

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:28:25*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/140
8
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1408 .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_185/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_185_S275_L002 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_185/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_185_S275_L002 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:28:24 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	57,502,611
Mapped reads	53,519,149 / 93.07%
Unmapped reads	3,983,462 / 6.93%
Mapped paired reads	53,519,149 / 93.07%
Mapped reads, first in pair	26,812,477 / 46.63%
Mapped reads, second in pair	26,706,672 / 46.44%
Mapped reads, both in pair	52,343,854 / 91.03%
Mapped reads, singletons	1,175,295 / 2.04%
Read min/max/mean length	30 / 151 / 148.21
Duplicated reads (flagged)	8,299,068 / 14.43%
Clipped reads	11,647,677 / 20.26%

### 2.2. ACGT Content

Number/percentage of A's	2,300,457,691 / 30.95%
Number/percentage of C's	1,417,252,344 / 19.07%
Number/percentage of T's	2,300,727,599 / 30.95%
Number/percentage of G's	1,414,073,929 / 19.03%
Number/percentage of N's	31,708 / 0%
GC Percentage	38.09%

### 2.3. Coverage

Mean	23.9109
Standard Deviation	177.3684

## 2.4. Mapping Quality

Mean Mapping Quality	44.62
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## 2.5. Insert size

Mean	233,271.3
Standard Deviation	2,291,117.79
P25/Median/P75	343 / 447 / 584

## 2.6. Mismatches and indels

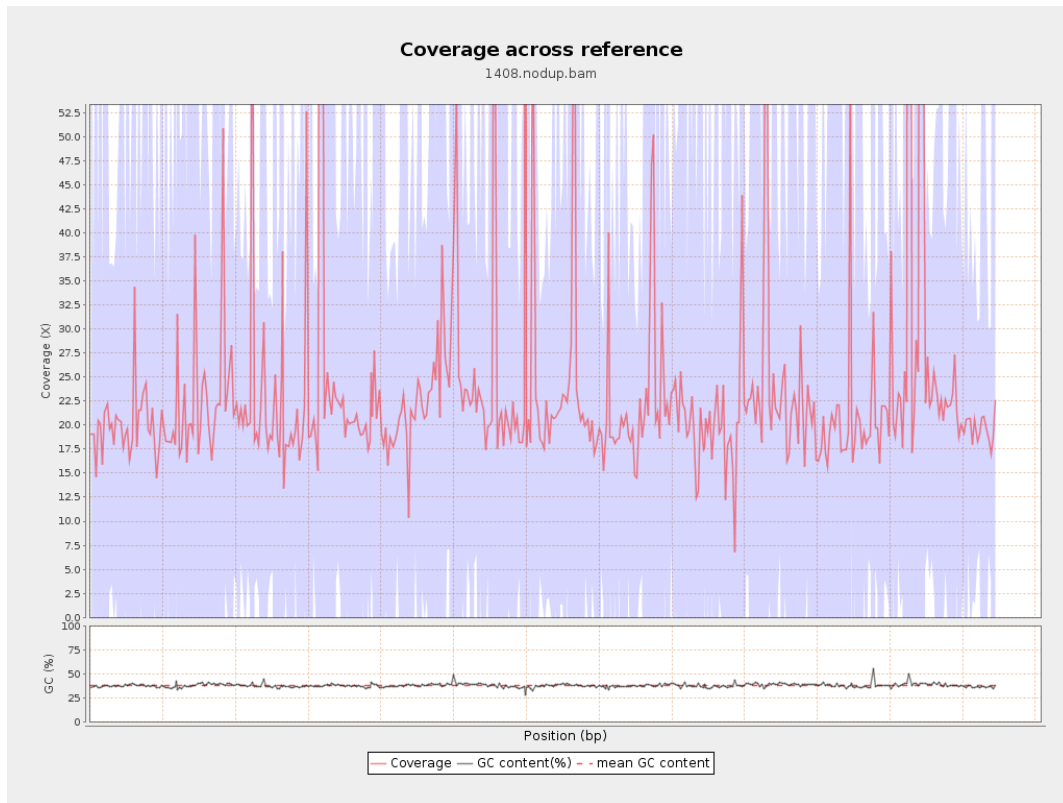
General error rate	2.25%
Mismatches	153,411,951
Insertions	4,908,879
Mapped reads with at least one insertion	8.23%
Deletions	5,013,466
Mapped reads with at least one deletion	8.32%
Homopolymer indels	57.06%

## 2.7. Chromosome stats

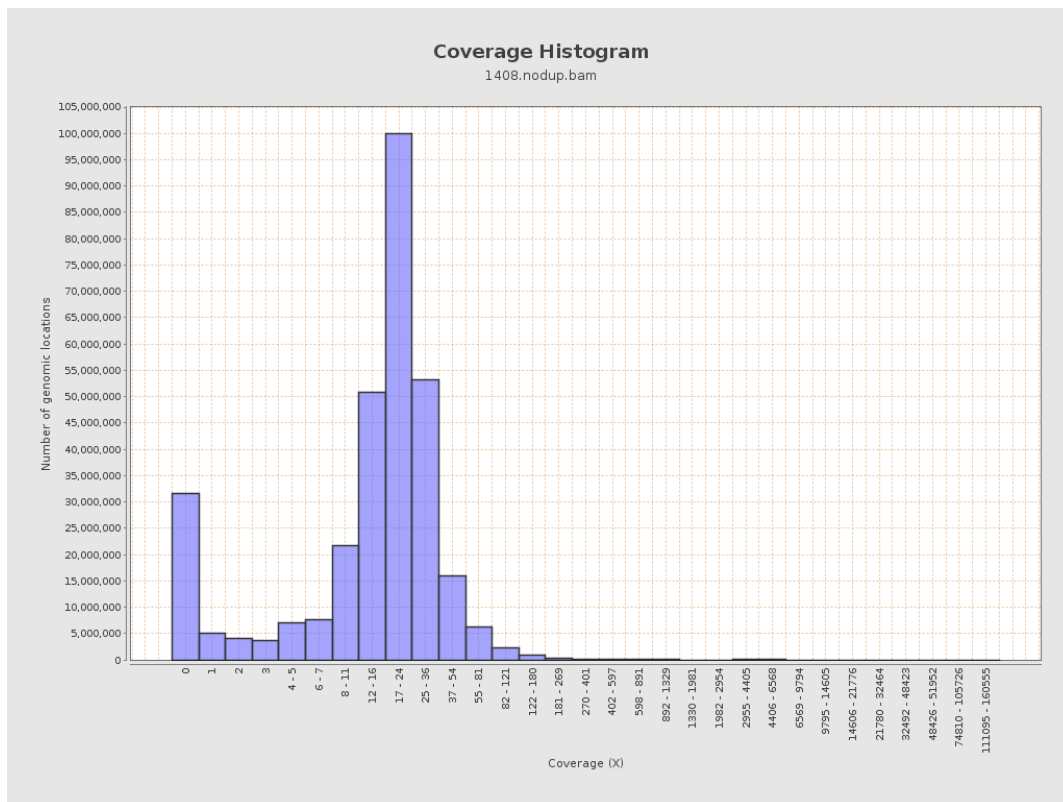
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	588029935	19.7828	52.2253

LT669789.1	36598175	856883181	23.4133	161.4073
LT669790.1	30422129	791998348	26.0336	189.918
LT669791.1	52758100	1238758762	23.48	144.6447
LT669792.1	28376109	671959082	23.6805	175.6181
LT669793.1	33388210	729232813	21.841	116.0455
LT669794.1	50579949	1134988342	22.4395	141.8275
LT669795.1	49795044	1439778149	28.9141	291.2555

### 3. Results : Coverage across reference

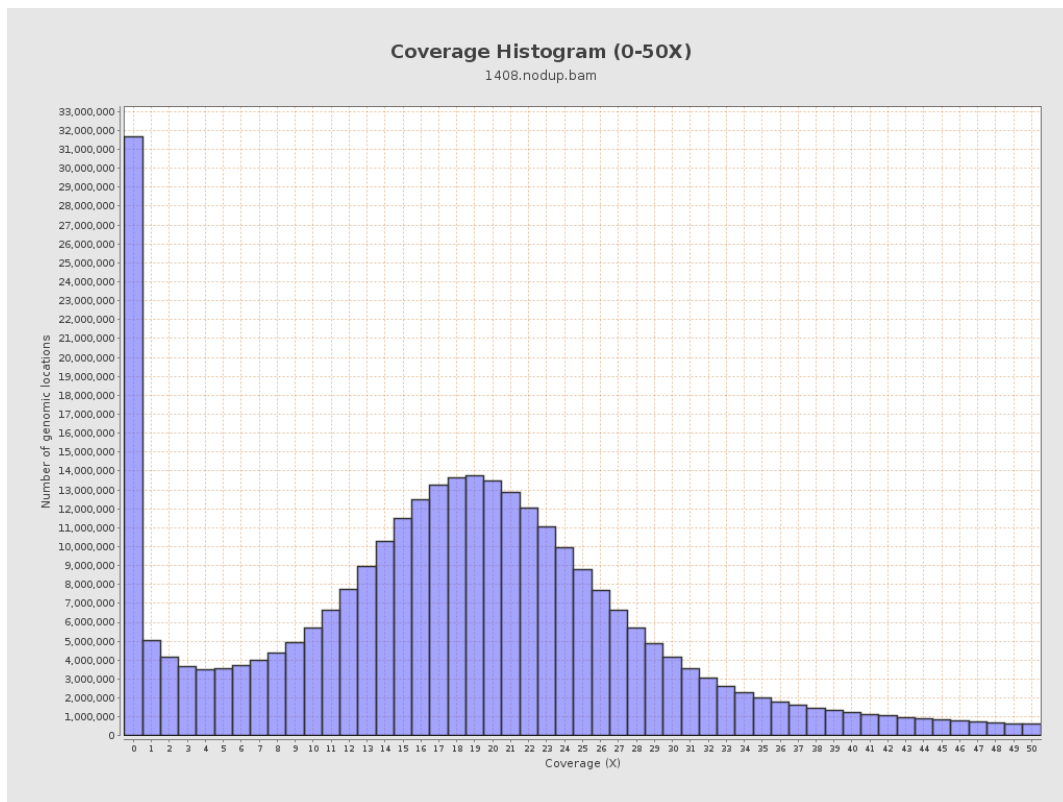


## 4. Results : Coverage Histogram

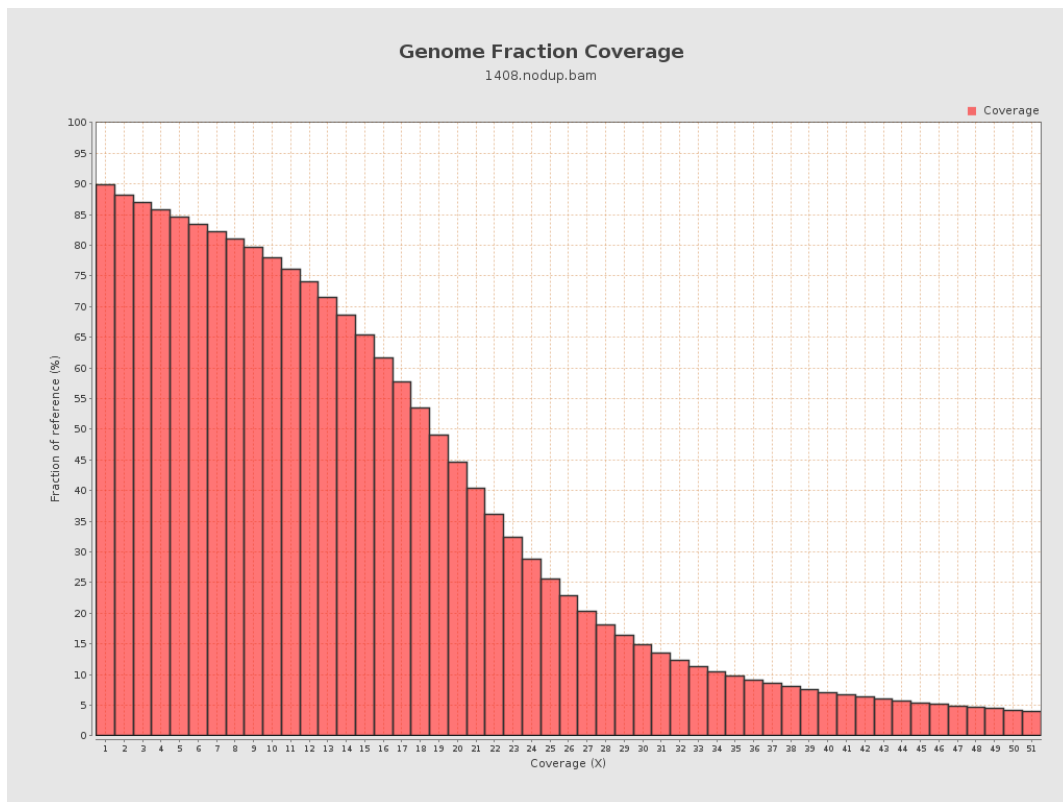




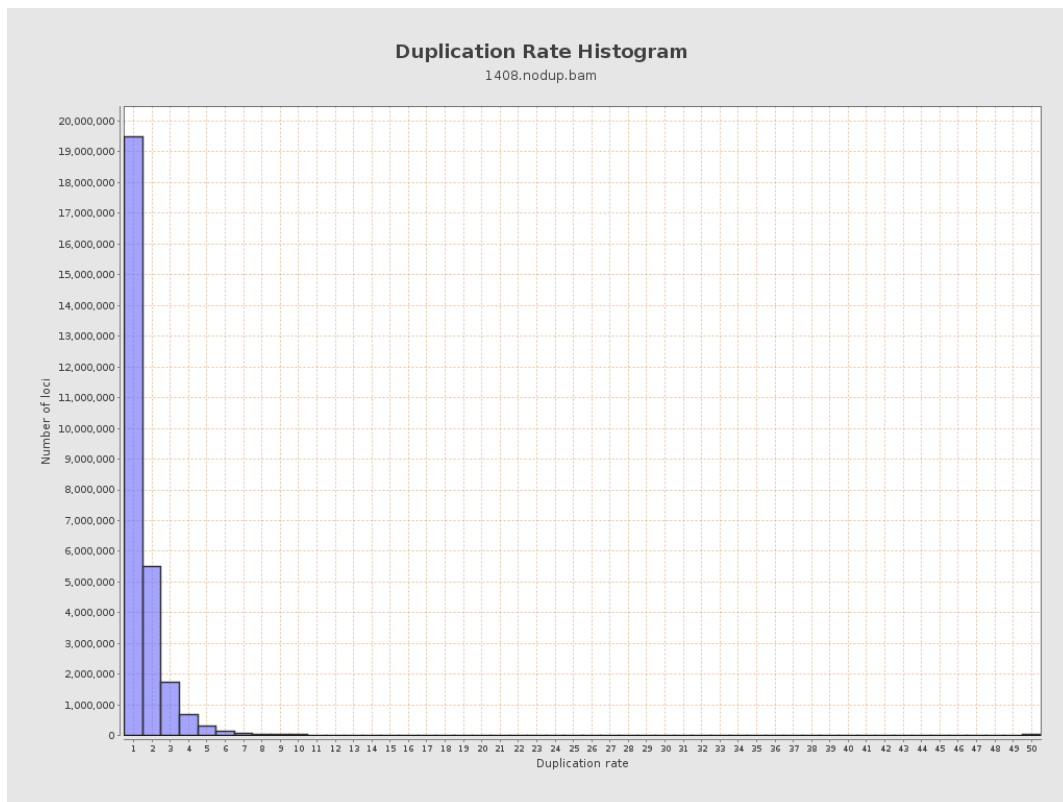
## 5. Results : Coverage Histogram (0-50X)



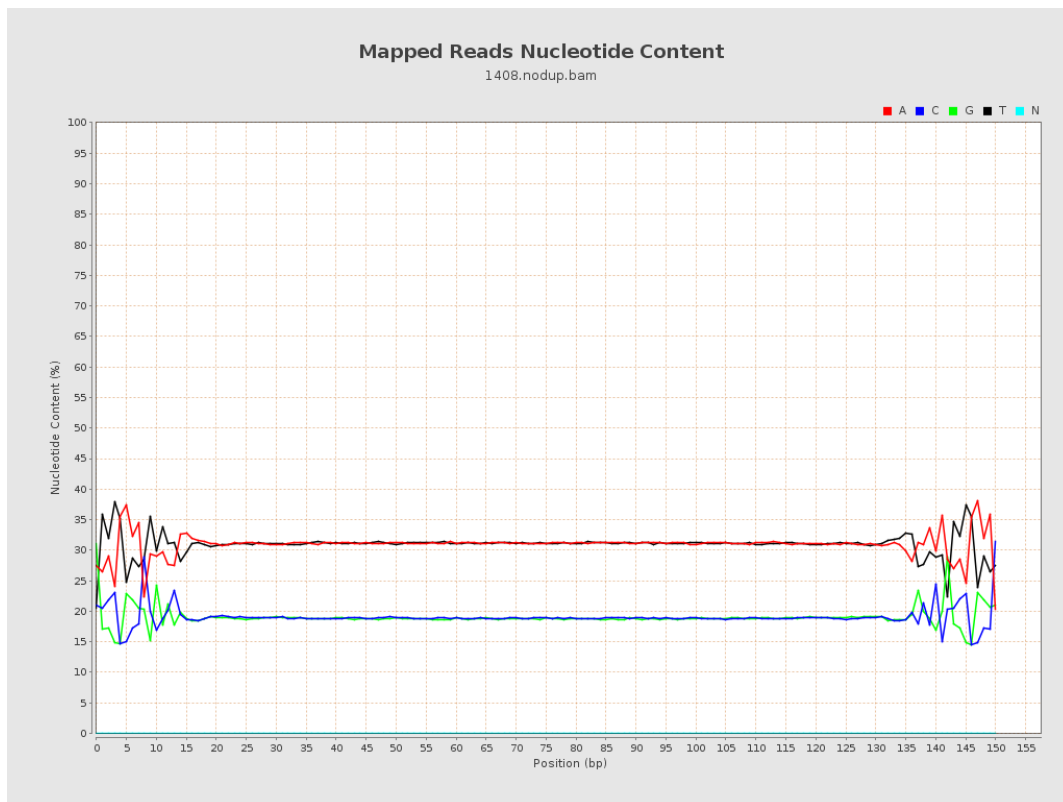
## 6. Results : Genome Fraction Coverage



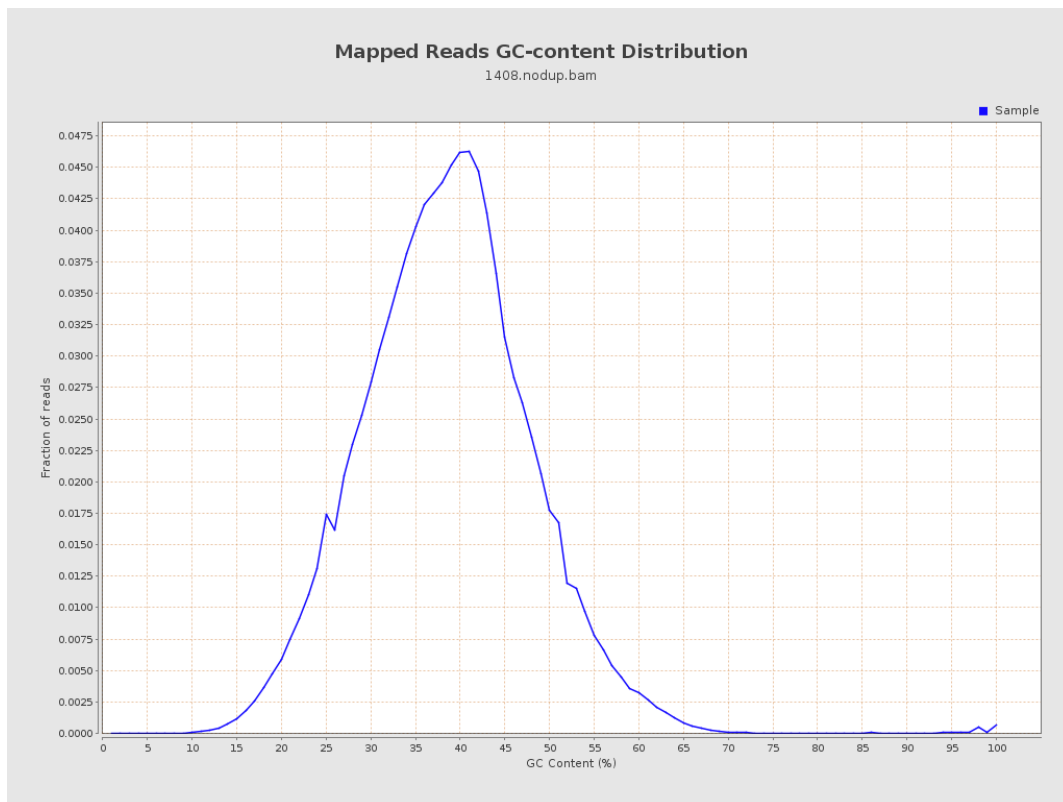
## 7. Results : Duplication Rate Histogram



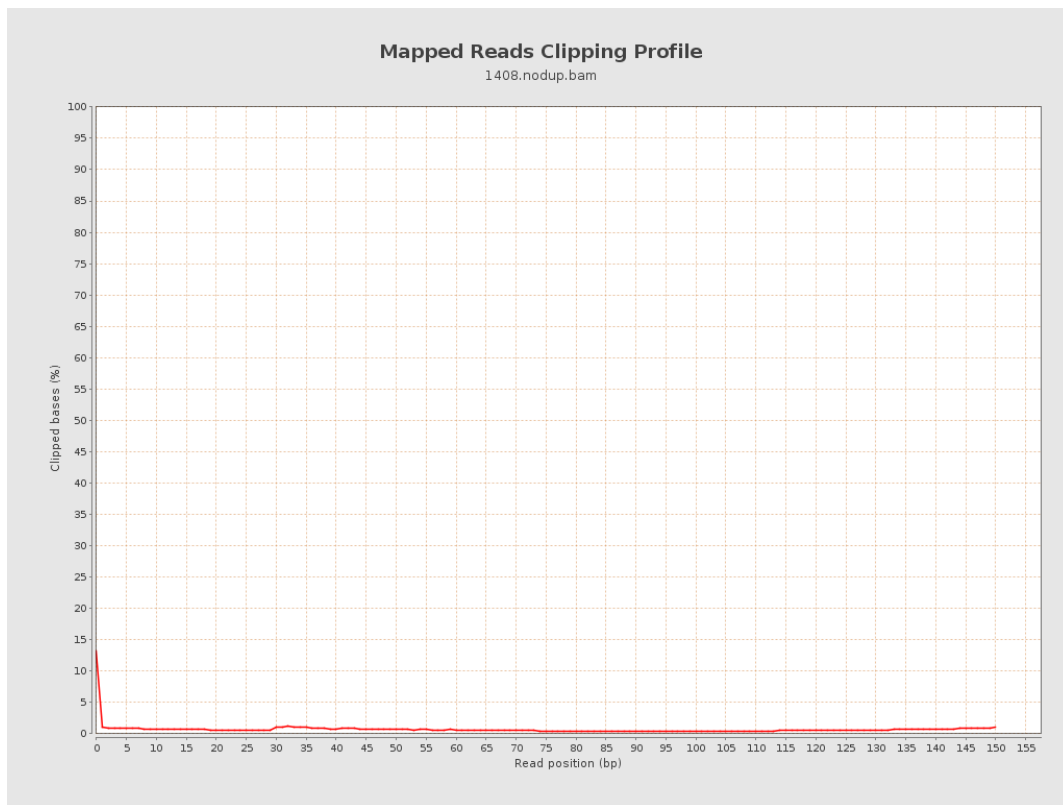
## 8. Results : Mapped Reads Nucleotide Content



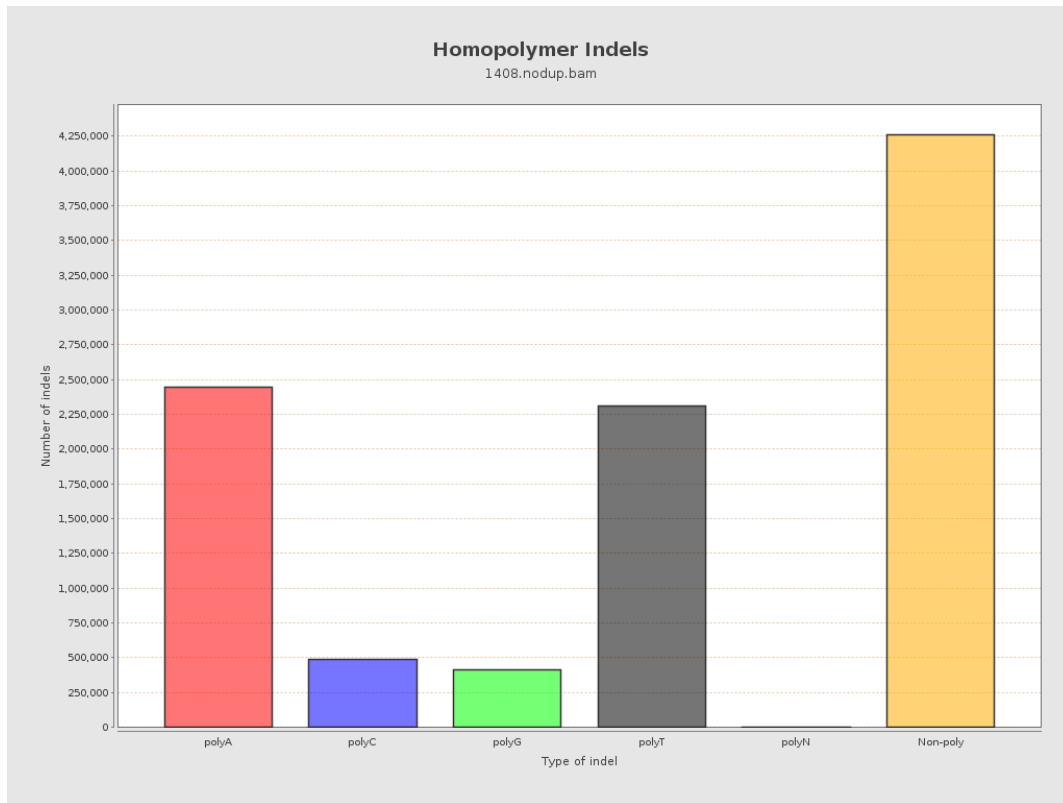
## 9. Results : Mapped Reads GC-content Distribution



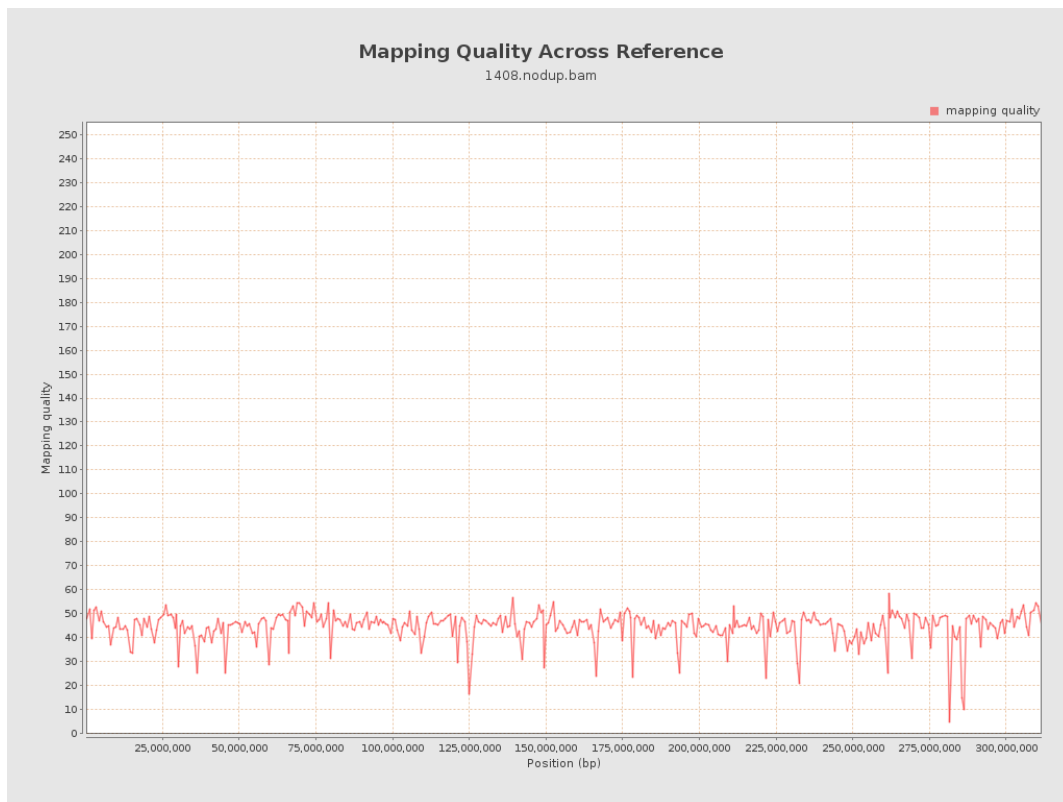
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

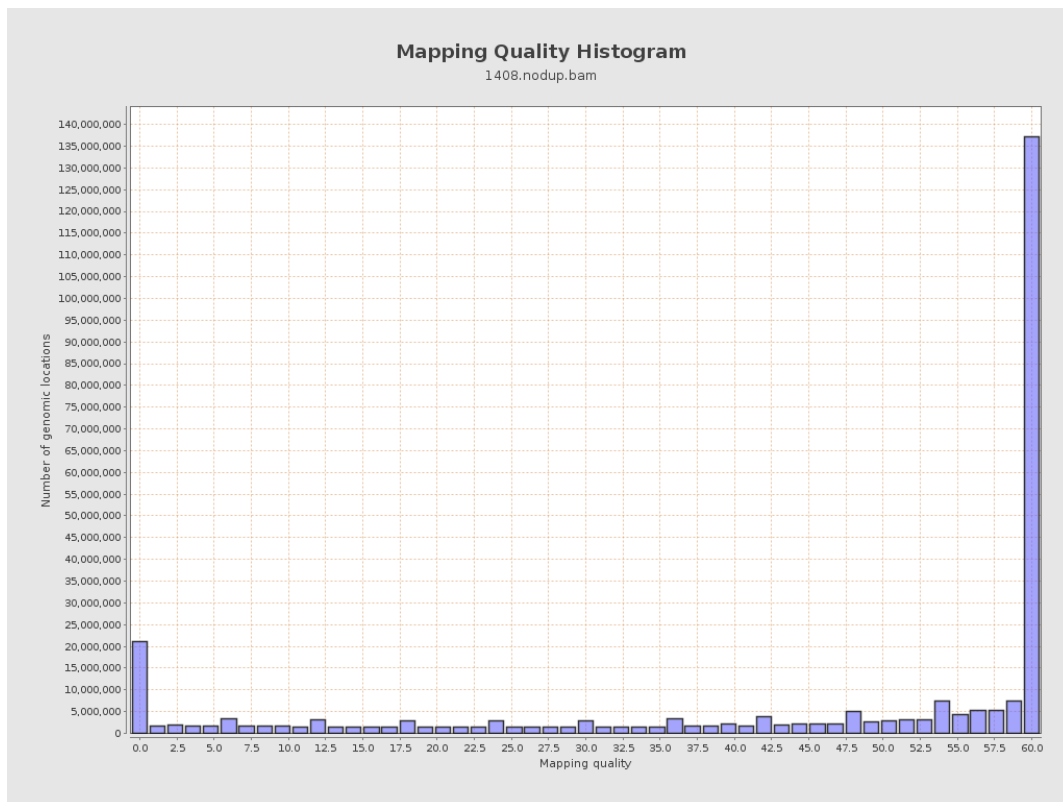


## 12. Results : Mapping Quality Across Reference

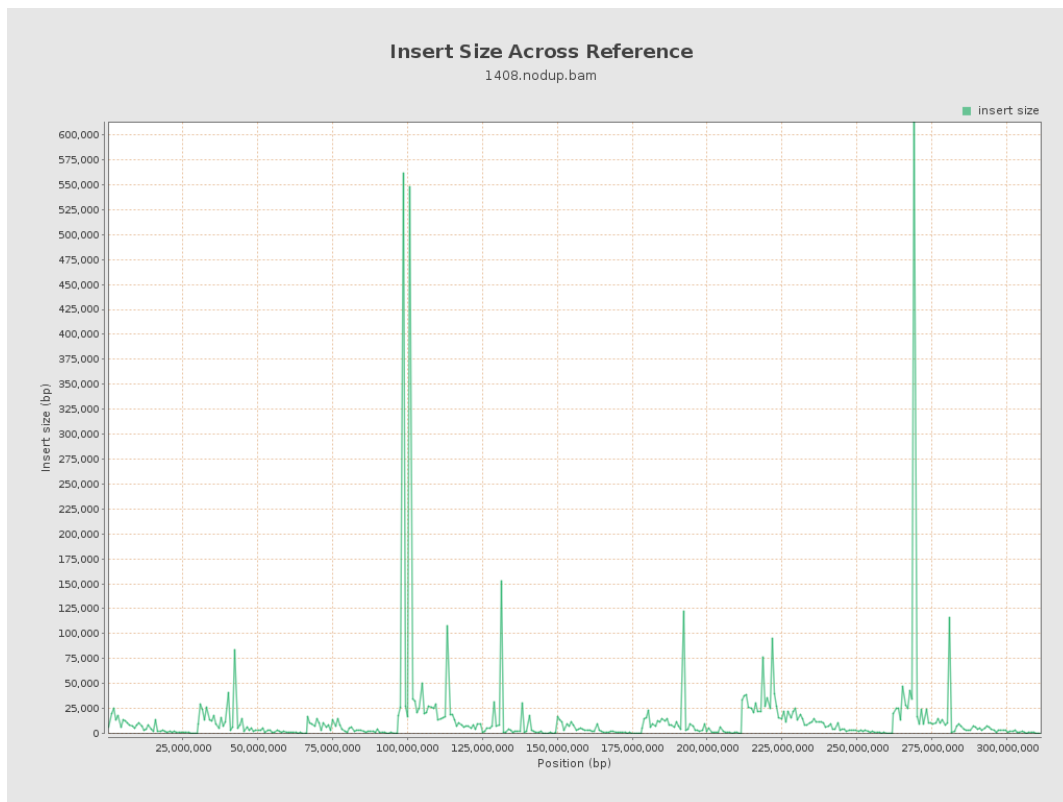




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

