

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:25:08*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/111
1
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1111 .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_570/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_570_S137_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_570/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_570_S137_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:25:08 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	48,337,431
Mapped reads	46,057,368 / 95.28%
Unmapped reads	2,280,063 / 4.72%
Mapped paired reads	46,057,368 / 95.28%
Mapped reads, first in pair	23,101,467 / 47.79%
Mapped reads, second in pair	22,955,901 / 47.49%
Mapped reads, both in pair	45,278,009 / 93.67%
Mapped reads, singletons	779,359 / 1.61%
Read min/max/mean length	30 / 151 / 148.15
Duplicated reads (flagged)	6,171,351 / 12.77%
Clipped reads	10,492,118 / 21.71%

### 2.2. ACGT Content

Number/percentage of A's	1,975,071,591 / 30.85%
Number/percentage of C's	1,227,956,645 / 19.18%
Number/percentage of T's	1,976,355,395 / 30.87%
Number/percentage of G's	1,223,564,917 / 19.11%
Number/percentage of N's	45,433 / 0%
GC Percentage	38.29%

### 2.3. Coverage

Mean	20.5981
Standard Deviation	165.1848

## 2.4. Mapping Quality

Mean Mapping Quality	43.89
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## 2.5. Insert size

Mean	211,135.96
Standard Deviation	2,161,261.72
P25/Median/P75	324 / 421 / 542

## 2.6. Mismatches and indels

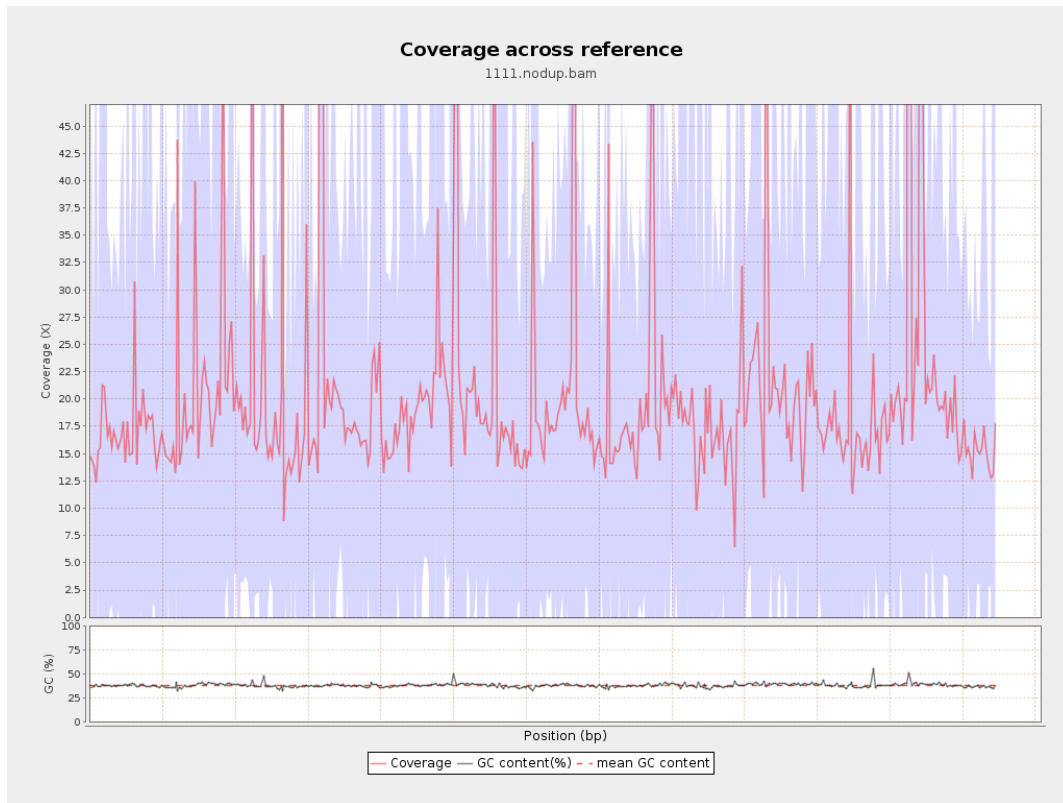
General error rate	2.53%
Mismatches	150,452,745
Insertions	4,189,453
Mapped reads with at least one insertion	8.22%
Deletions	4,387,615
Mapped reads with at least one deletion	8.47%
Homopolymer indels	55.71%

## 2.7. Chromosome stats

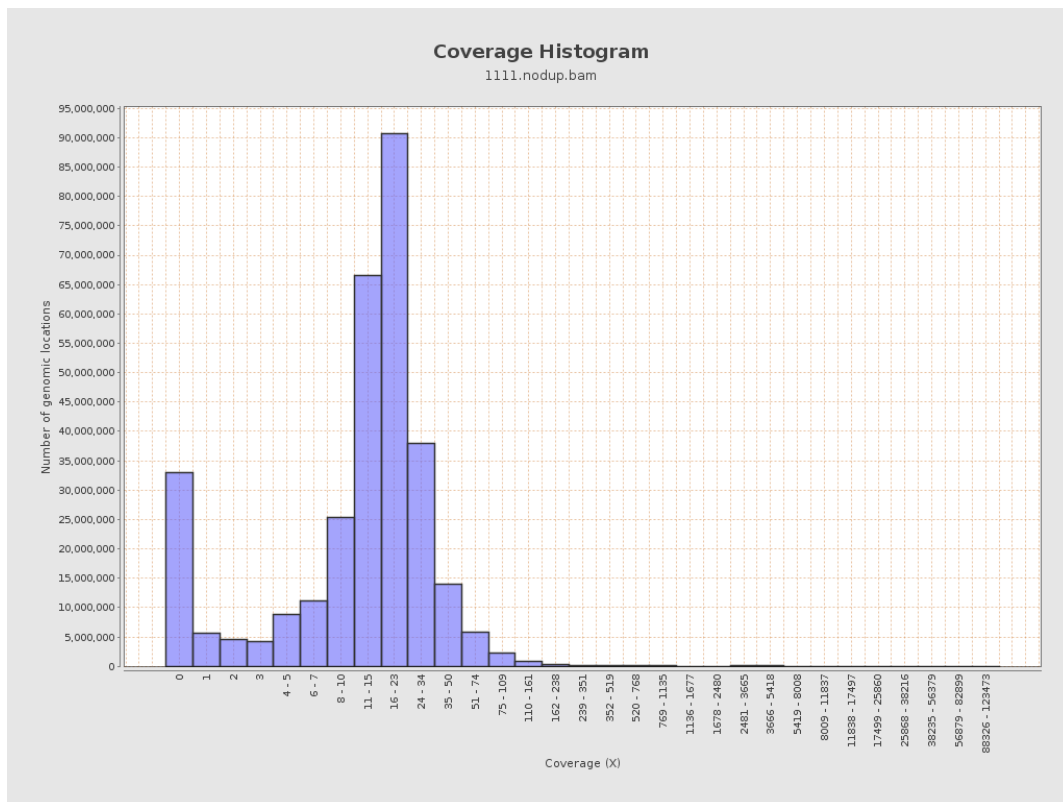
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	495438002	16.6678	58.033

LT669789.1	36598175	804558243	21.9836	195.7138
LT669790.1	30422129	633596447	20.8268	146.4123
LT669791.1	52758100	1079960676	20.47	159.0107
LT669792.1	28376109	565870142	19.9418	191.2467
LT669793.1	33388210	638585212	19.1261	88.6887
LT669794.1	50579949	1024659292	20.2582	181.1669
LT669795.1	49795044	1176553885	23.6279	203.0857

### 3. Results : Coverage across reference

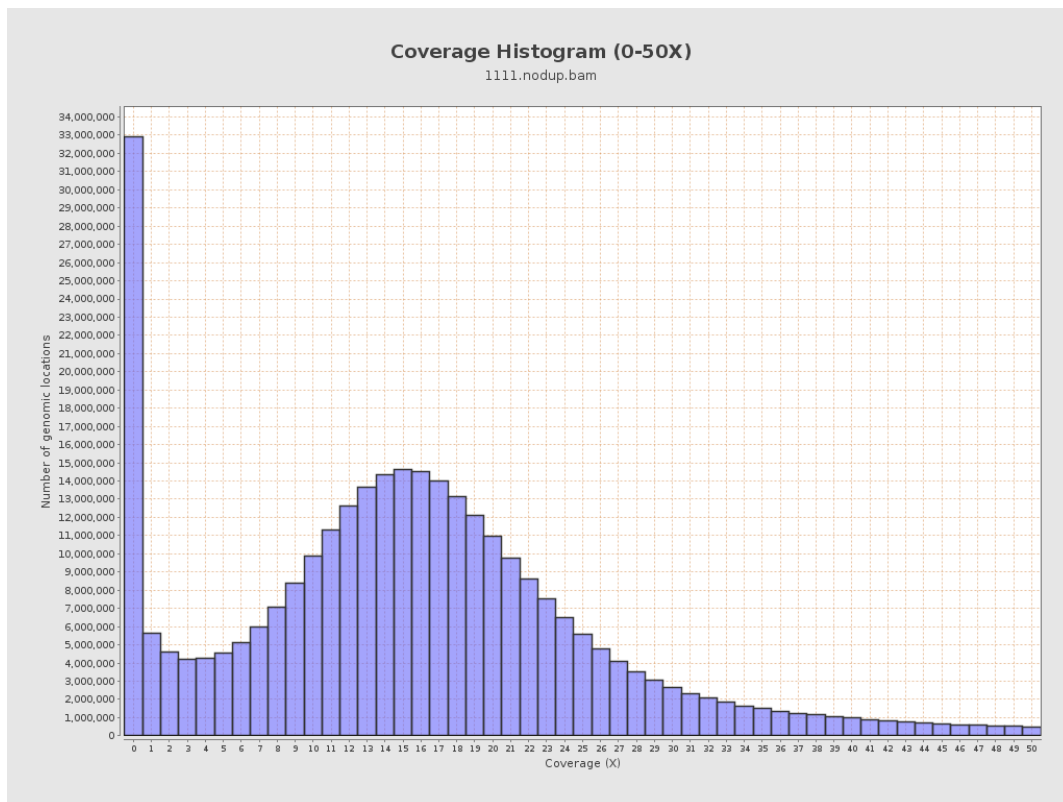


## 4. Results : Coverage Histogram

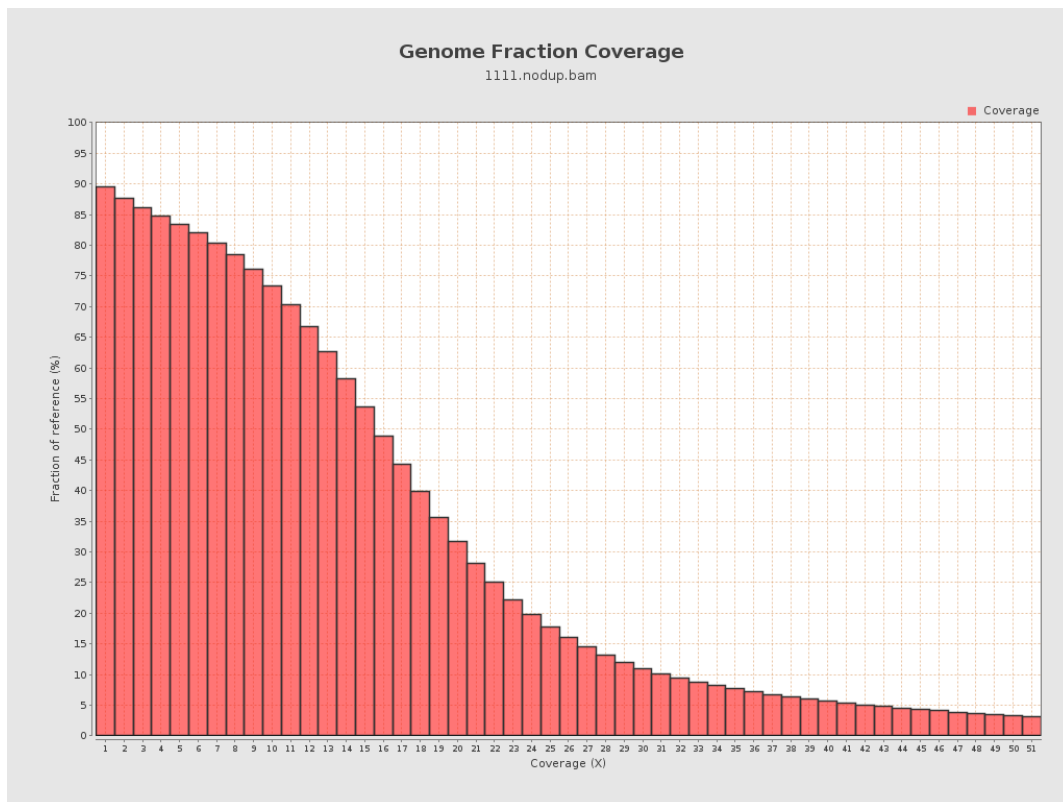




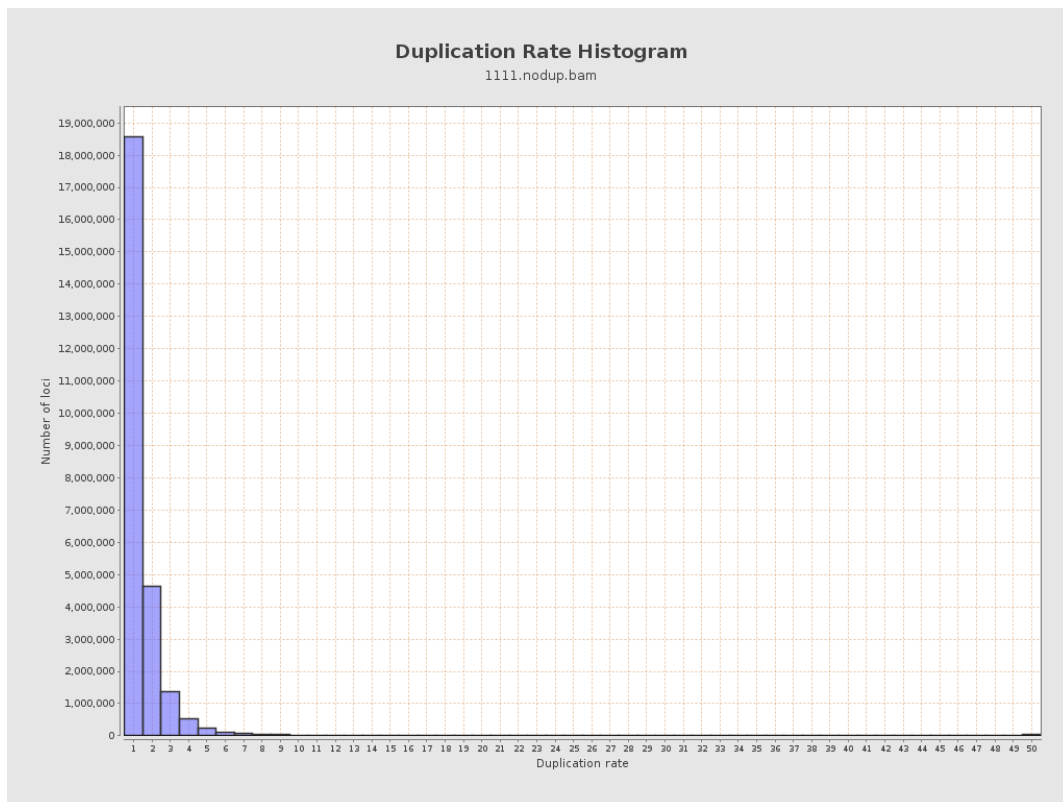
## 5. Results : Coverage Histogram (0-50X)



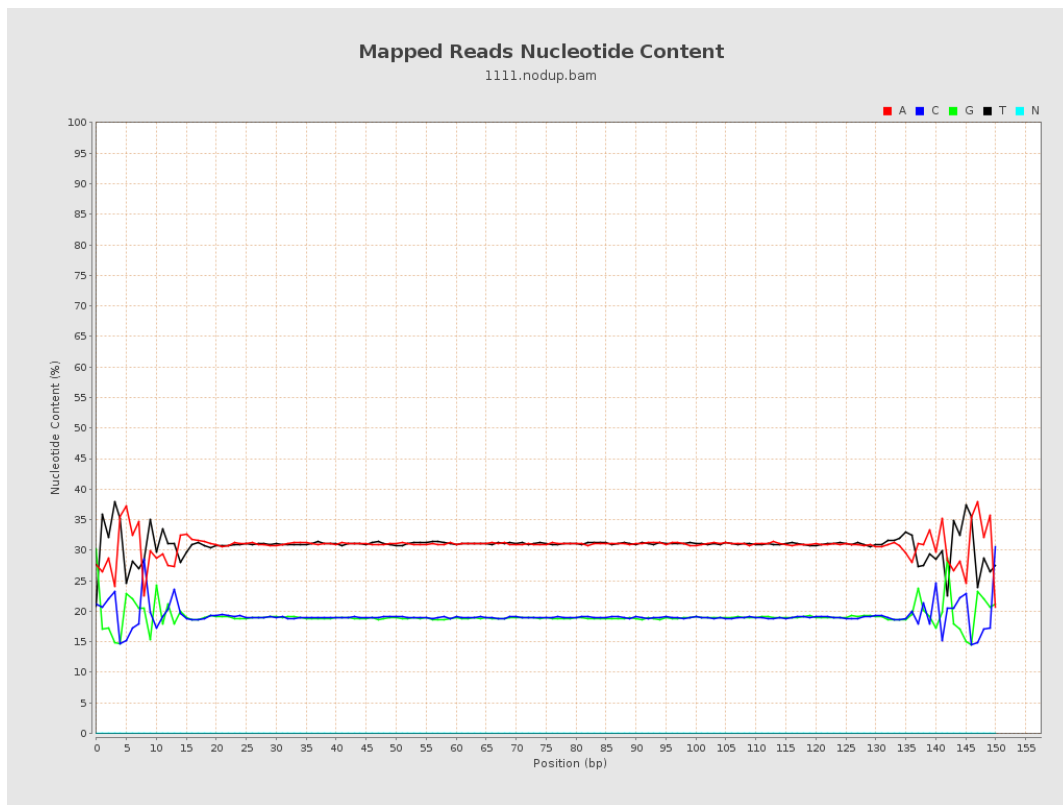
## 6. Results : Genome Fraction Coverage



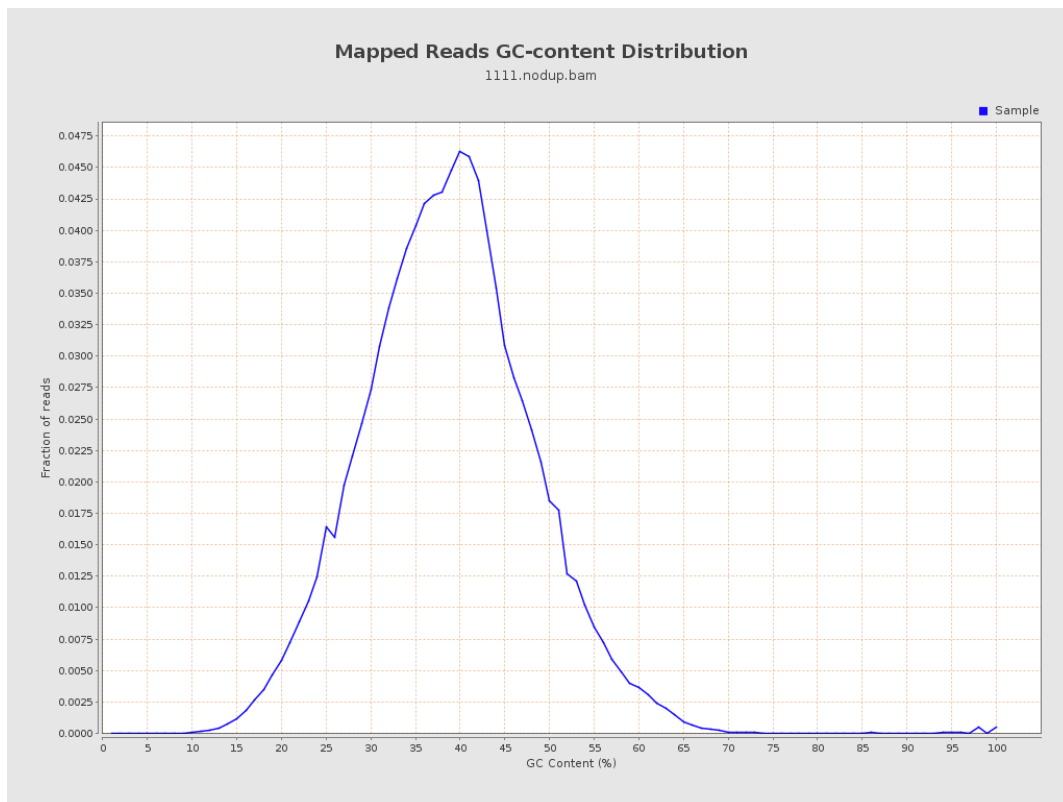
## 7. Results : Duplication Rate Histogram



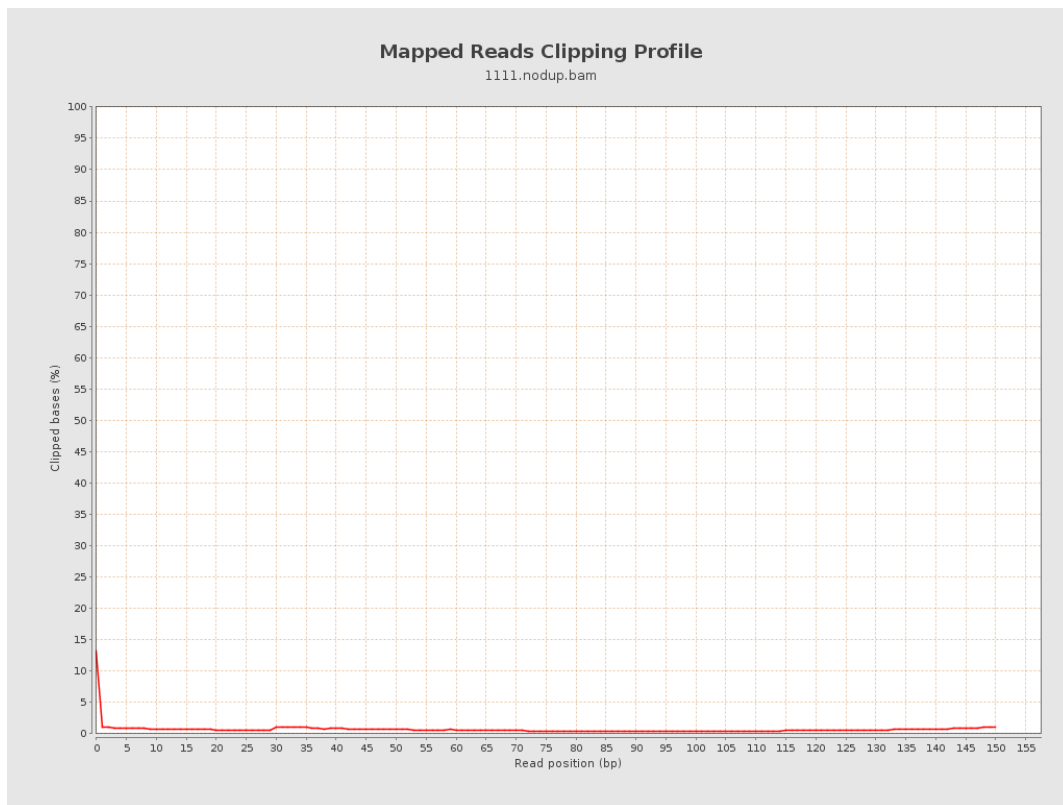
## 8. Results : Mapped Reads Nucleotide Content



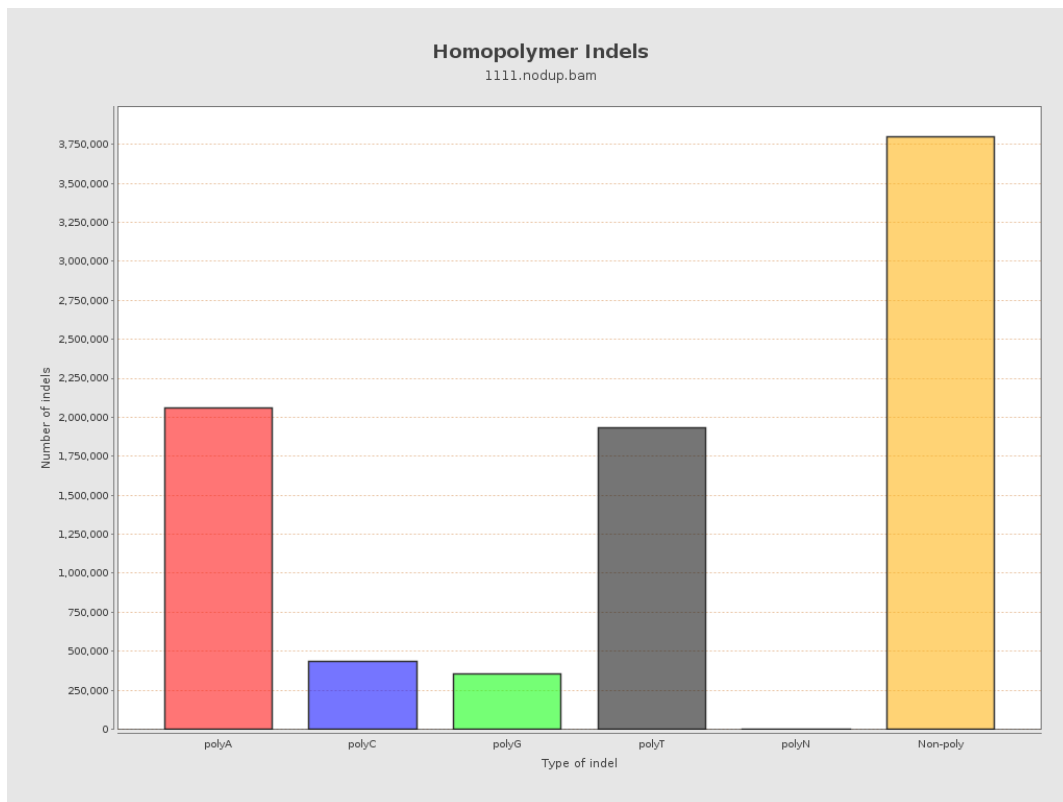
## 9. Results : Mapped Reads GC-content Distribution



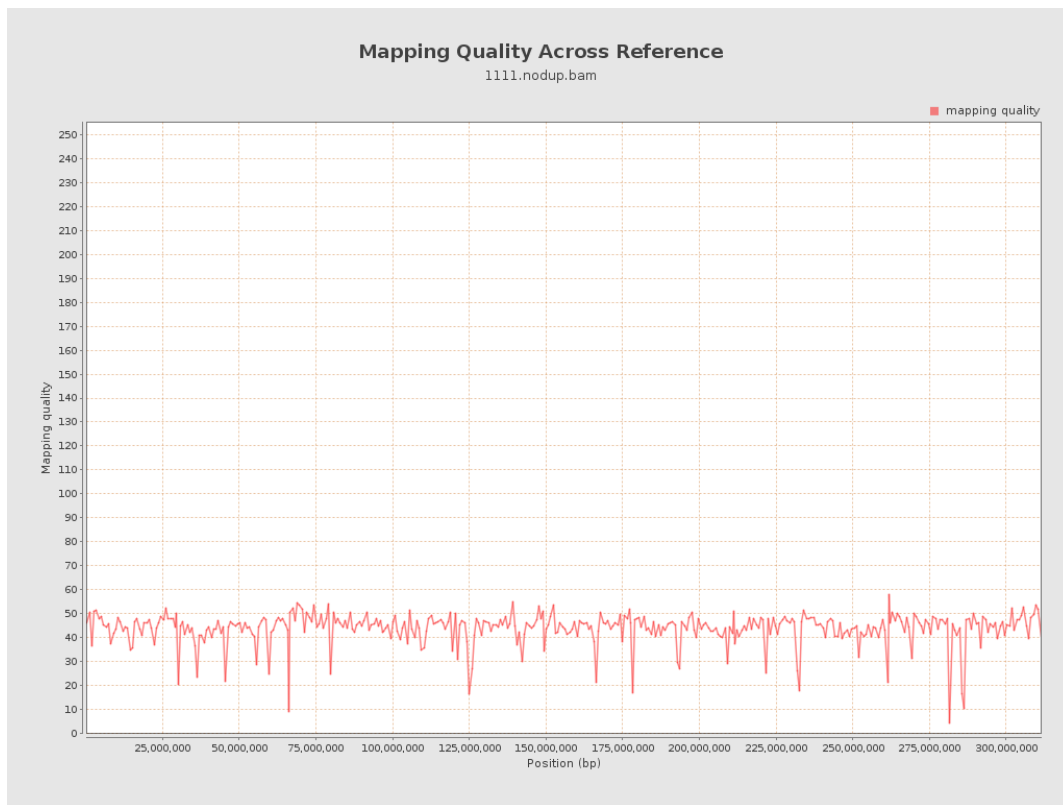
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

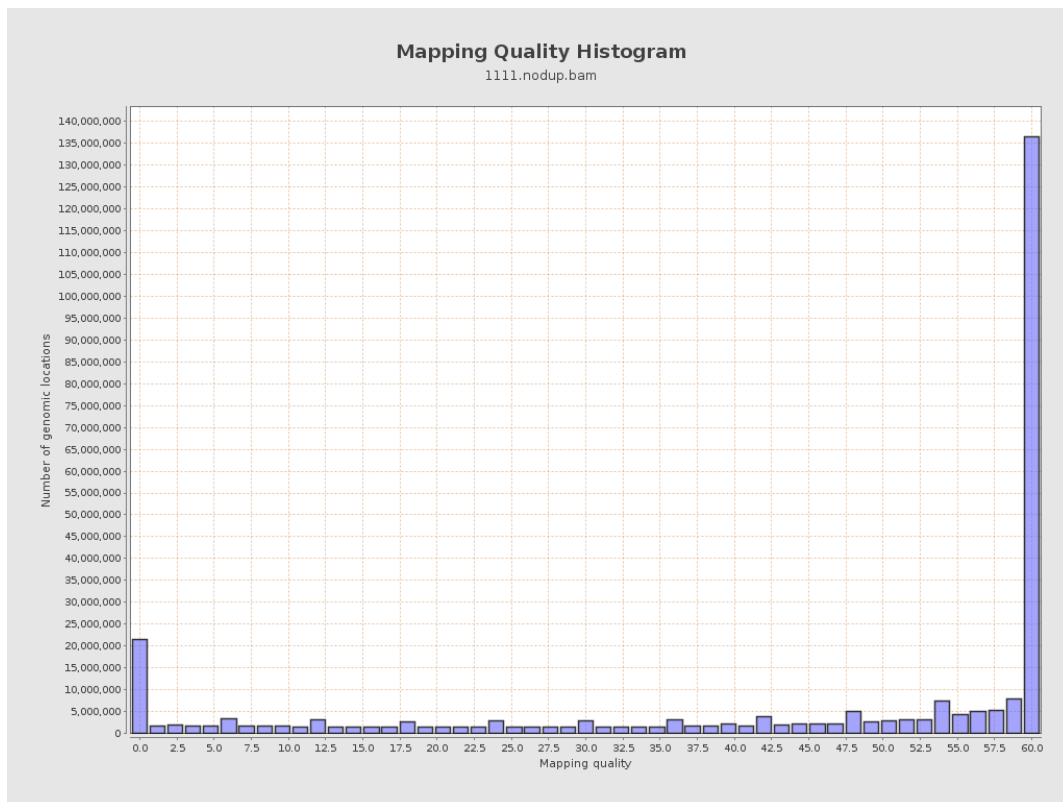


## 12. Results : Mapping Quality Across Reference

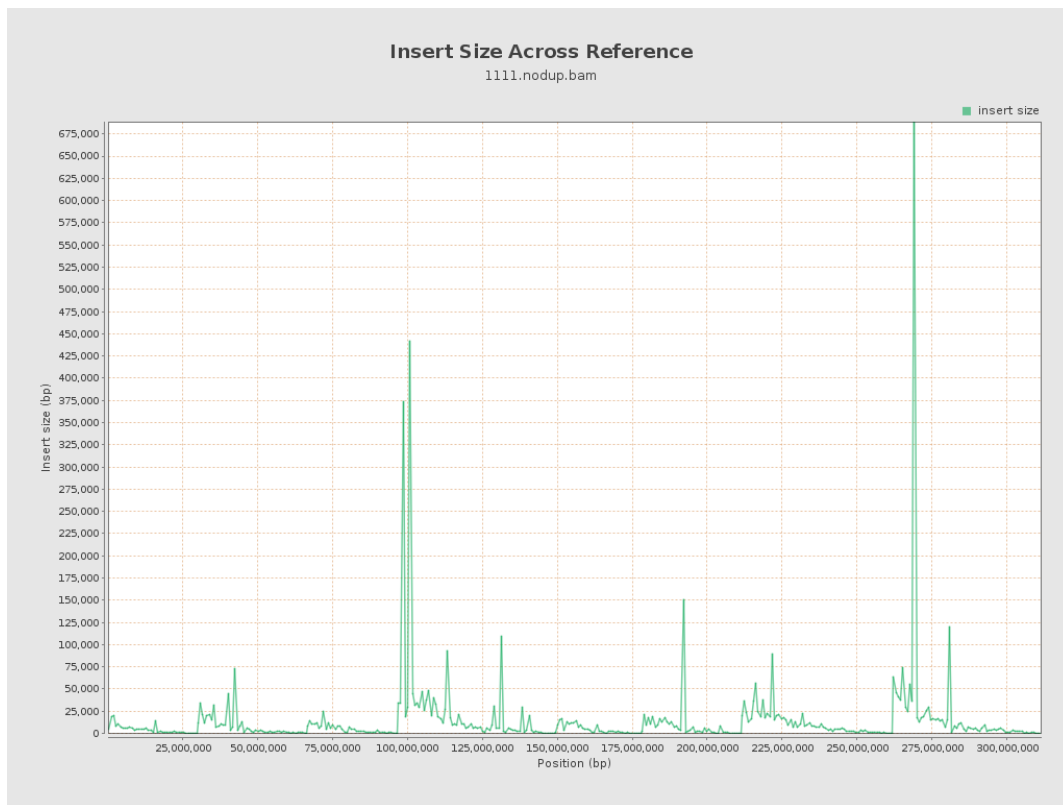




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

