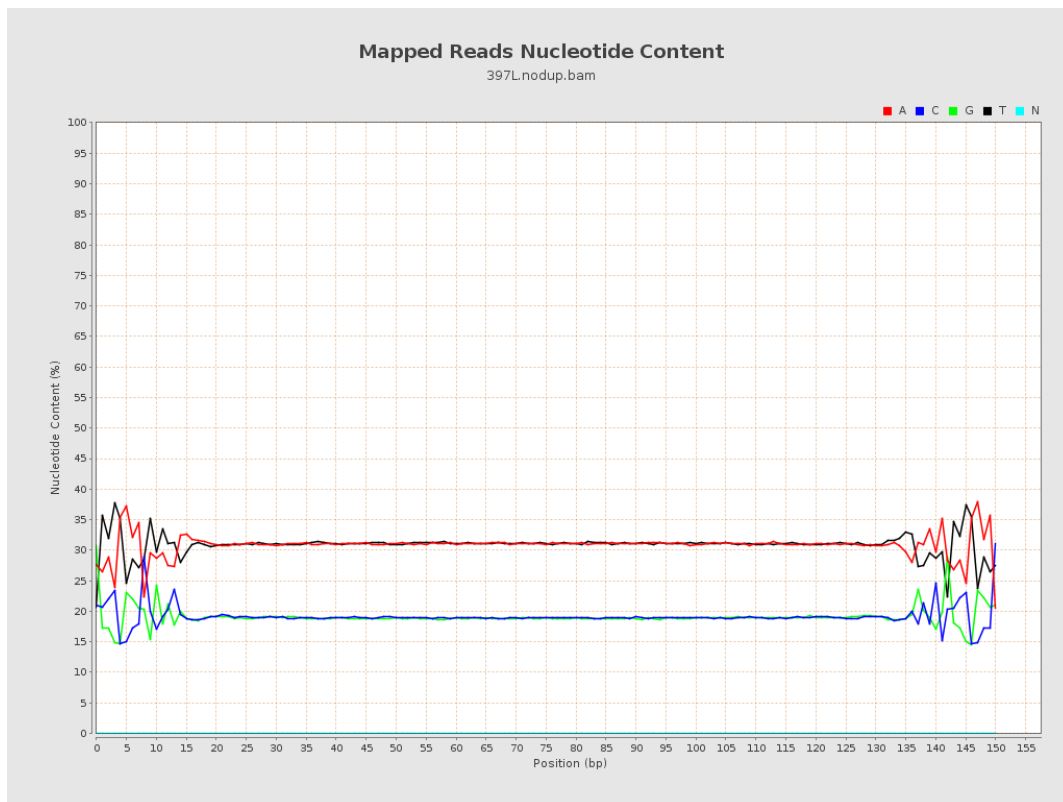
## 6. Results : Genome Fraction Coverage



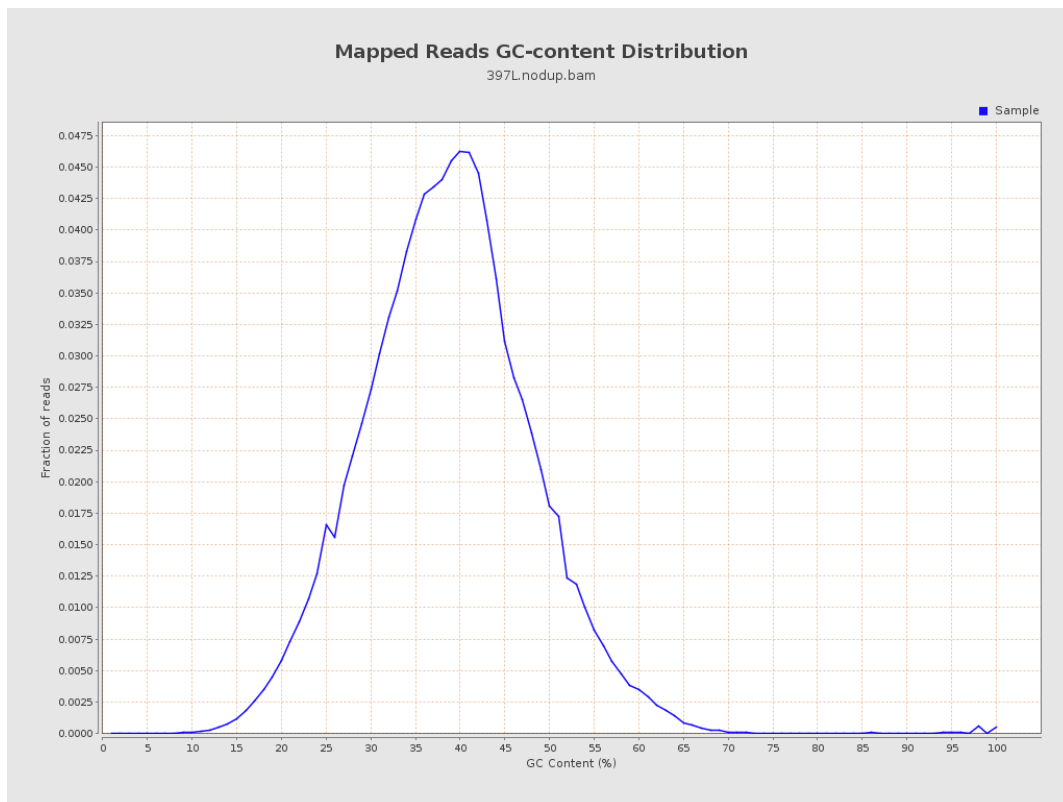
## 7. Results : Duplication Rate Histogram



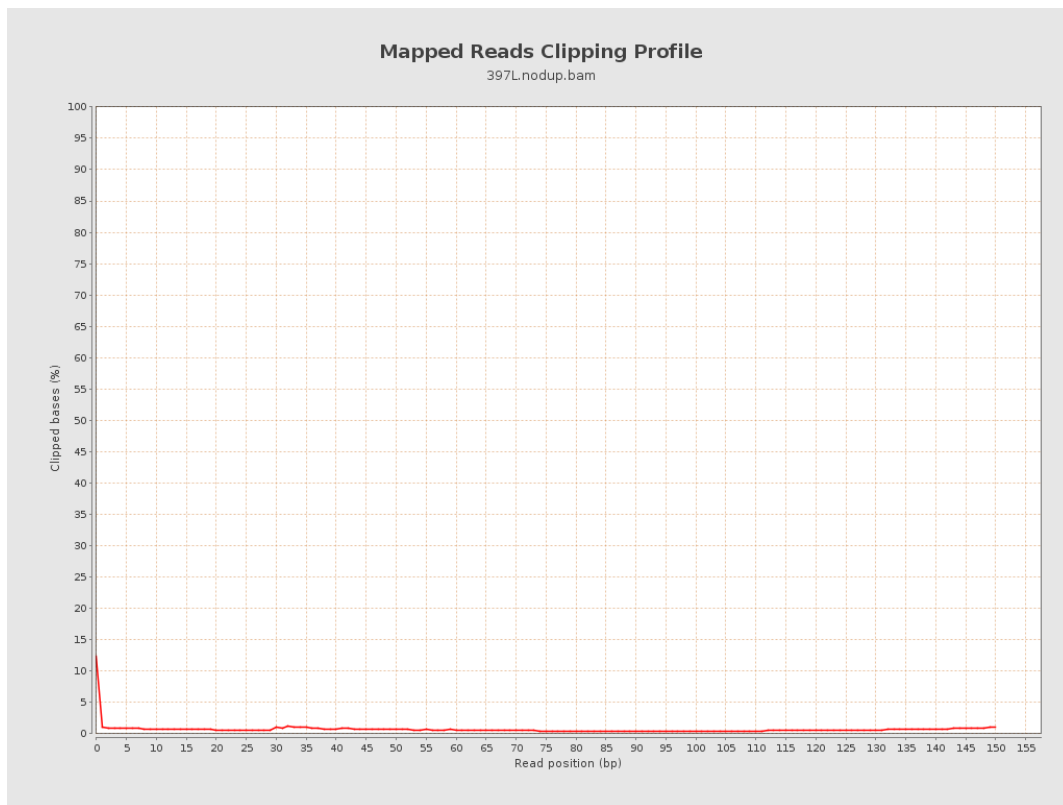
## 8. Results : Mapped Reads Nucleotide Content



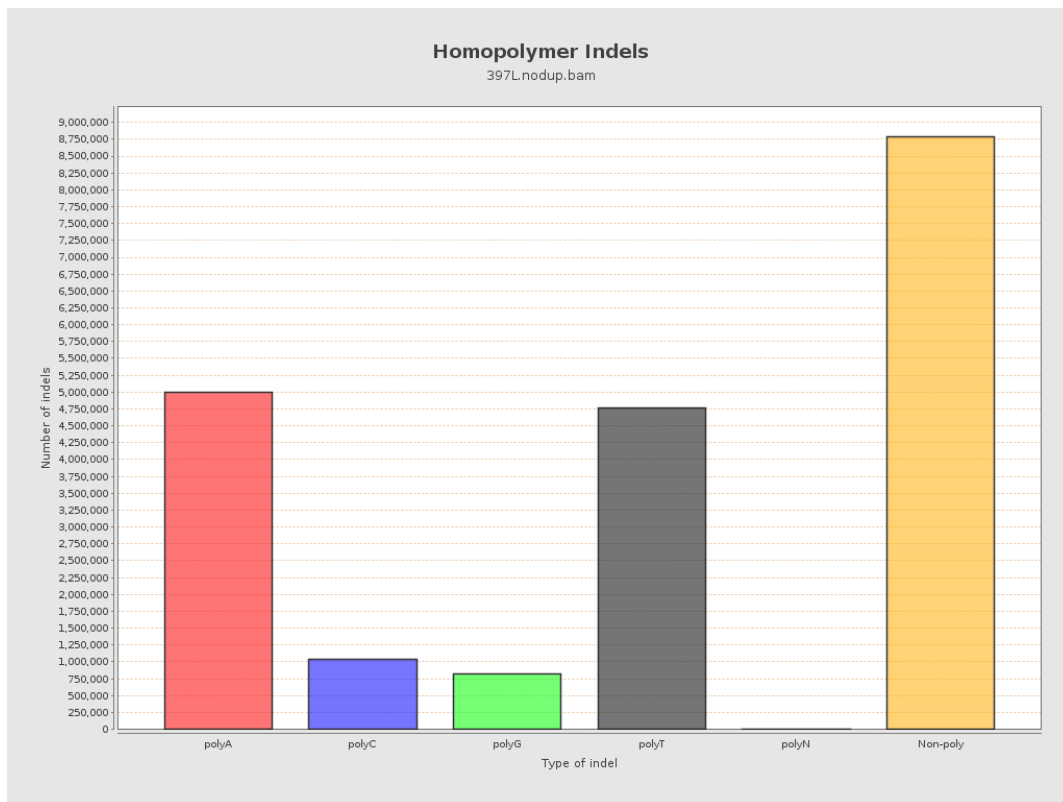
## 9. Results : Mapped Reads GC-content Distribution



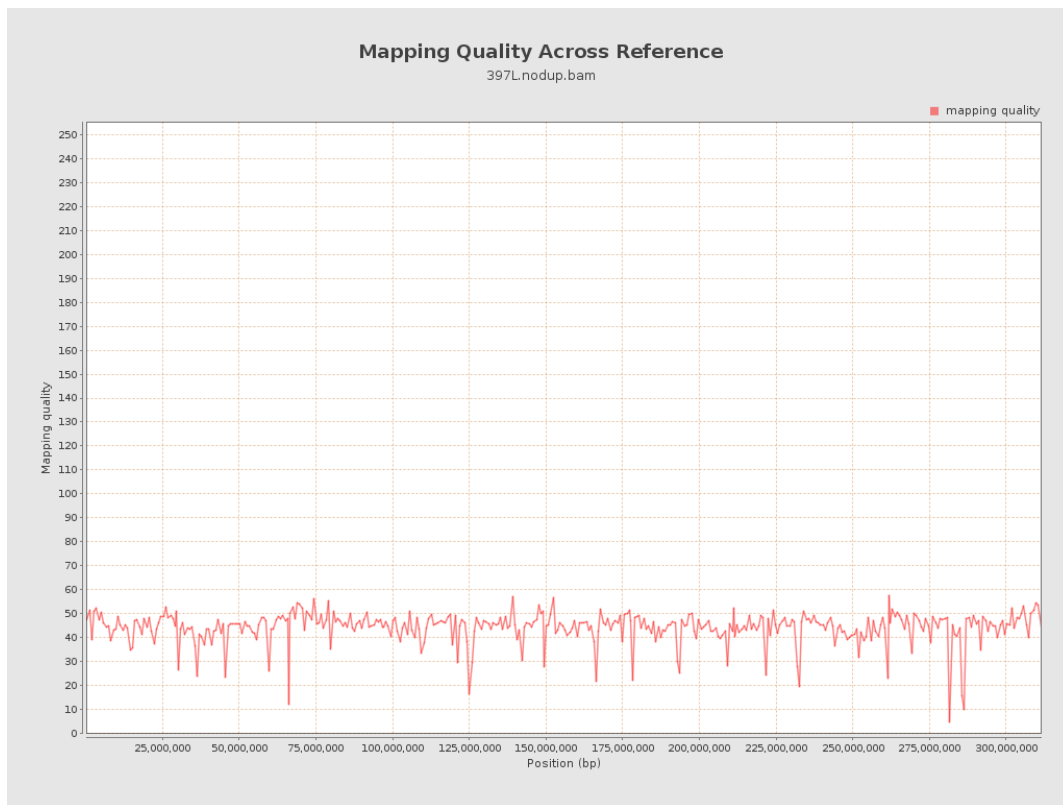
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

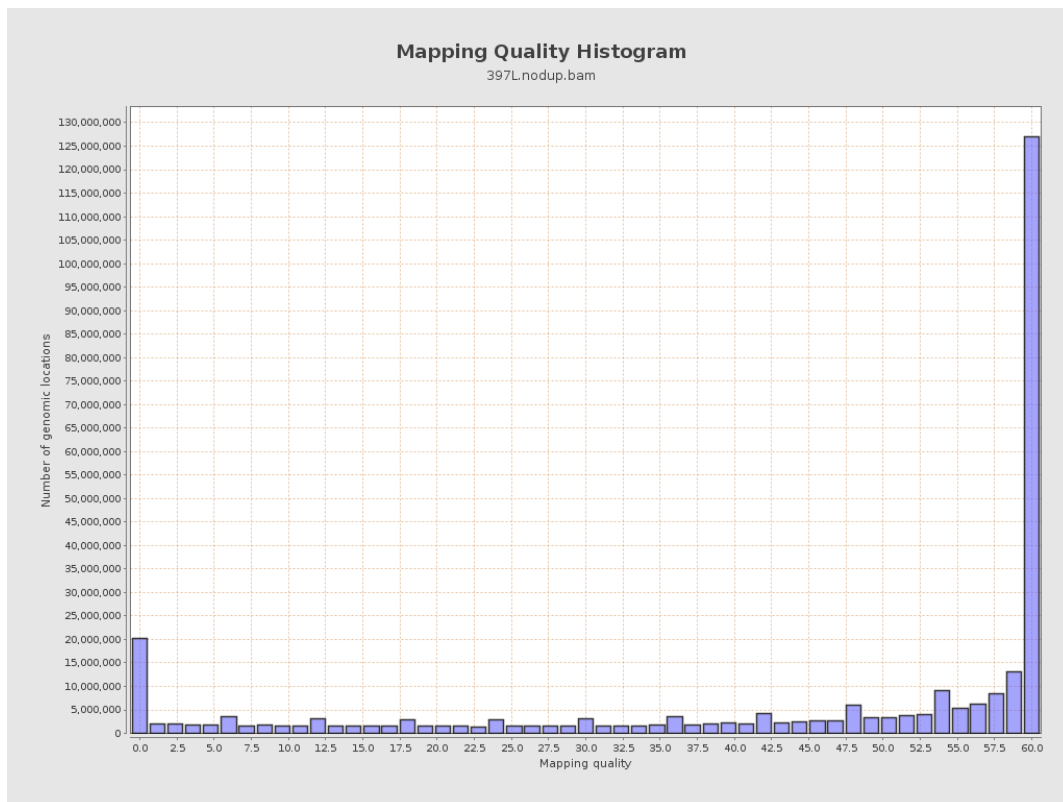


## 12. Results : Mapping Quality Across Reference

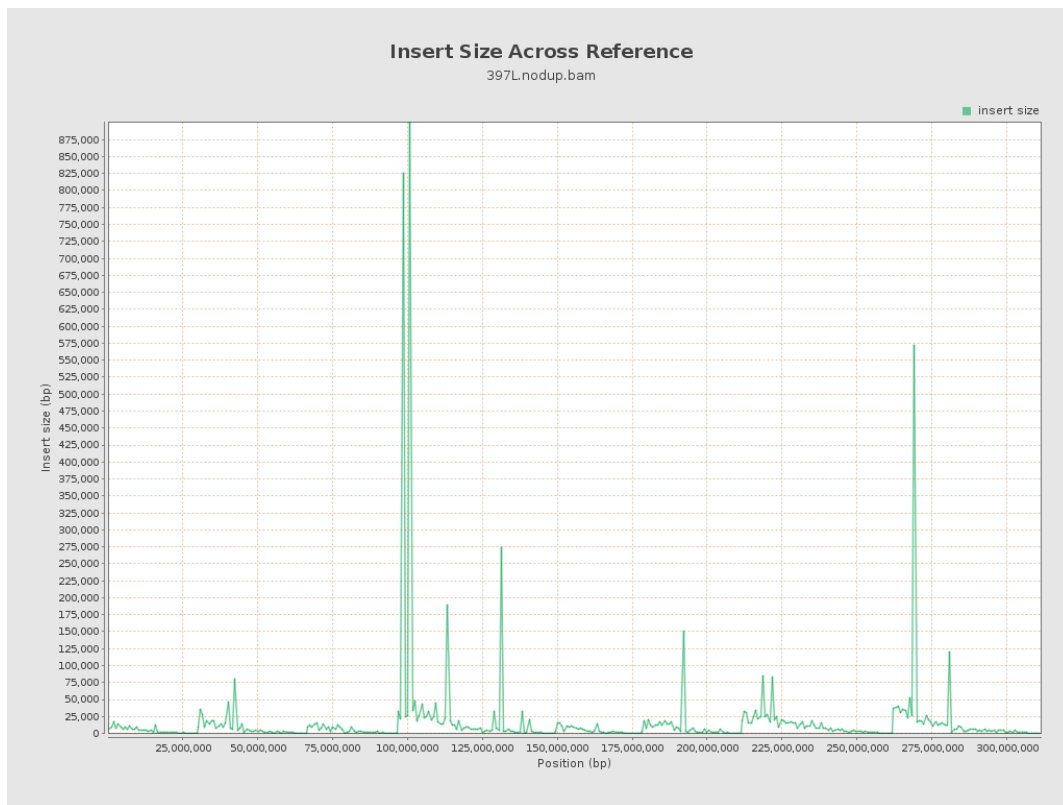




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

