

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

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

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/594
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/594.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_544/02-FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_544_S111_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_544/02-FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_544_S111_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:29:48 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	62,162,289
Mapped reads	56,360,195 / 90.67%
Unmapped reads	5,802,094 / 9.33%
Mapped paired reads	56,360,195 / 90.67%
Mapped reads, first in pair	28,296,070 / 45.52%
Mapped reads, second in pair	28,064,125 / 45.15%
Mapped reads, both in pair	54,482,200 / 87.65%
Mapped reads, singletons	1,877,995 / 3.02%
Read min/max/mean length	30 / 151 / 148.26
Duplicated reads (flagged)	9,544,412 / 15.35%
Clipped reads	13,974,384 / 22.48%

### 2.2. ACGT Content

Number/percentage of A's	2,392,632,124 / 31.04%
Number/percentage of C's	1,462,577,308 / 18.97%
Number/percentage of T's	2,393,290,275 / 31.04%
Number/percentage of G's	1,460,641,459 / 18.95%
Number/percentage of N's	53,700 / 0%
GC Percentage	37.92%

### 2.3. Coverage

Mean	24.799
Standard Deviation	235.8687

## 2.4. Mapping Quality

Mean Mapping Quality	44.8
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## 2.5. Insert size

Mean	246,403.26
Standard Deviation	2,404,370.88
P25/Median/P75	326 / 427 / 551

## 2.6. Mismatches and indels

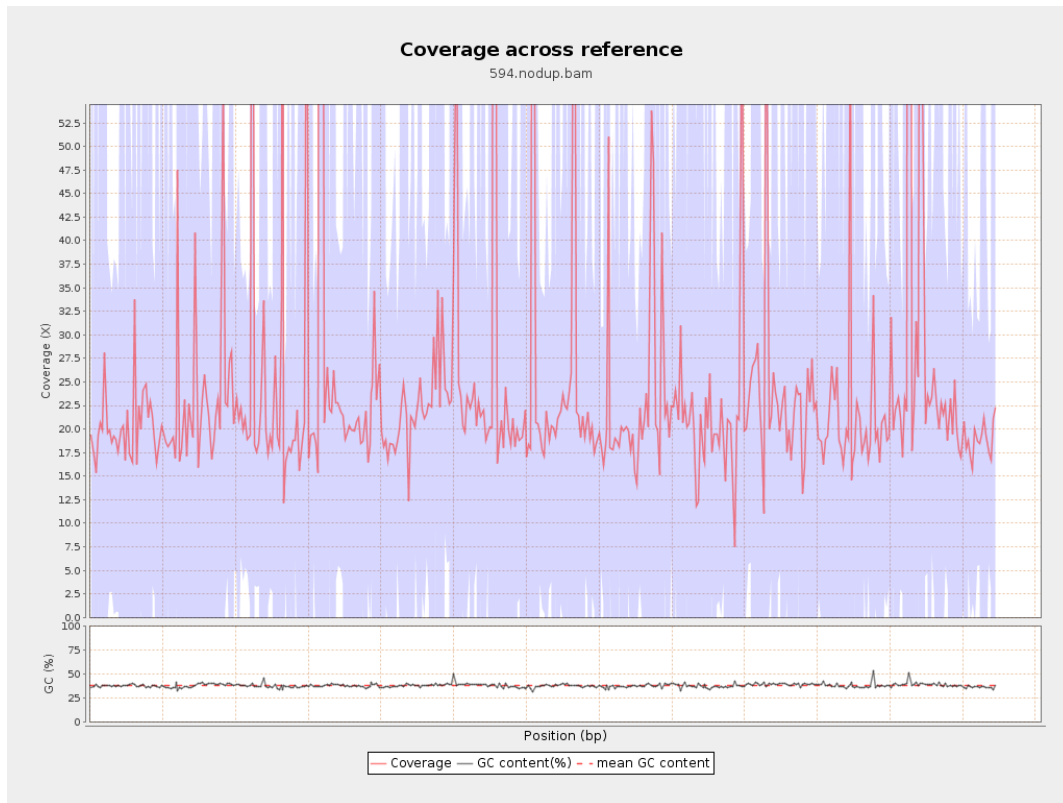
General error rate	2.59%
Mismatches	184,403,302
Insertions	5,599,868
Mapped reads with at least one insertion	8.86%
Deletions	5,270,961
Mapped reads with at least one deletion	8.32%
Homopolymer indels	57.45%

## 2.7. Chromosome stats

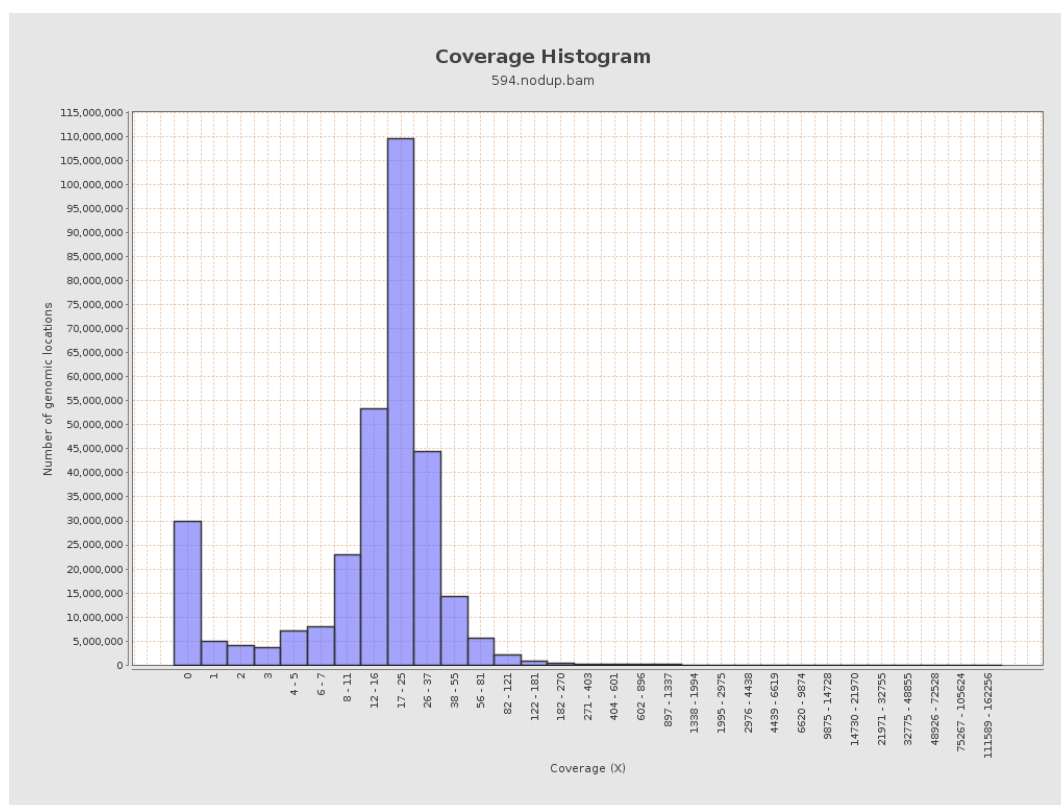
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	593486430	19.9663	93.5904

LT669789.1	36598175	923529647	25.2343	249.8039
LT669790.1	30422129	933687615	30.6911	354.7665
LT669791.1	52758100	1307703541	24.7868	260.8278
LT669792.1	28376109	703998408	24.8095	253.145
LT669793.1	33388210	743055485	22.255	132.5946
LT669794.1	50579949	1175774733	23.2459	203.2342
LT669795.1	49795044	1347175000	27.0544	240.4404

### 3. Results : Coverage across reference

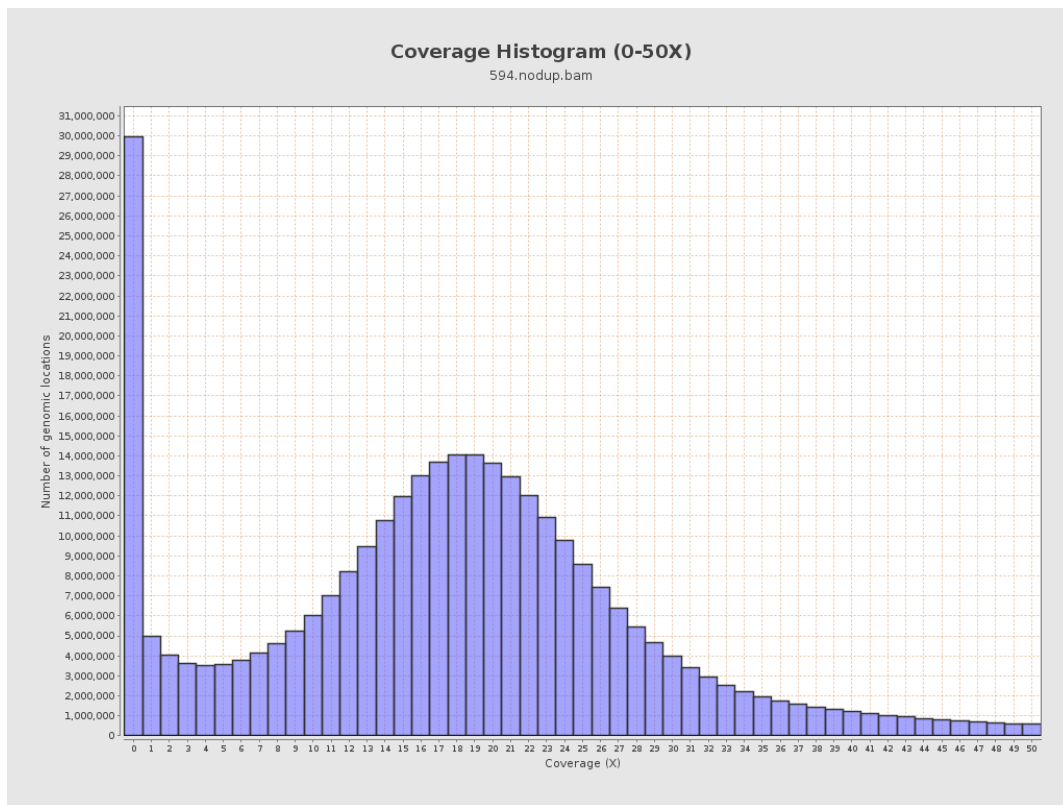


## 4. Results : Coverage Histogram

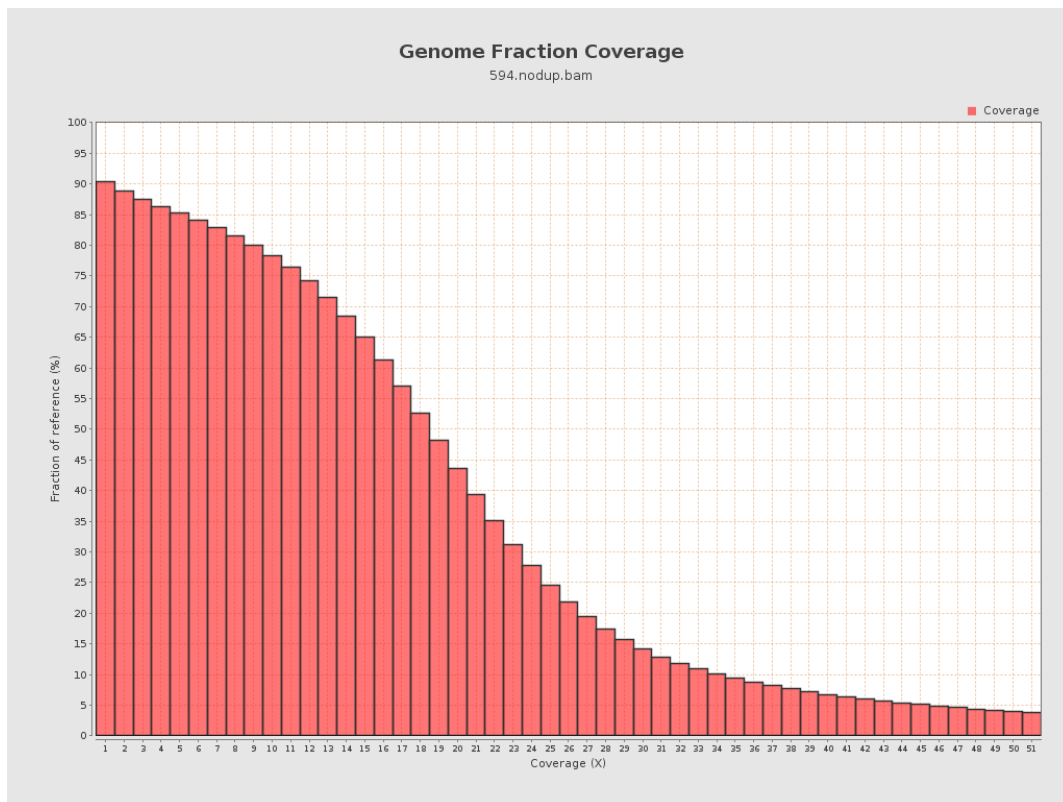




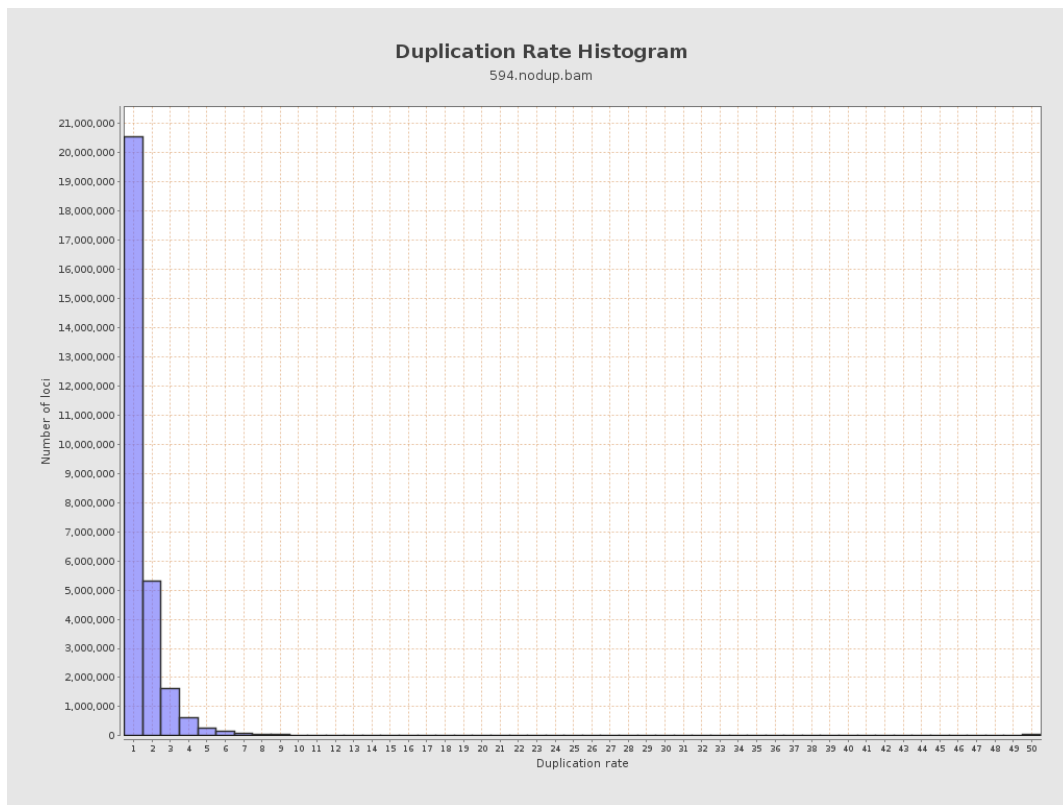
## 5. Results : Coverage Histogram (0-50X)



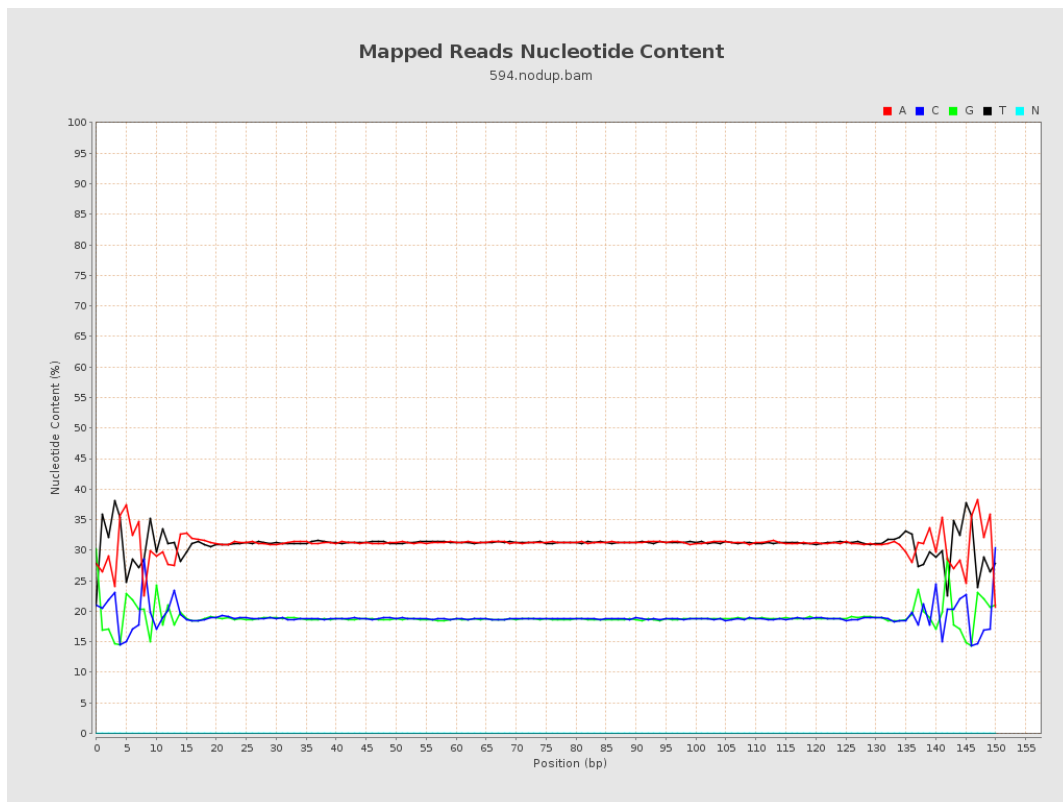
## 6. Results : Genome Fraction Coverage



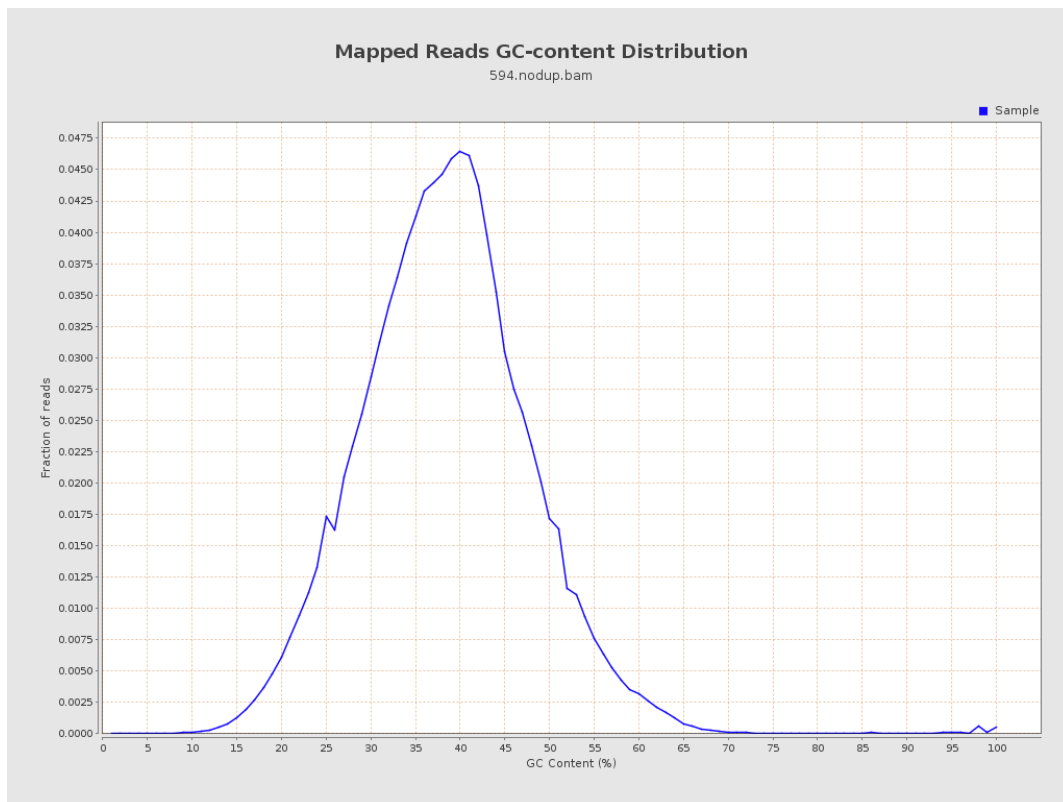
## 7. Results : Duplication Rate Histogram



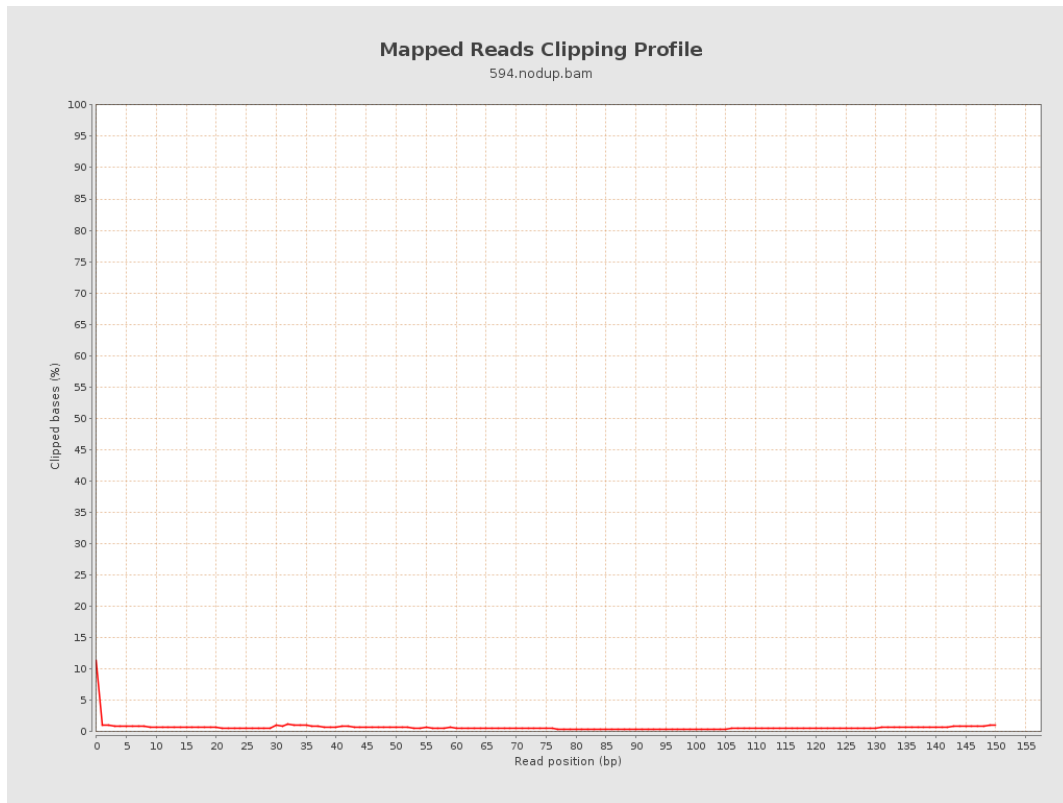
## 8. Results : Mapped Reads Nucleotide Content



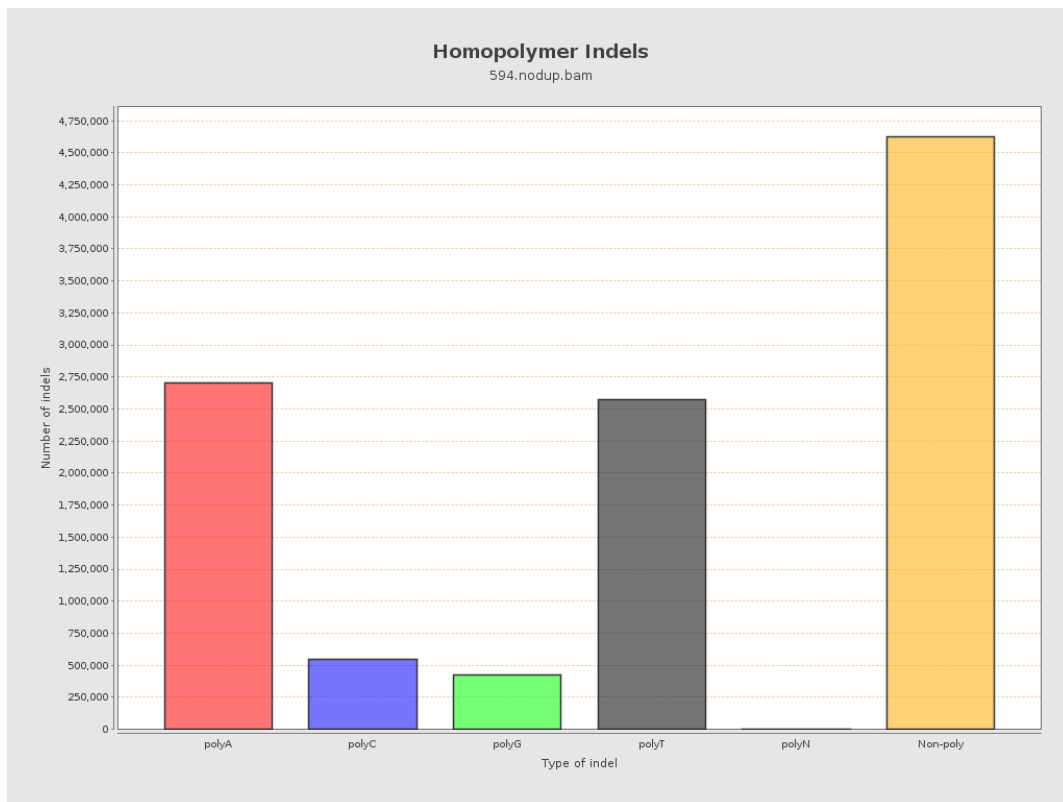
## 9. Results : Mapped Reads GC-content Distribution



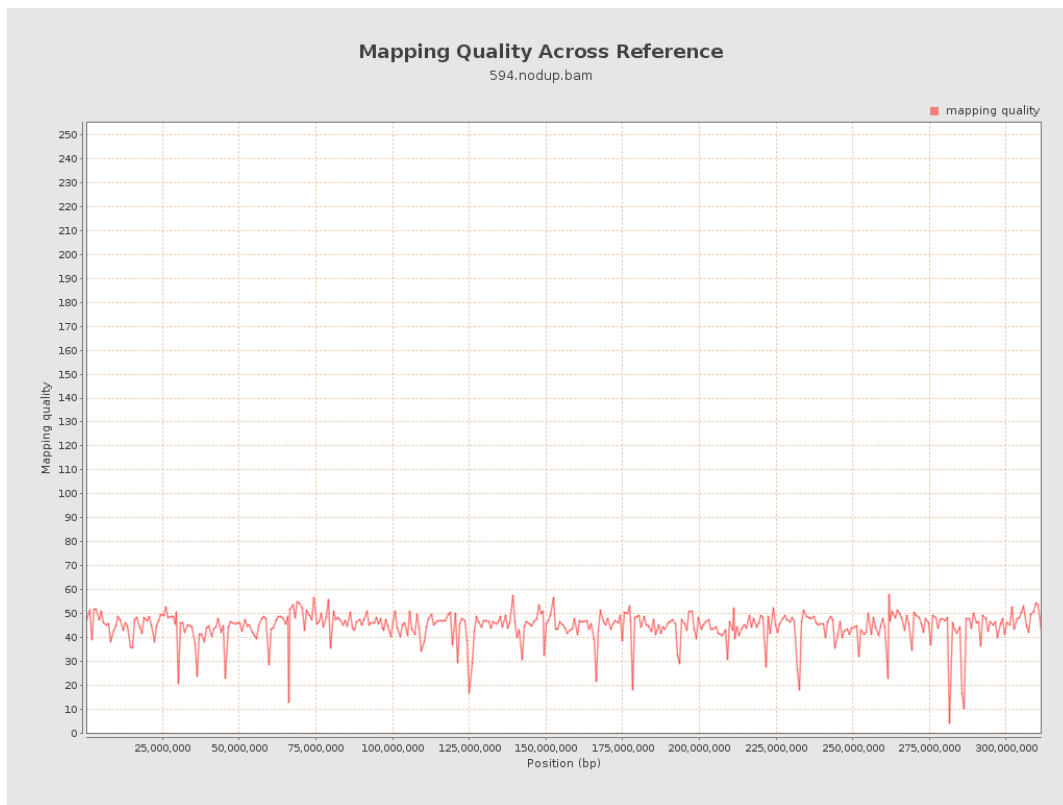
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

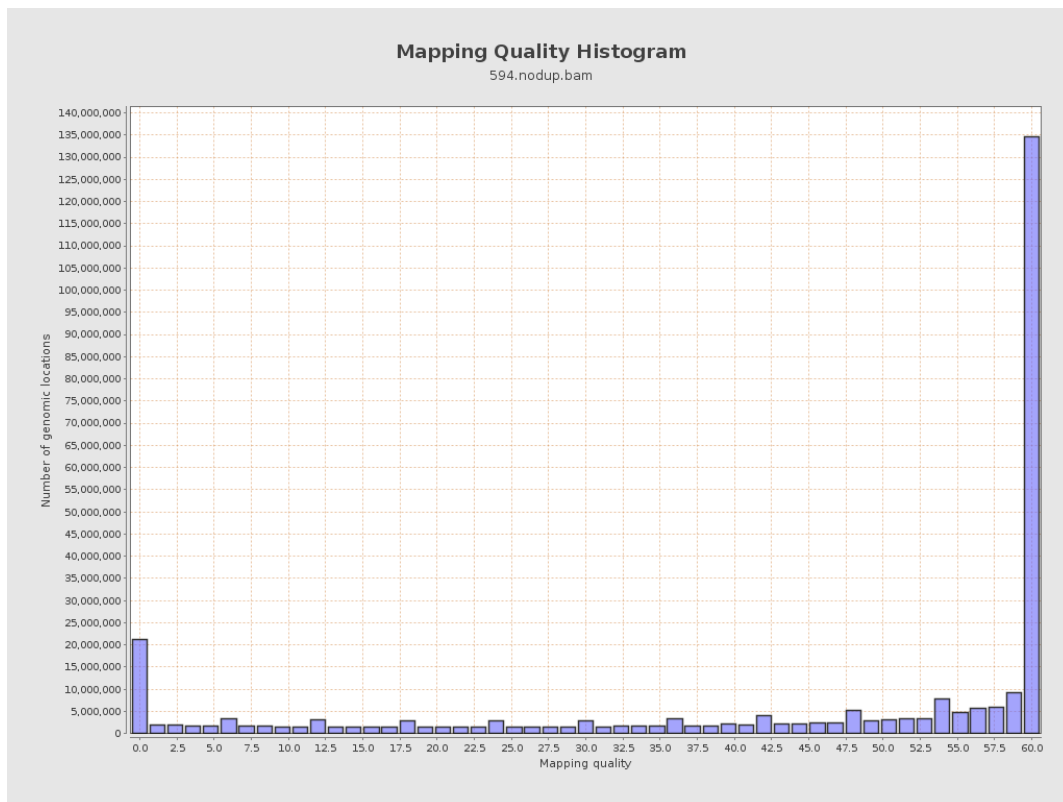


## 12. Results : Mapping Quality Across Reference

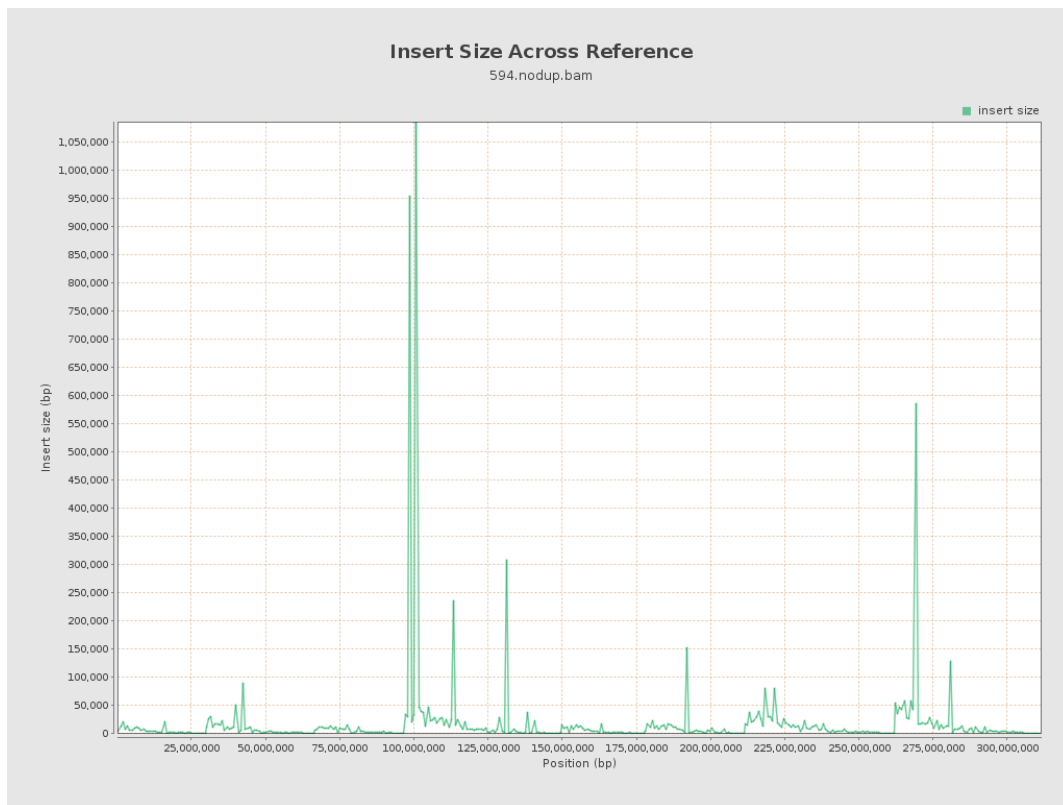




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

