

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:27:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/998
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/998 .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_106/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_106_S196_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_106/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_106_S196_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:27:23 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	56,121,640
Mapped reads	50,907,913 / 90.71%
Unmapped reads	5,213,727 / 9.29%
Mapped paired reads	50,907,913 / 90.71%
Mapped reads, first in pair	25,482,804 / 45.41%
Mapped reads, second in pair	25,425,109 / 45.3%
Mapped reads, both in pair	49,261,002 / 87.78%
Mapped reads, singletons	1,646,911 / 2.93%
Read min/max/mean length	30 / 151 / 148.02
Duplicated reads (flagged)	9,264,948 / 16.51%
Clipped reads	12,195,847 / 21.73%

### 2.2. ACGT Content

Number/percentage of A's	2,157,156,272 / 30.9%
Number/percentage of C's	1,331,869,443 / 19.08%
Number/percentage of T's	2,159,616,241 / 30.94%
Number/percentage of G's	1,332,108,825 / 19.08%
Number/percentage of N's	28,012 / 0%
GC Percentage	38.16%

### 2.3. Coverage

Mean	22.4619
Standard Deviation	208.172

## 2.4. Mapping Quality

Mean Mapping Quality	43.77
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## 2.5. Insert size

Mean	273,630.85
Standard Deviation	2,513,080.63
P25/Median/P75	328 / 427 / 558

## 2.6. Mismatches and indels

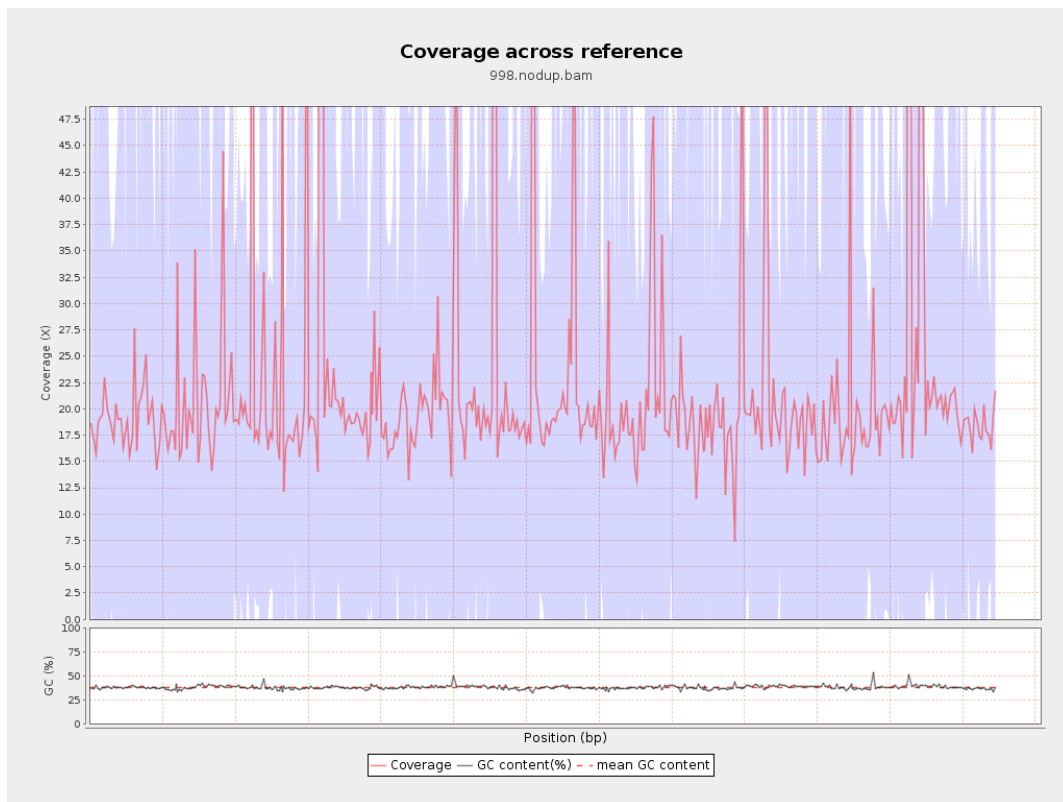
General error rate	2.44%
Mismatches	155,609,551
Insertions	5,228,125
Mapped reads with at least one insertion	9.14%
Deletions	5,090,638
Mapped reads with at least one deletion	8.84%
Homopolymer indels	56.69%

## 2.7. Chromosome stats

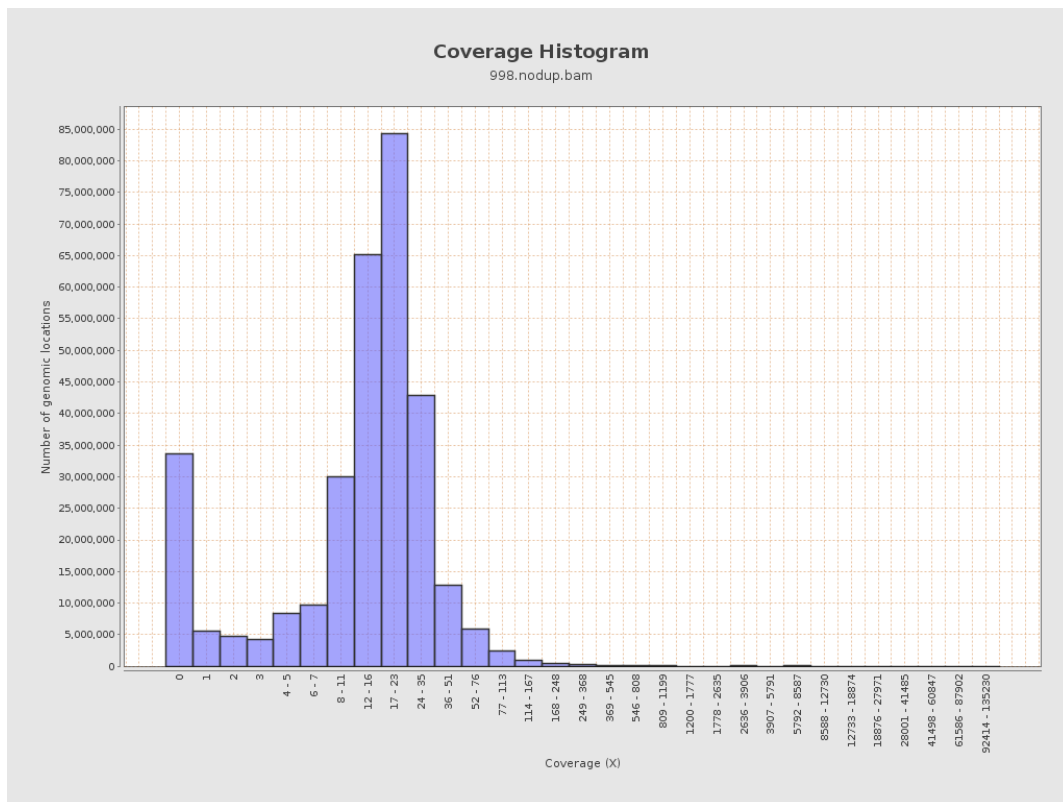
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	559984135	18.8392	80.4963

LT669789.1	36598175	820397011	22.4163	217.6852
LT669790.1	30422129	831812490	27.3423	284.4621
LT669791.1	52758100	1159225794	21.9725	231.5074
LT669792.1	28376109	646386659	22.7793	213.8479
LT669793.1	33388210	679510784	20.3518	148.5332
LT669794.1	50579949	1046148169	20.6831	165.486
LT669795.1	49795044	1256605146	25.2355	239.9805

### 3. Results : Coverage across reference

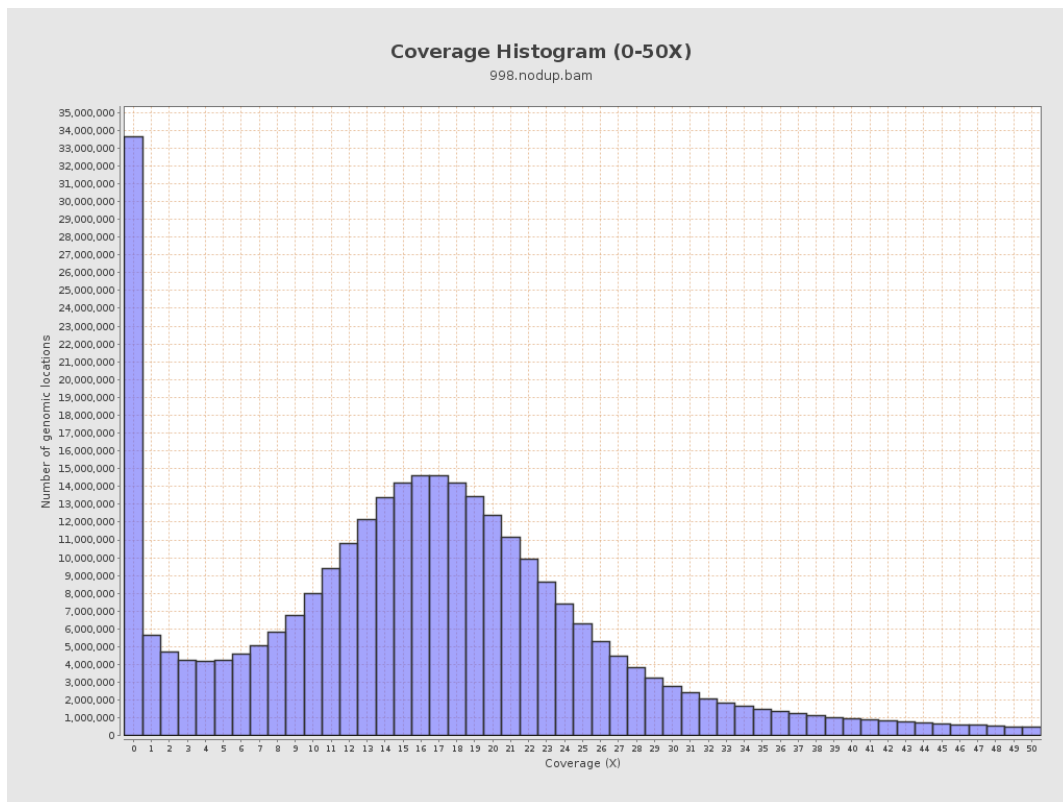


## 4. Results : Coverage Histogram

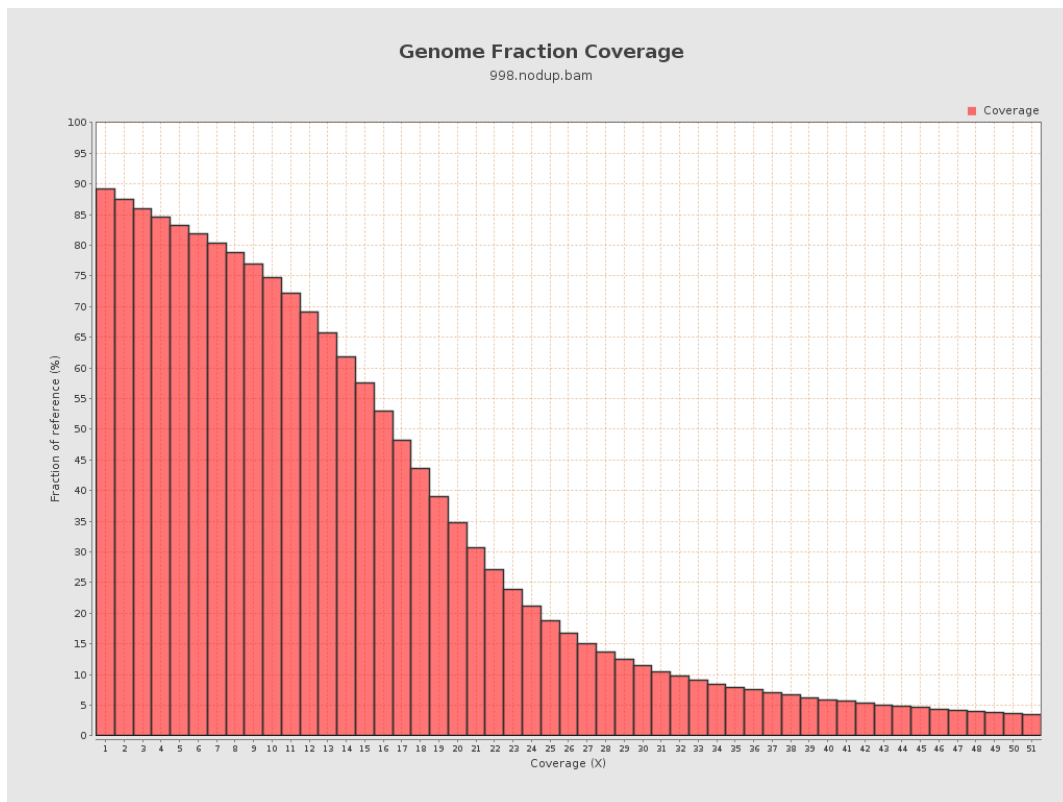




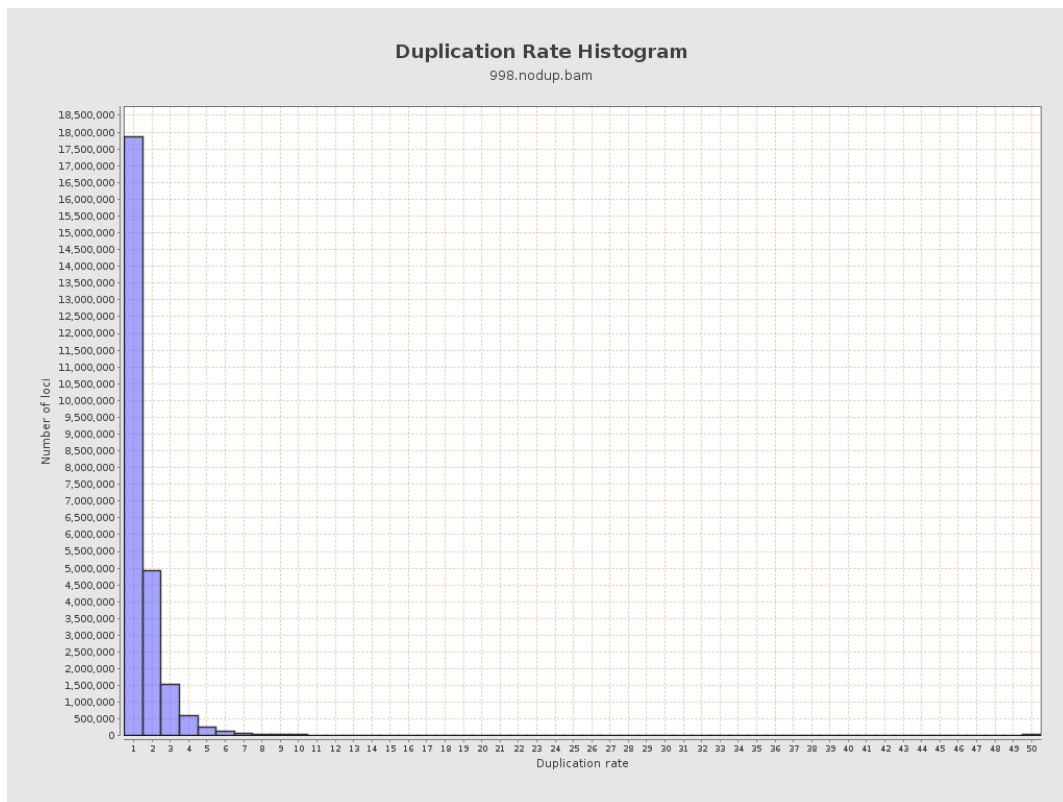
## 5. Results : Coverage Histogram (0-50X)



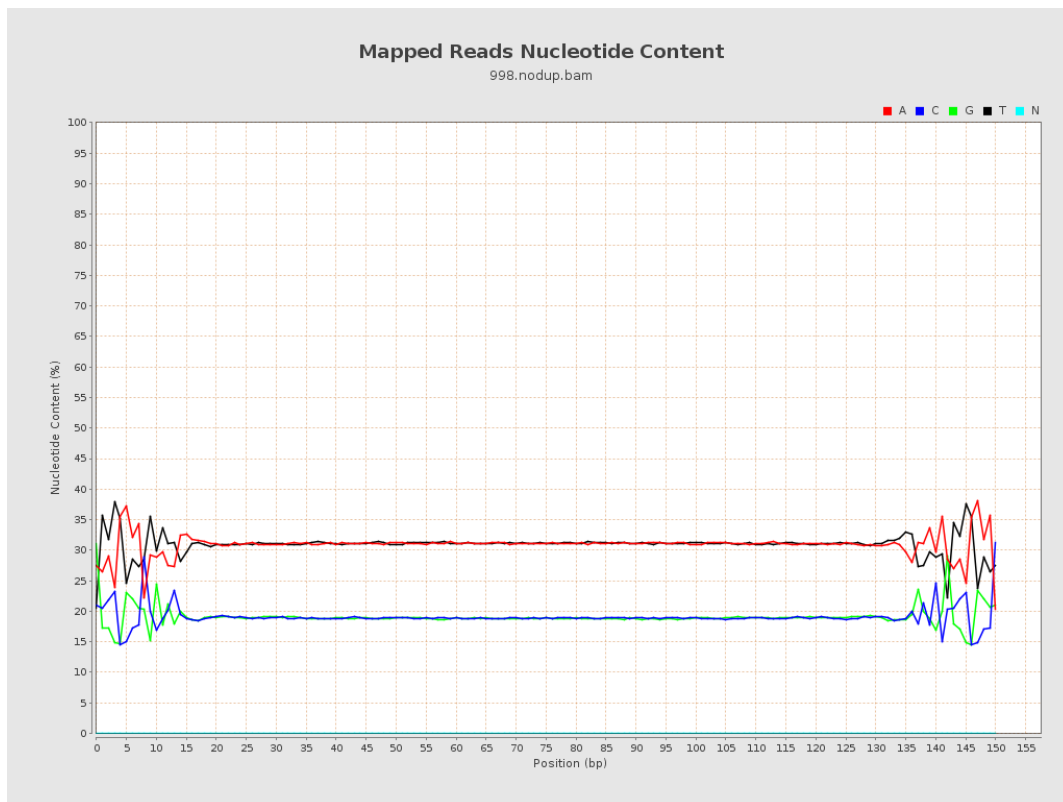
## 6. Results : Genome Fraction Coverage



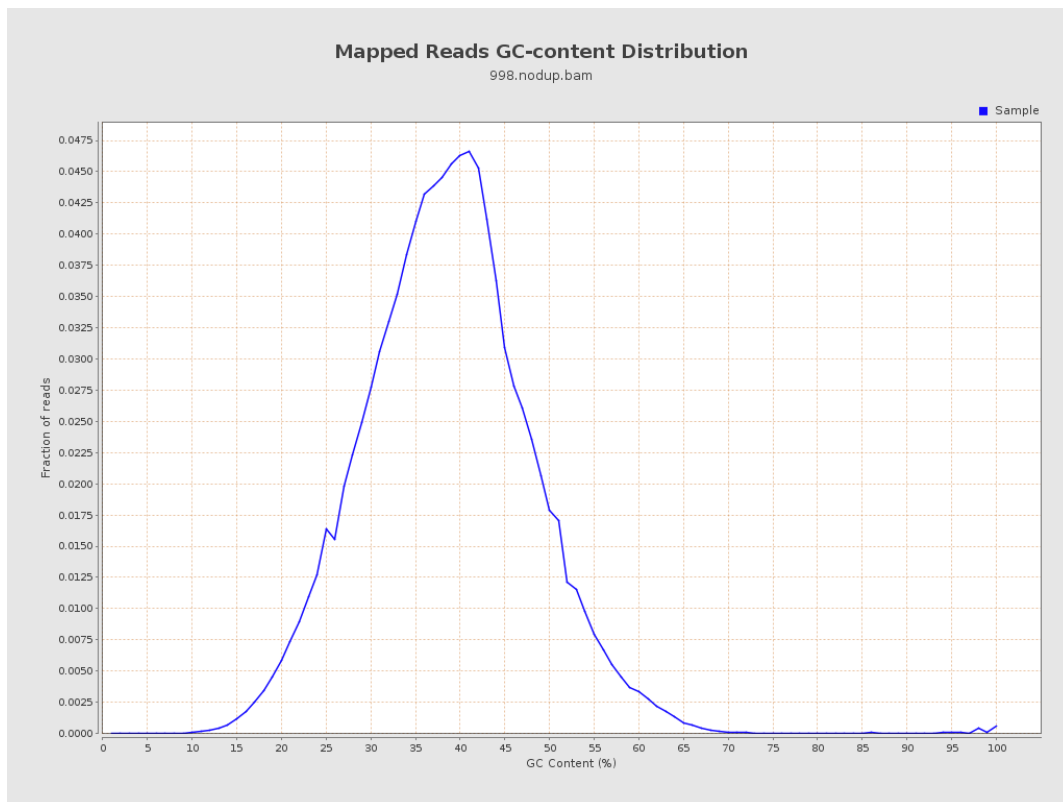
## 7. Results : Duplication Rate Histogram



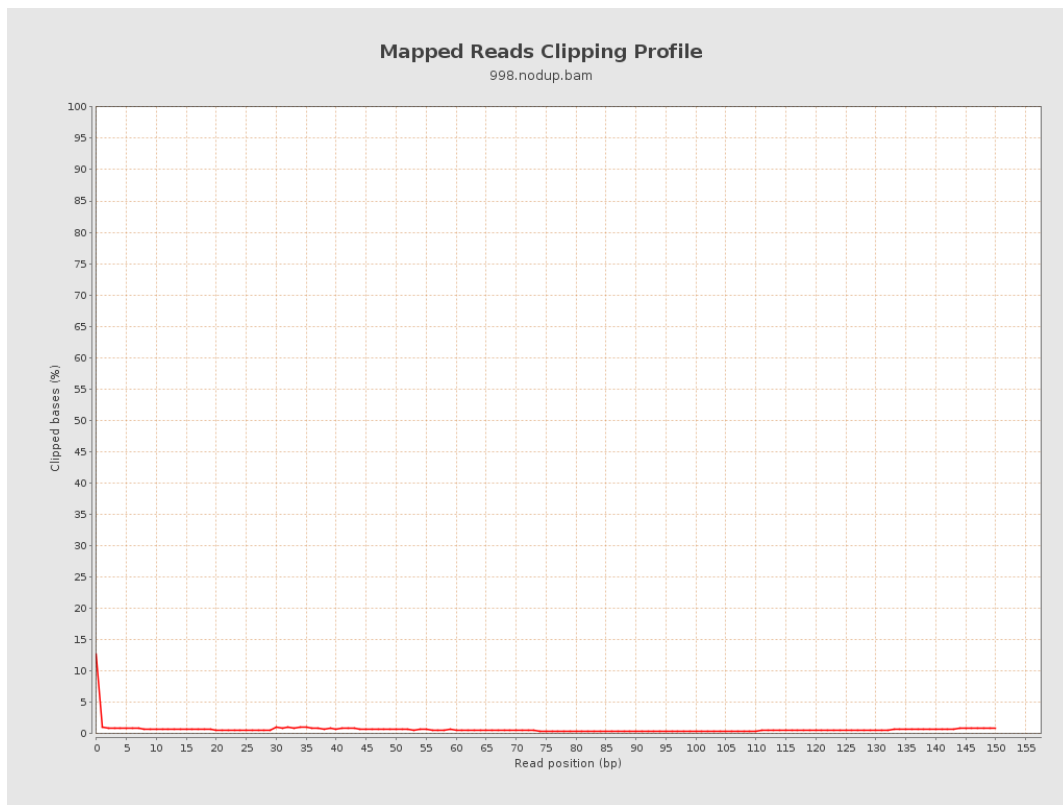
## 8. Results : Mapped Reads Nucleotide Content



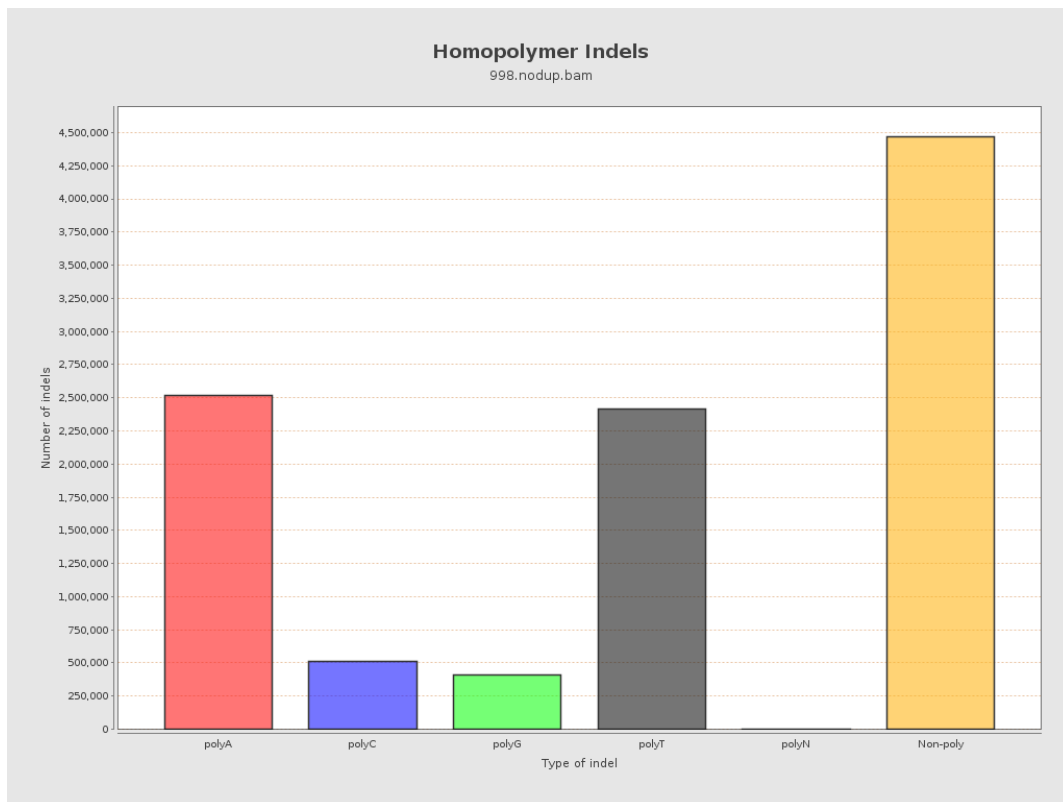
## 9. Results : Mapped Reads GC-content Distribution



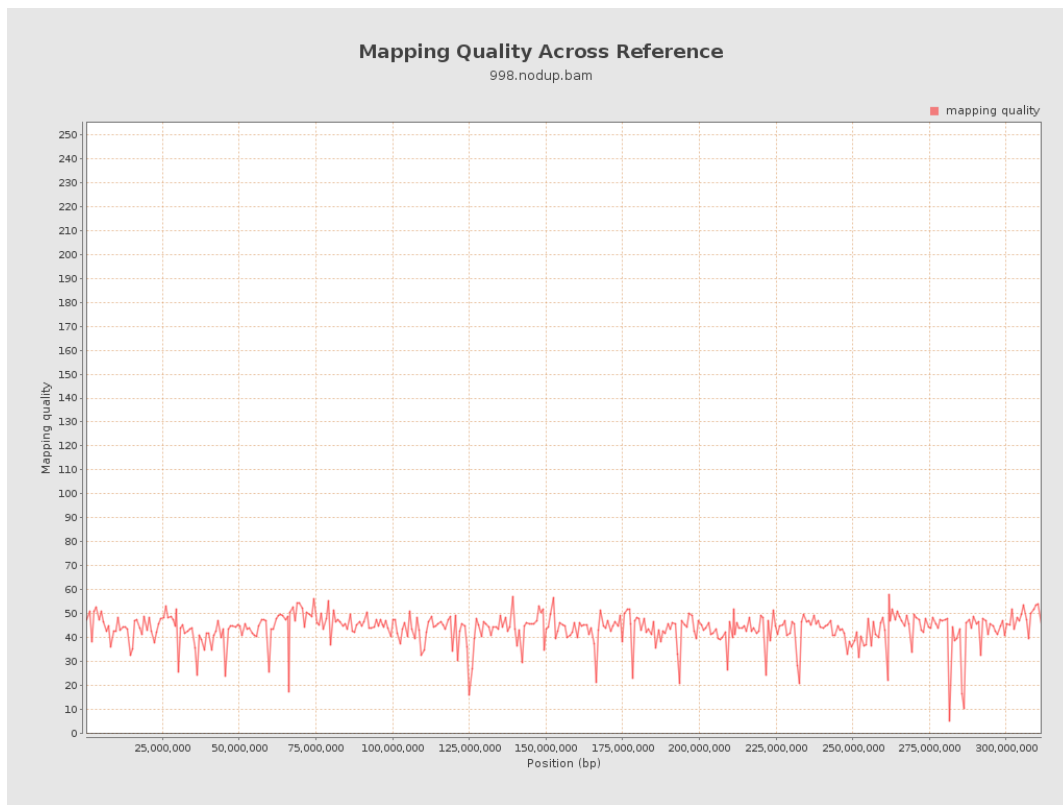
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

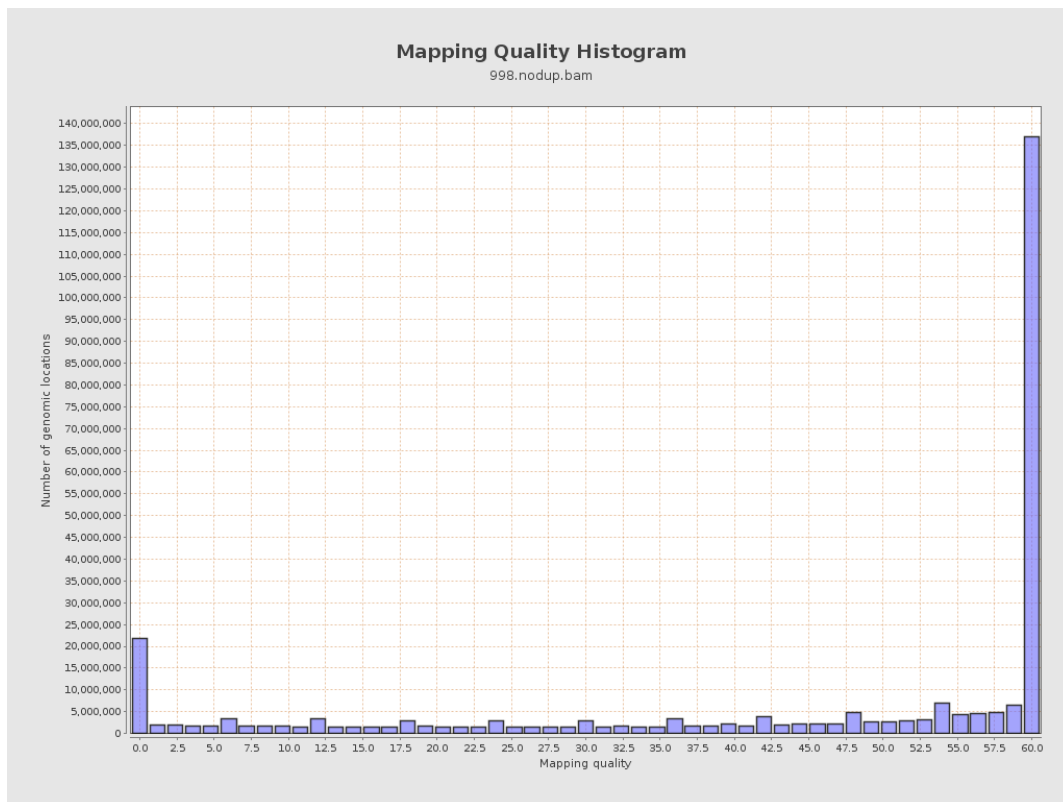


## 12. Results : Mapping Quality Across Reference

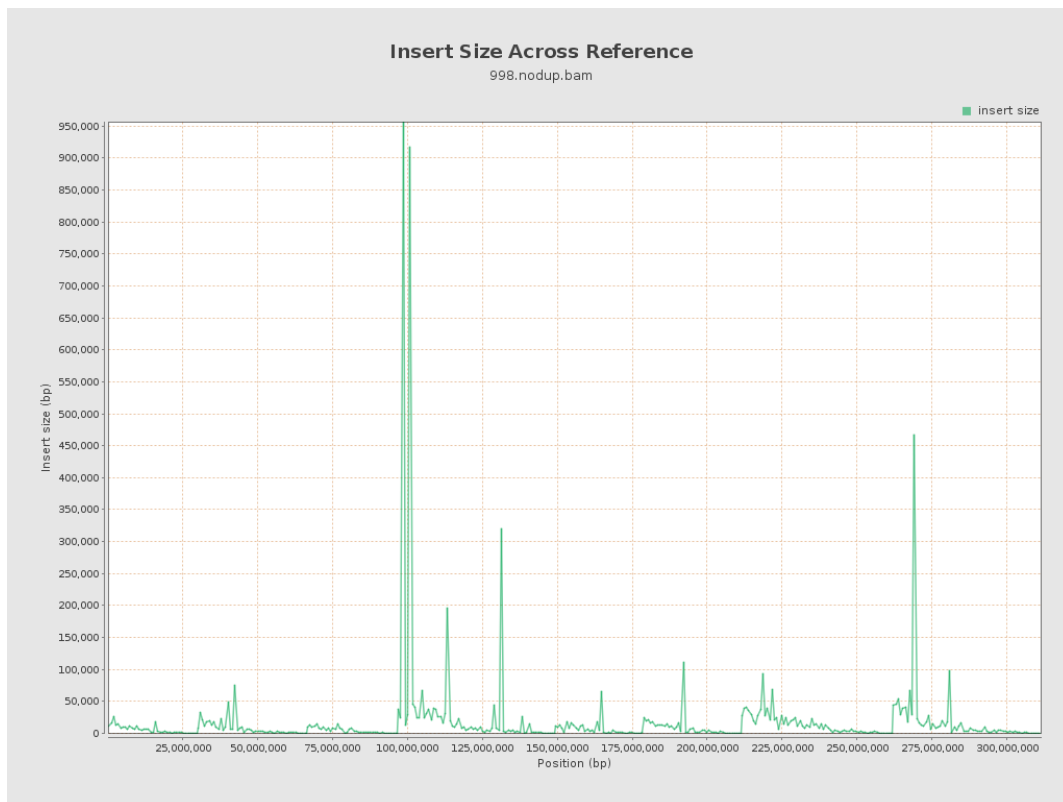




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

