

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:33:22*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/140
2
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1402 .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_125/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_125_S215_L002 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_125/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_125_S215_L002 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:33:21 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	73,755,392
Mapped reads	66,719,988 / 90.46%
Unmapped reads	7,035,404 / 9.54%
Mapped paired reads	66,719,988 / 90.46%
Mapped reads, first in pair	33,409,400 / 45.3%
Mapped reads, second in pair	33,310,588 / 45.16%
Mapped reads, both in pair	64,903,560 / 88%
Mapped reads, singletons	1,816,428 / 2.46%
Read min/max/mean length	30 / 151 / 148.2
Duplicated reads (flagged)	11,921,189 / 16.16%
Clipped reads	15,203,666 / 20.61%

### 2.2. ACGT Content

Number/percentage of A's	2,841,506,109 / 30.86%
Number/percentage of C's	1,762,075,713 / 19.13%
Number/percentage of T's	2,847,198,317 / 30.92%
Number/percentage of G's	1,757,899,584 / 19.09%
Number/percentage of N's	38,328 / 0%
GC Percentage	38.22%

### 2.3. Coverage

Mean	29.6273
Standard Deviation	256.3006

## 2.4. Mapping Quality

Mean Mapping Quality	43.91
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## 2.5. Insert size

Mean	248,708.31
Standard Deviation	2,389,289.33
P25/Median/P75	319 / 418 / 549

## 2.6. Mismatches and indels

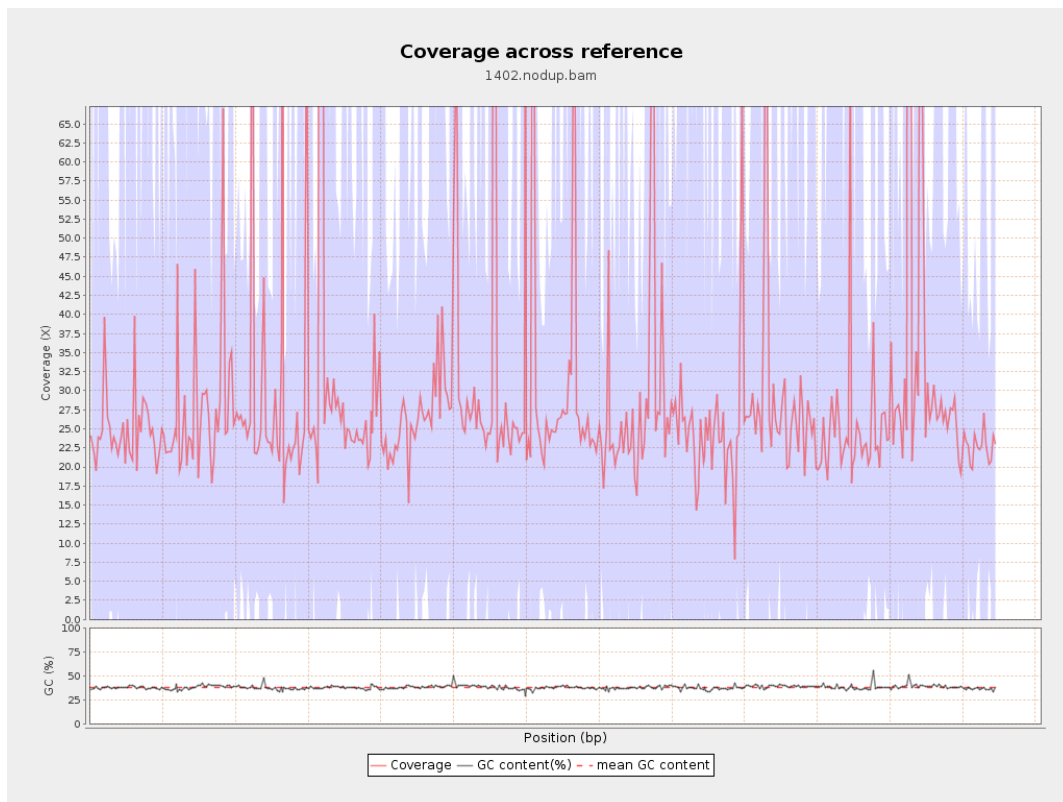
General error rate	2.35%
Mismatches	198,533,716
Insertions	6,568,443
Mapped reads with at least one insertion	8.79%
Deletions	6,429,800
Mapped reads with at least one deletion	8.53%
Homopolymer indels	56.68%

## 2.7. Chromosome stats

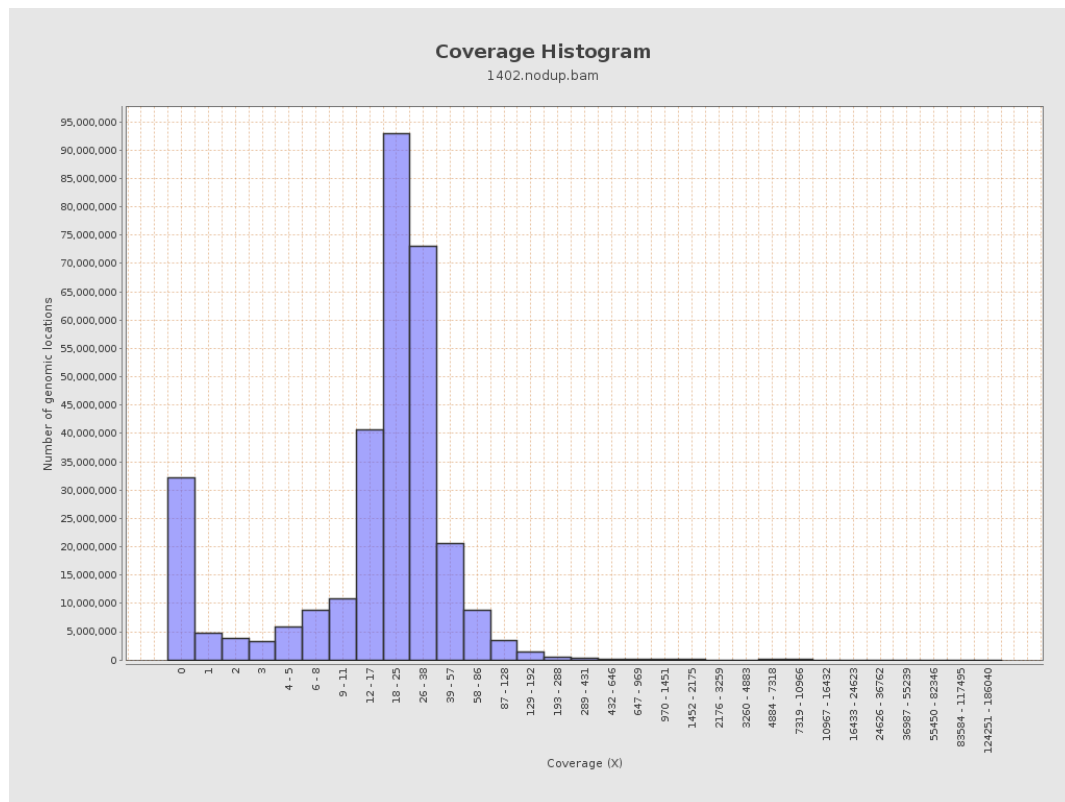
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	727512572	24.4753	95.2167

LT669789.1	36598175	1073406651	29.3295	269.168
LT669790.1	30422129	1057662691	34.7662	336.731
LT669791.1	52758100	1547934690	29.3402	259.2305
LT669792.1	28376109	839389698	29.5809	267.2143
LT669793.1	33388210	921380069	27.596	223.0925
LT669794.1	50579949	1390647299	27.494	204.8088
LT669795.1	49795044	1675194518	33.6418	308.6435

### 3. Results : Coverage across reference

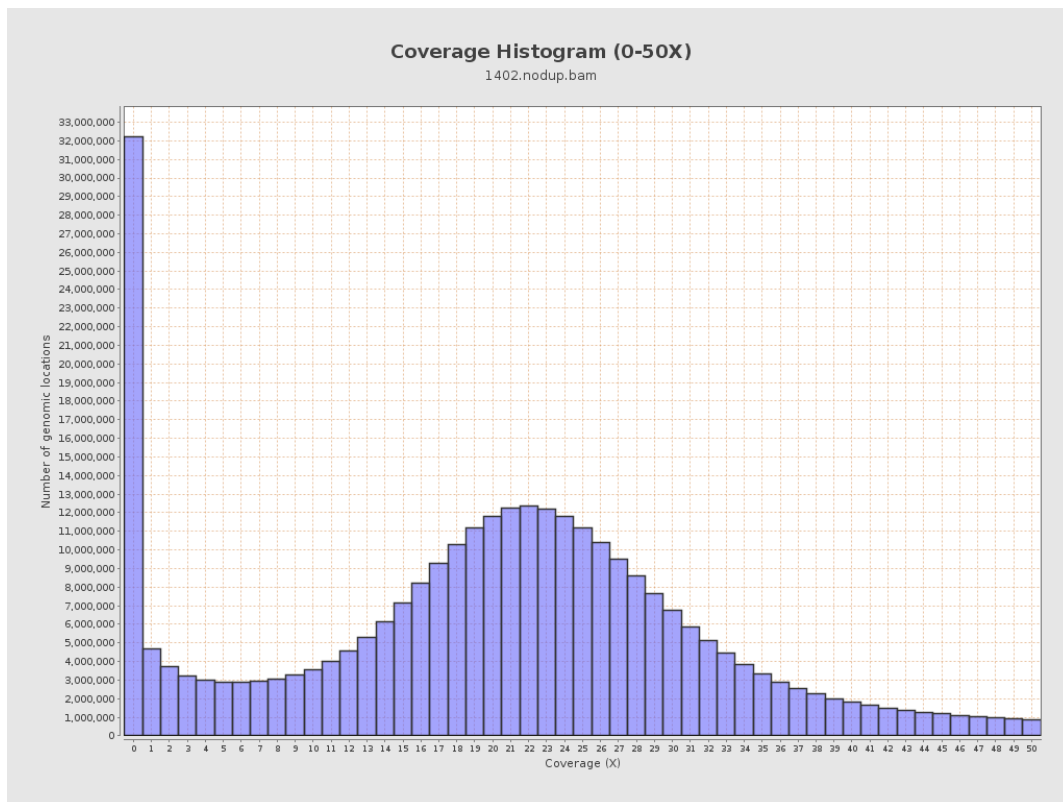


## 4. Results : Coverage Histogram

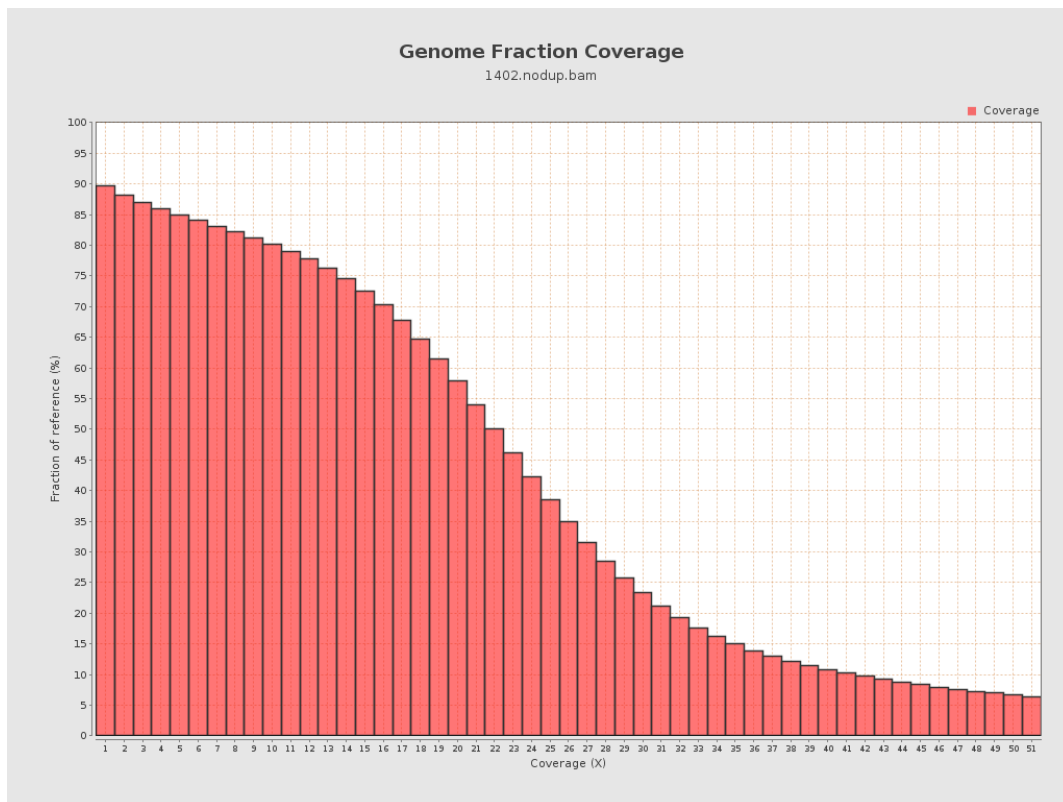




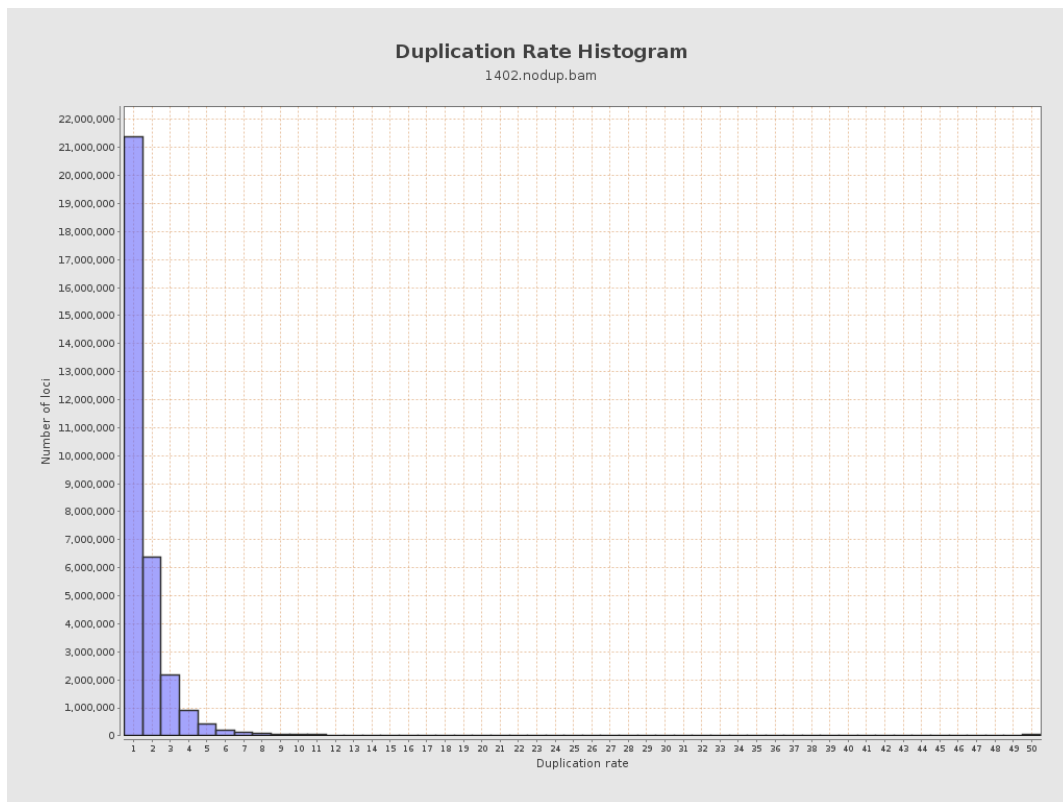
## 5. Results : Coverage Histogram (0-50X)



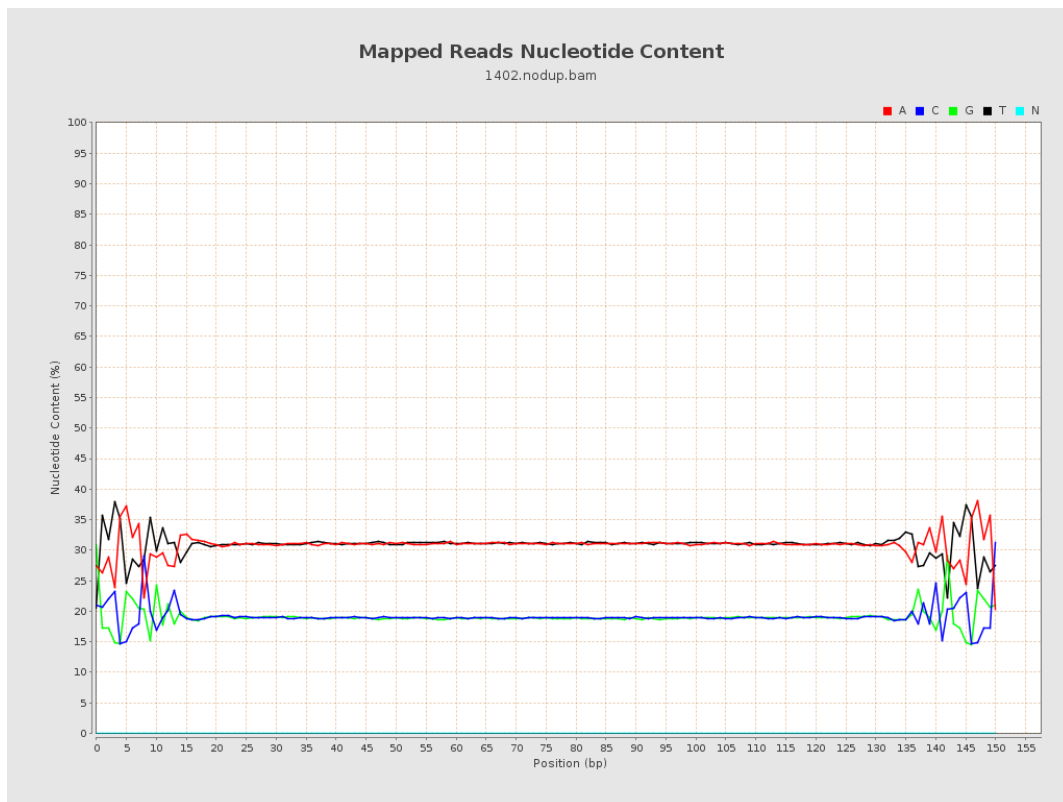
## 6. Results : Genome Fraction Coverage



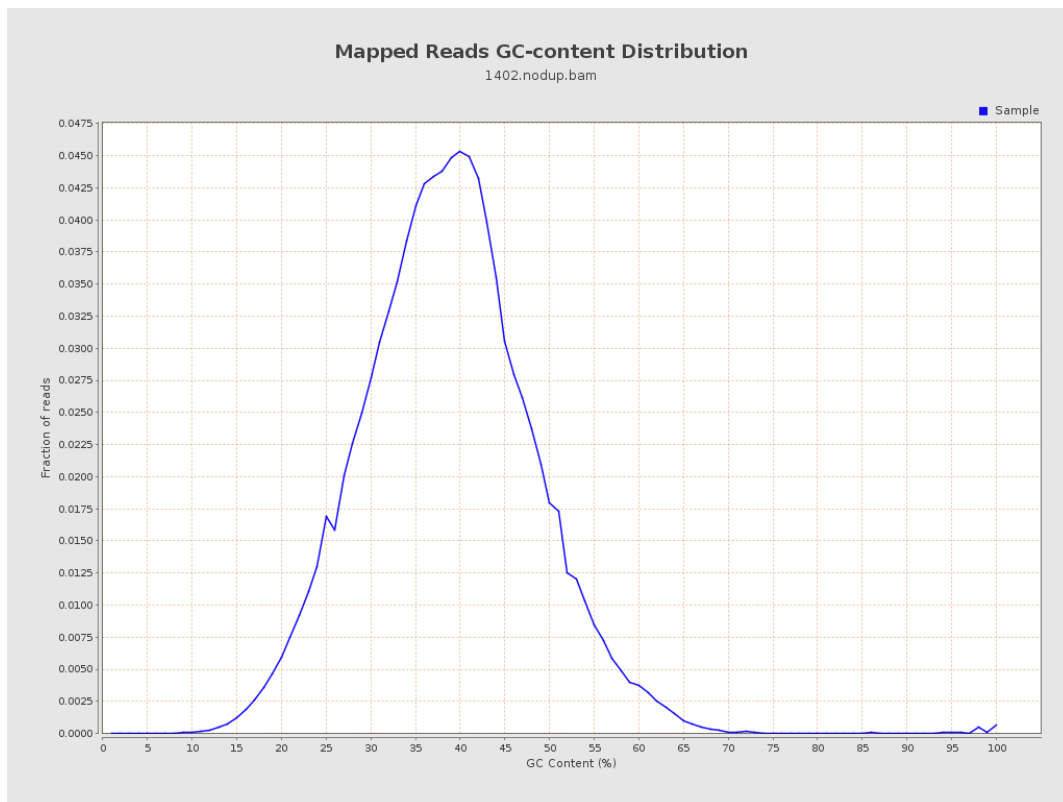
## 7. Results : Duplication Rate Histogram



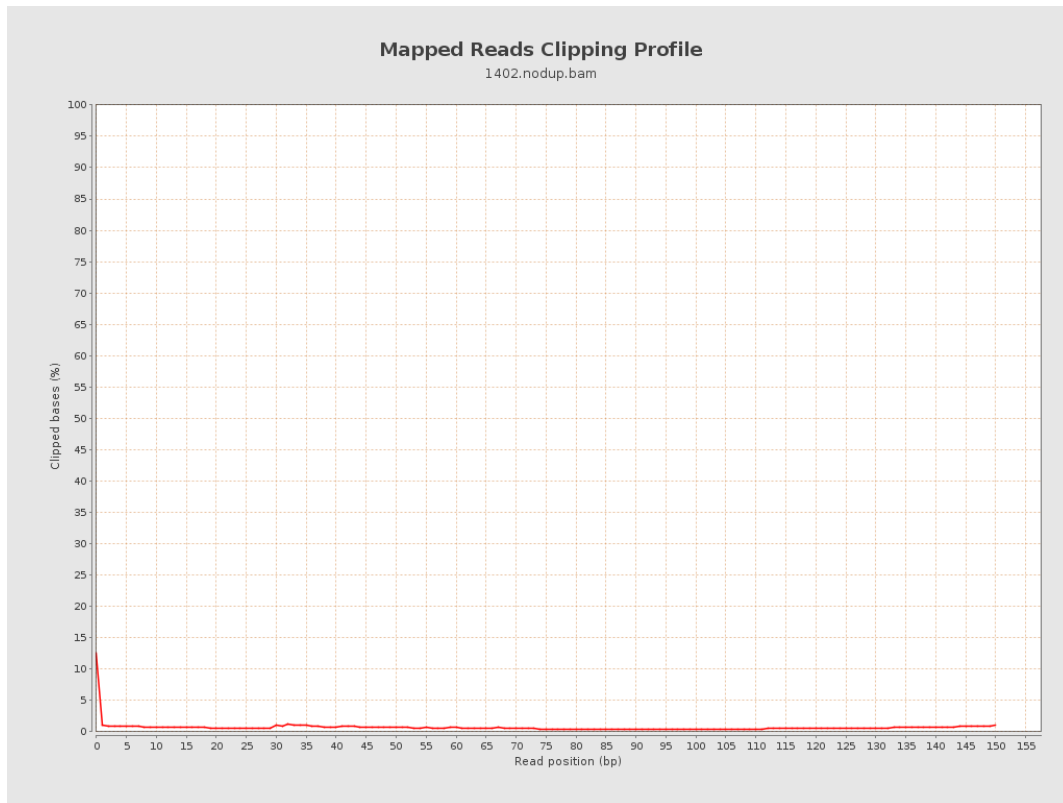
## 8. Results : Mapped Reads Nucleotide Content



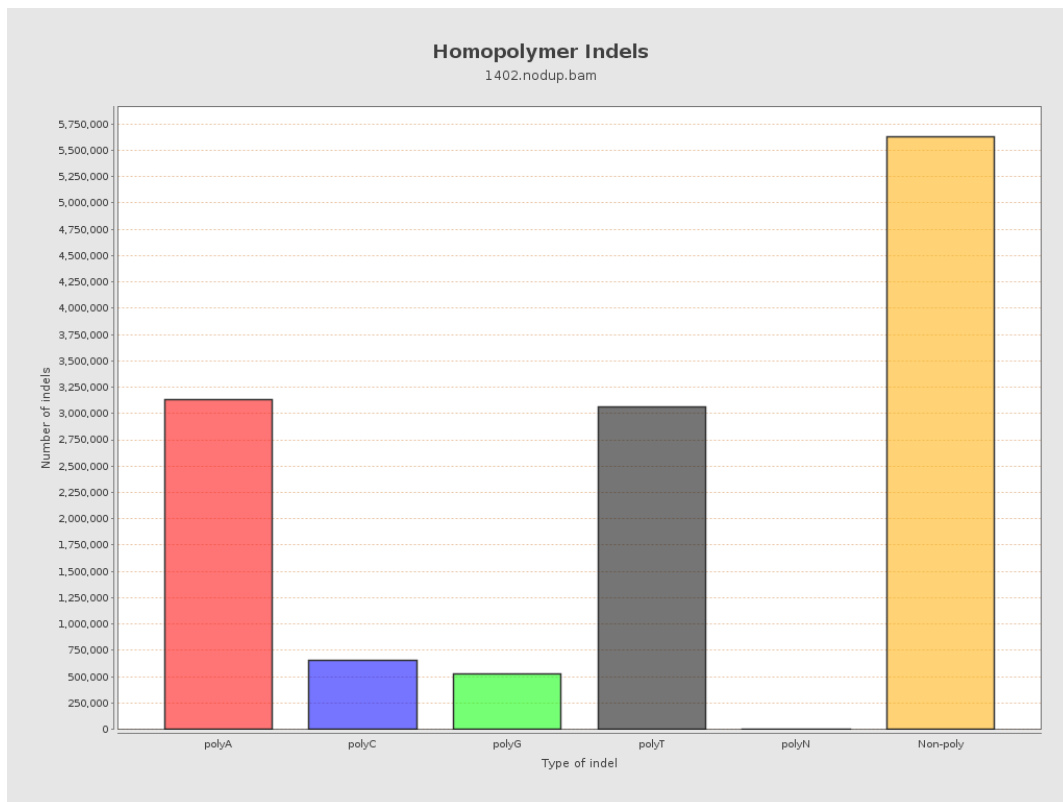
## 9. Results : Mapped Reads GC-content Distribution



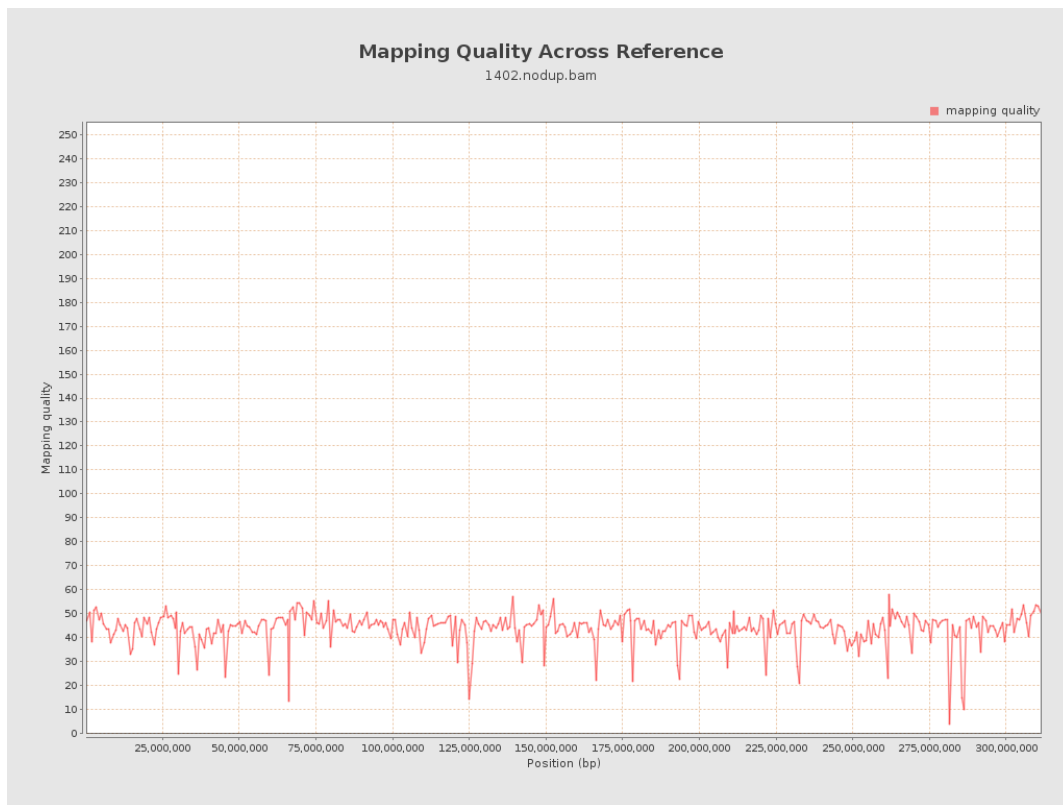
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

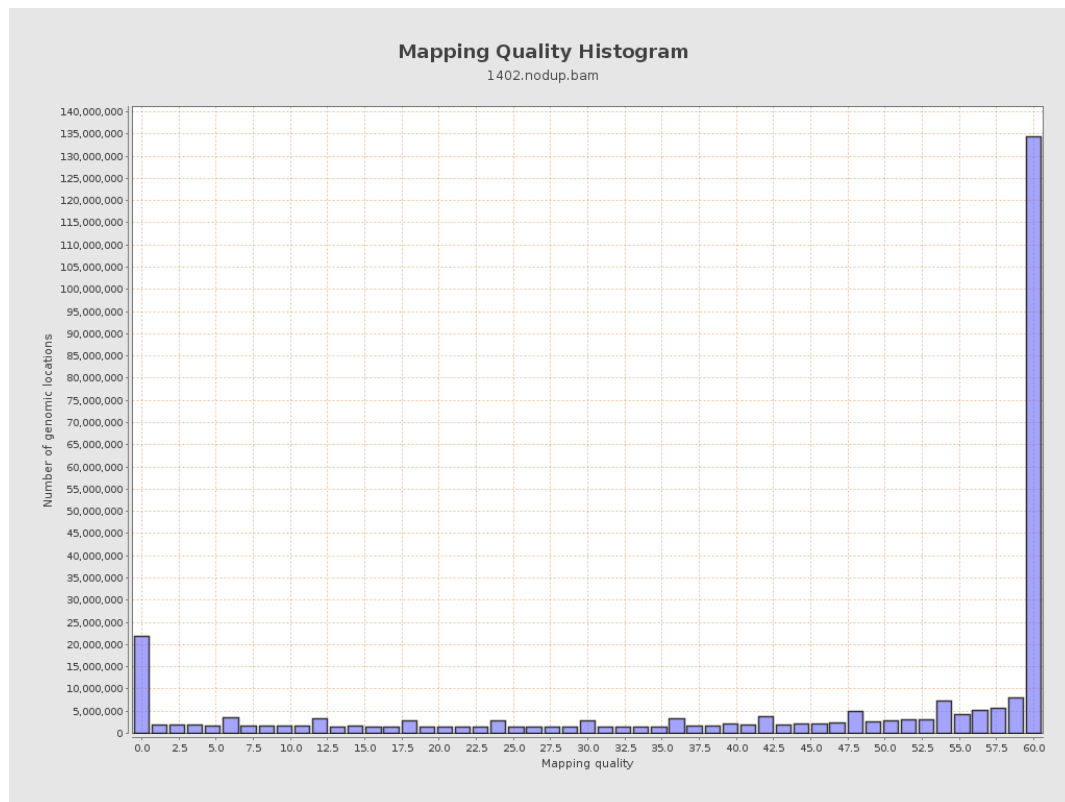


## 12. Results : Mapping Quality Across Reference

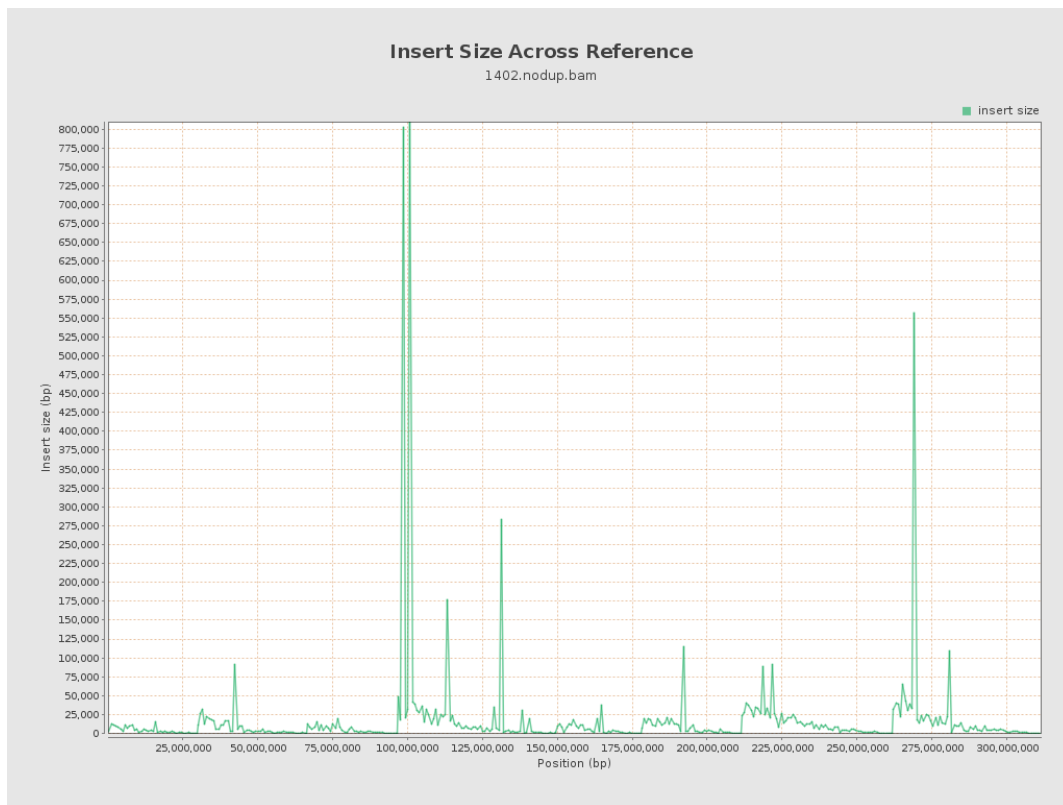




# 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

