

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:26:22*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/136
4
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1364 .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_406/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_406_S381_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_406/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_406_S381_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:26:21 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	51,996,587
Mapped reads	48,311,459 / 92.91%
Unmapped reads	3,685,128 / 7.09%
Mapped paired reads	48,311,459 / 92.91%
Mapped reads, first in pair	24,200,376 / 46.54%
Mapped reads, second in pair	24,111,083 / 46.37%
Mapped reads, both in pair	47,112,727 / 90.61%
Mapped reads, singletons	1,198,732 / 2.31%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	6,981,860 / 13.43%
Clipped reads	10,775,001 / 20.72%

### 2.2. ACGT Content

Number/percentage of A's	2,068,683,907 / 30.9%
Number/percentage of C's	1,277,928,804 / 19.09%
Number/percentage of T's	2,072,559,224 / 30.96%
Number/percentage of G's	1,274,595,282 / 19.04%
Number/percentage of N's	23,077 / 0%
GC Percentage	38.13%

### 2.3. Coverage

Mean	21.536
Standard Deviation	168.0473

## 2.4. Mapping Quality

Mean Mapping Quality	43.82
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## 2.5. Insert size

Mean	259,569.12
Standard Deviation	2,441,689.62
P25/Median/P75	361 / 469 / 605

## 2.6. Mismatches and indels

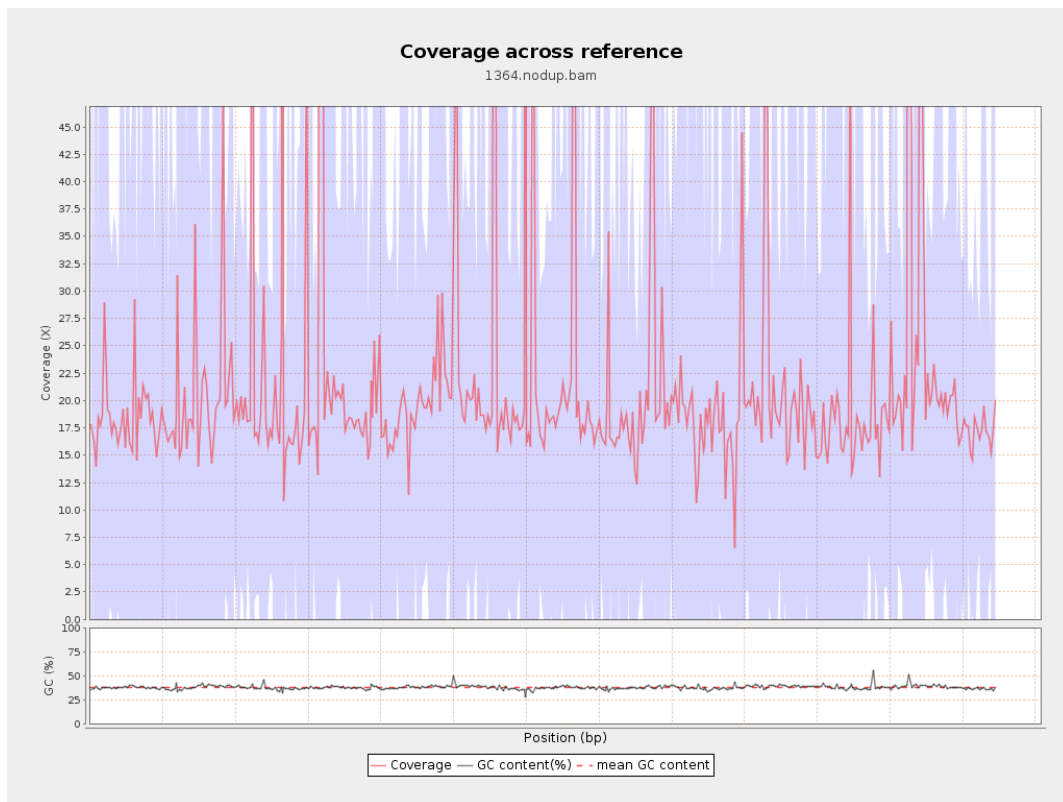
General error rate	2.34%
Mismatches	143,518,573
Insertions	4,674,283
Mapped reads with at least one insertion	8.67%
Deletions	4,676,946
Mapped reads with at least one deletion	8.57%
Homopolymer indels	56.54%

## 2.7. Chromosome stats

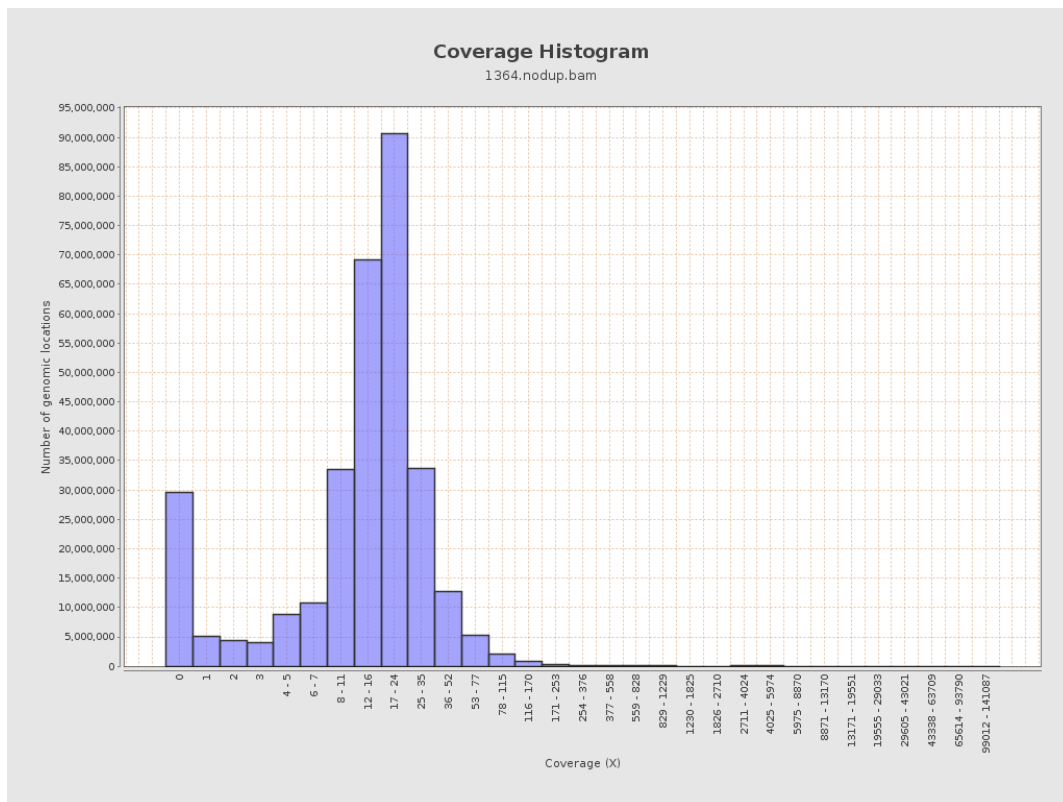
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	541993922	18.234	58.7294

LT669789.1	36598175	796109116	21.7527	181.0022
LT669790.1	30422129	729712289	23.9862	198.2748
LT669791.1	52758100	1121451296	21.2565	162.6502
LT669792.1	28376109	617014328	21.7441	203.0626
LT669793.1	33388210	666246713	19.9546	116.0844
LT669794.1	50579949	1020709720	20.1801	141.99
LT669795.1	49795044	1218300030	24.4663	213.3523

### 3. Results : Coverage across reference

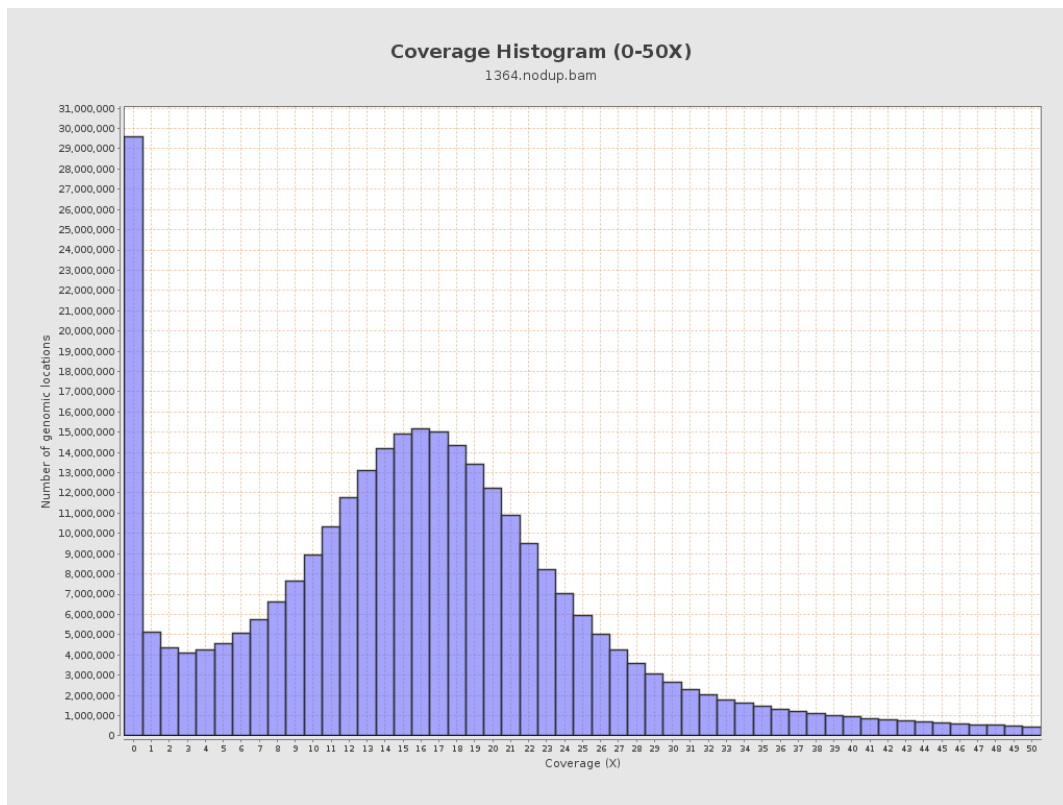


## 4. Results : Coverage Histogram

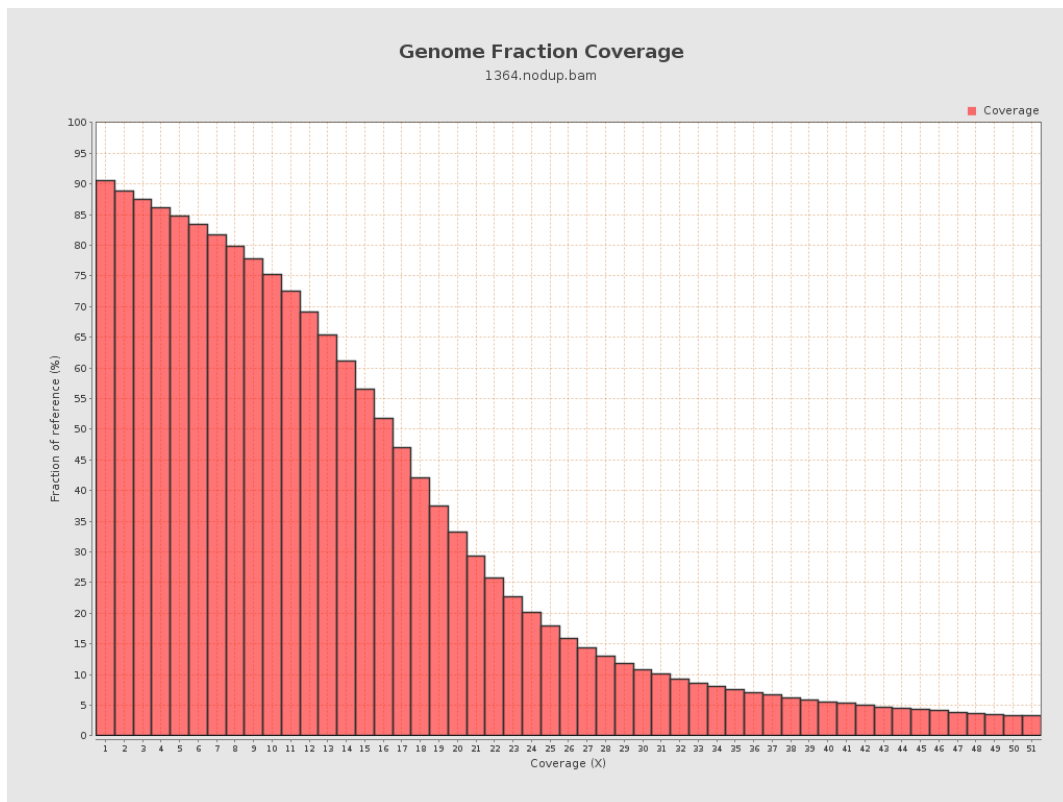




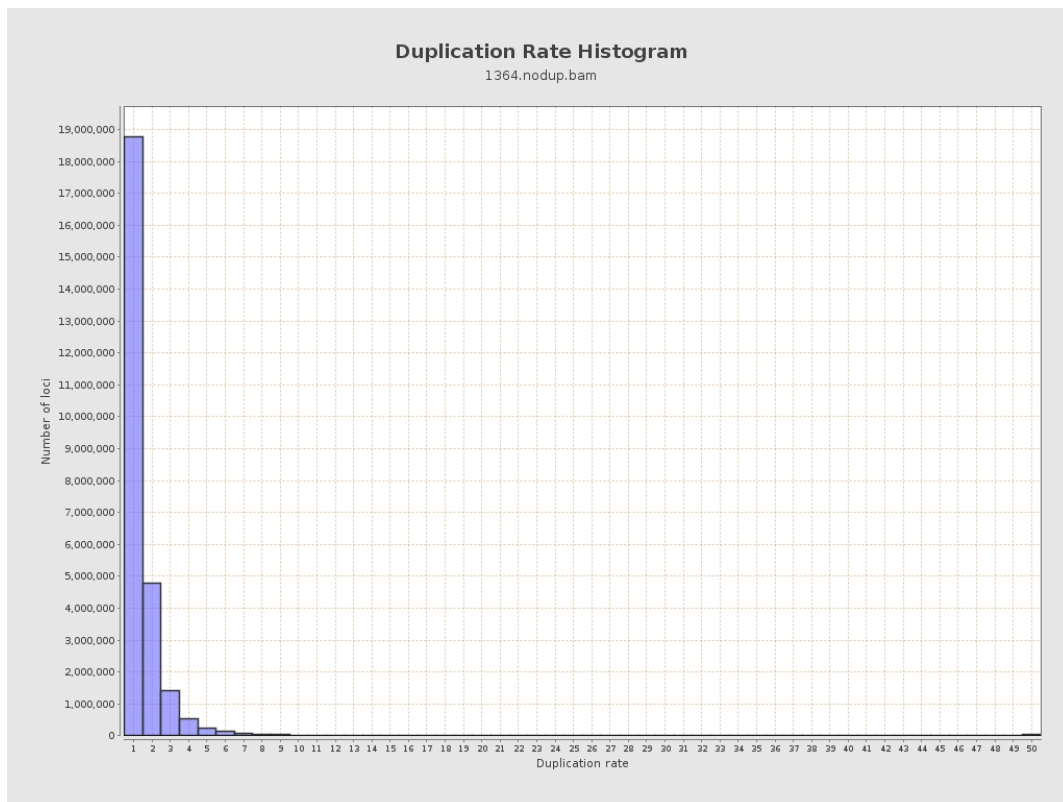
## 5. Results : Coverage Histogram (0-50X)



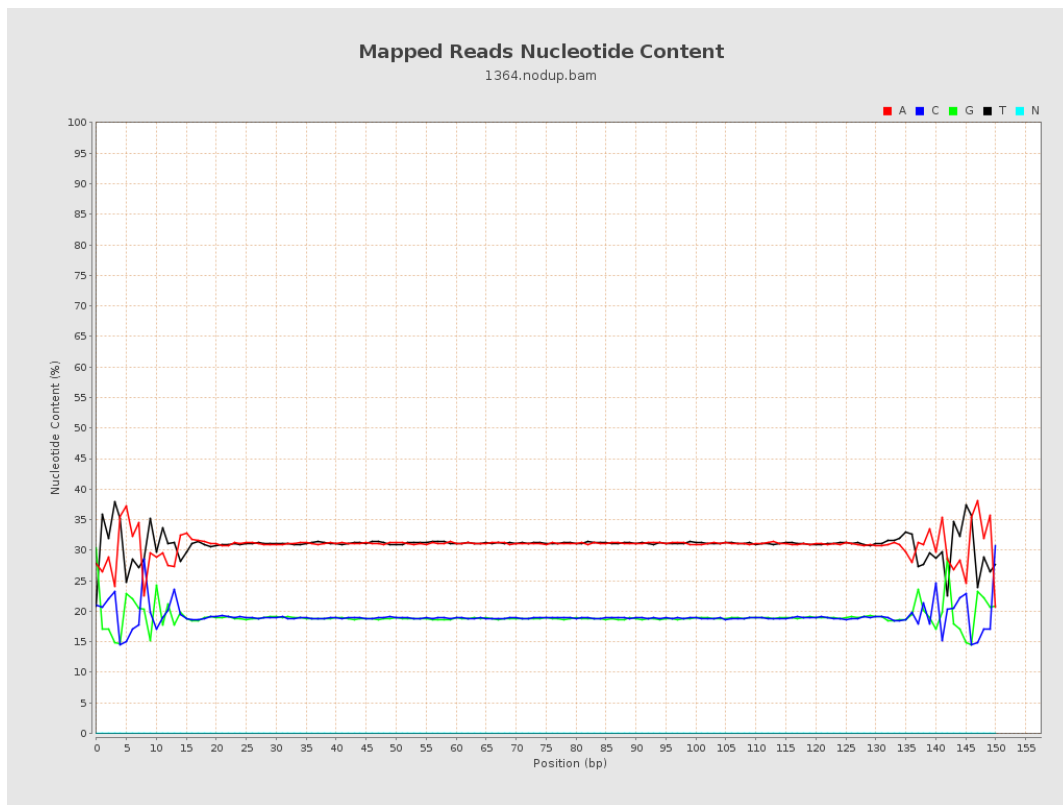
## 6. Results : Genome Fraction Coverage



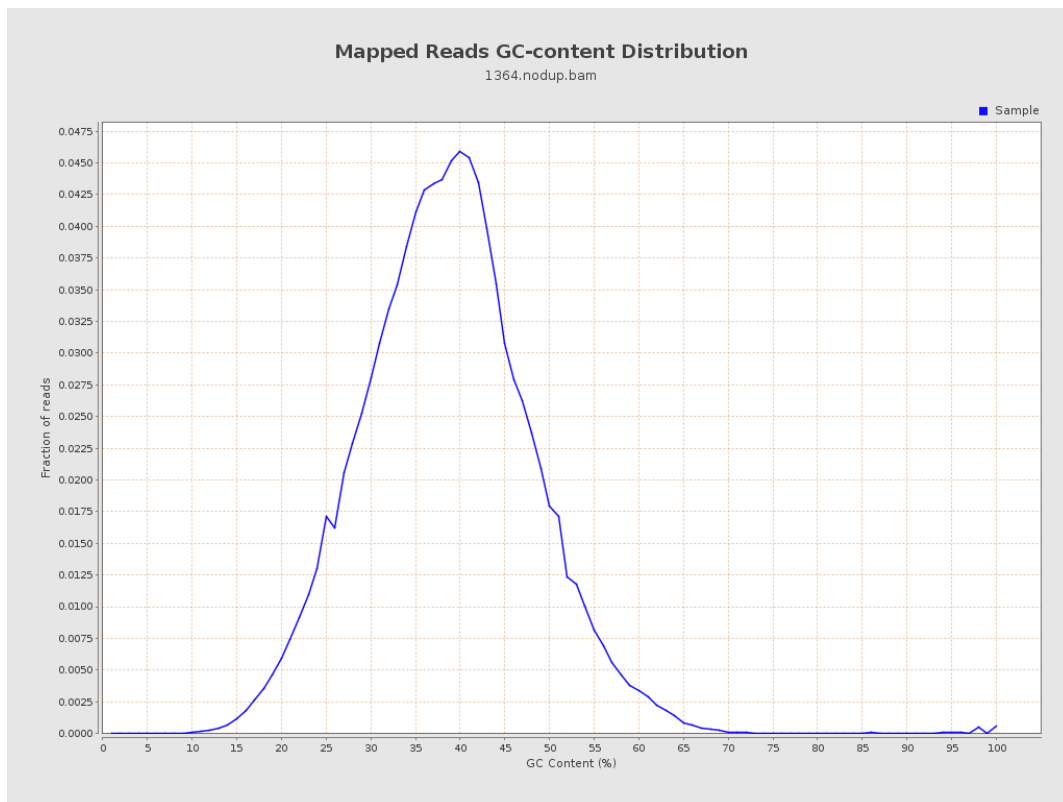
## 7. Results : Duplication Rate Histogram



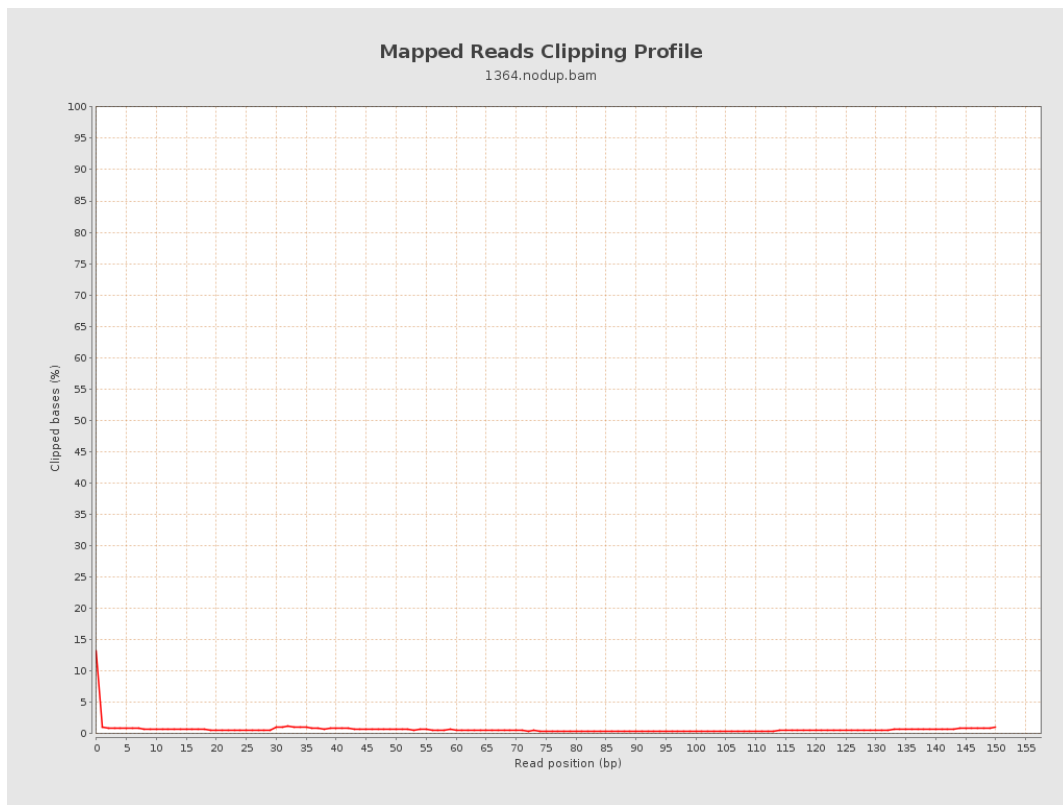
## 8. Results : Mapped Reads Nucleotide Content



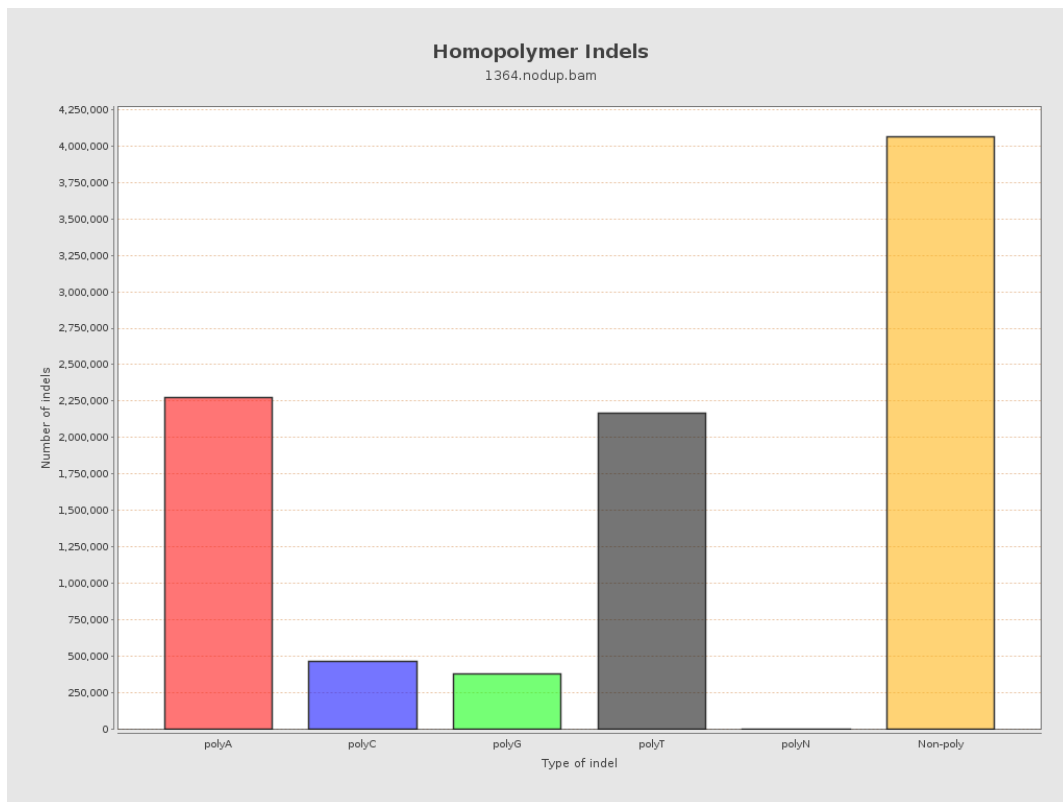
## 9. Results : Mapped Reads GC-content Distribution



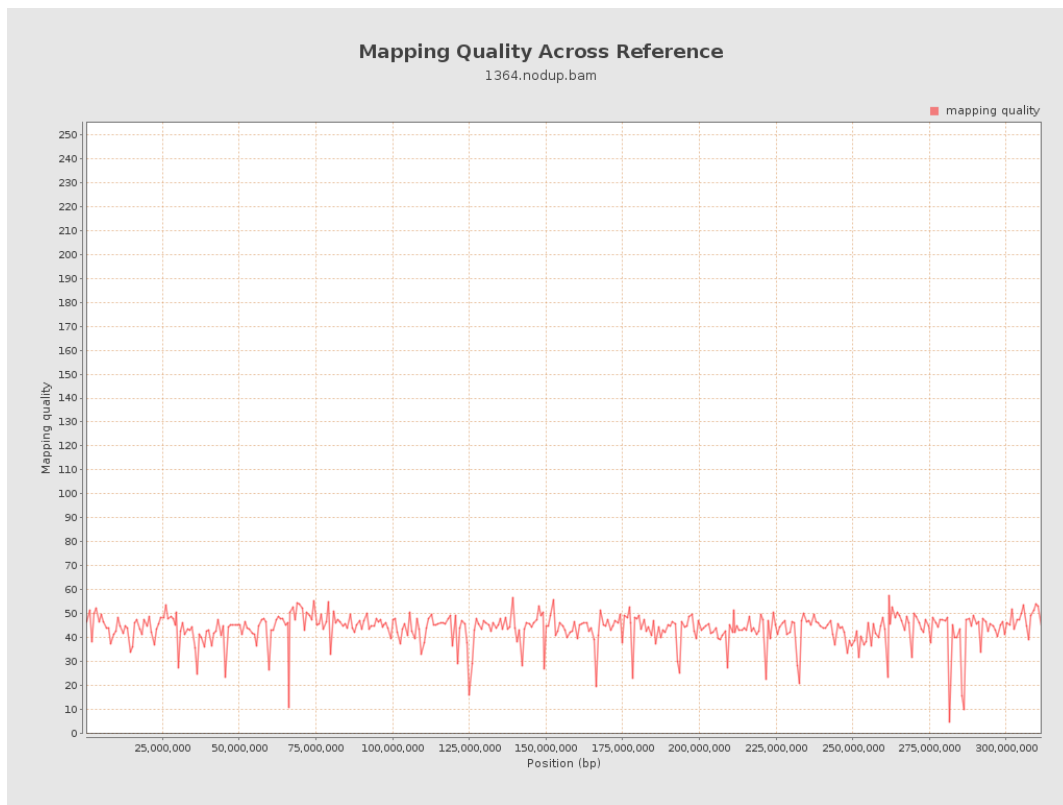
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

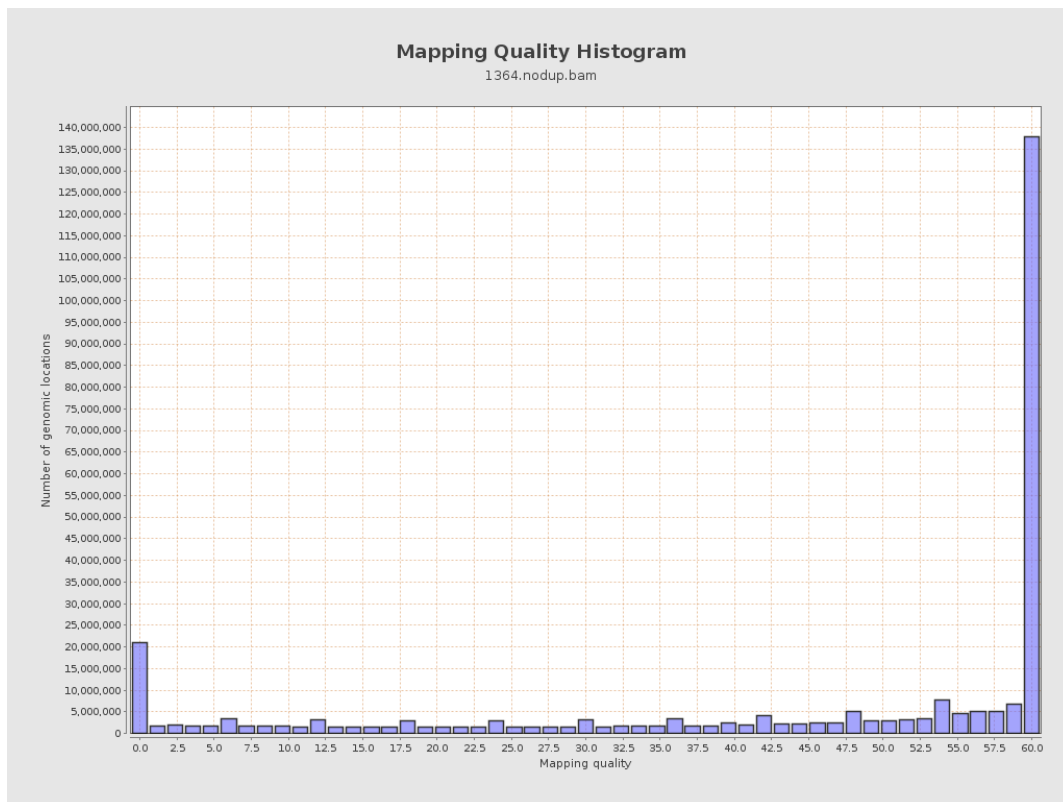


## 12. Results : Mapping Quality Across Reference

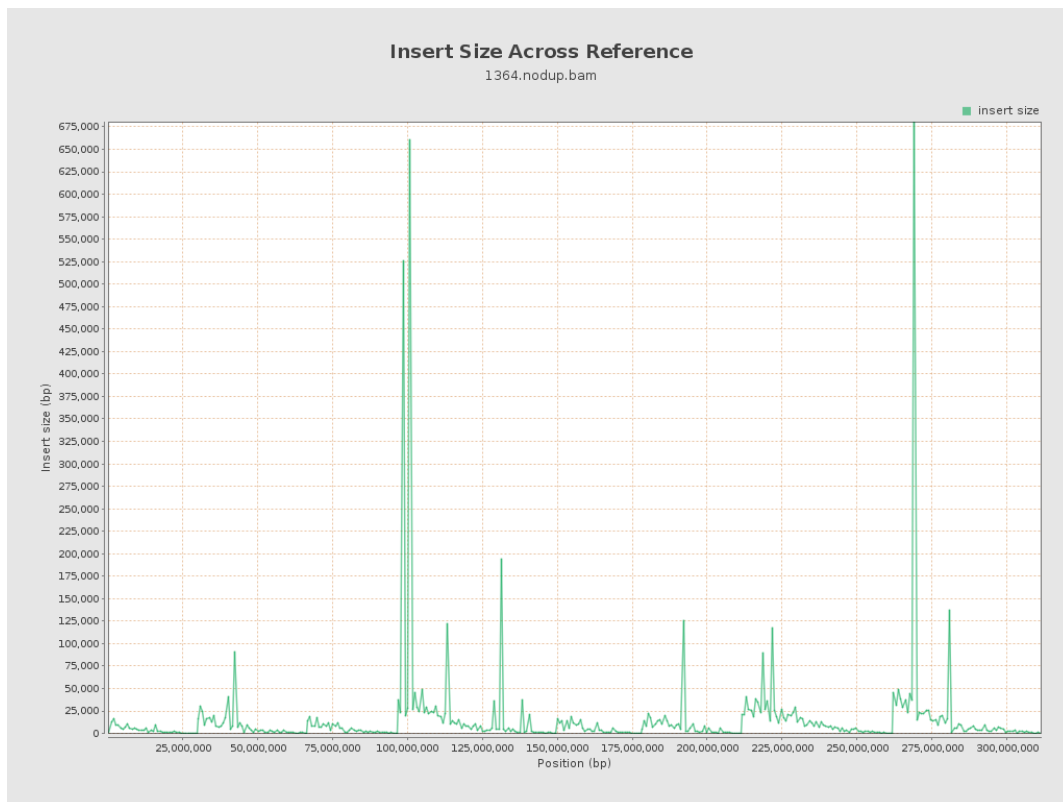




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

