

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:35:02*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/136
3
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1363 .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_260/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_260_S341_L003 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_260/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_260_S341_L003 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:01 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	78,446,549
Mapped reads	72,393,242 / 92.28%
Unmapped reads	6,053,307 / 7.72%
Mapped paired reads	72,393,242 / 92.28%
Mapped reads, first in pair	36,259,789 / 46.22%
Mapped reads, second in pair	36,133,453 / 46.06%
Mapped reads, both in pair	70,617,492 / 90.02%
Mapped reads, singletons	1,775,750 / 2.26%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	10,542,742 / 13.44%
Clipped reads	17,068,488 / 21.76%

### 2.2. ACGT Content

Number/percentage of A's	3,077,708,647 / 30.94%
Number/percentage of C's	1,893,877,796 / 19.04%
Number/percentage of T's	3,083,138,165 / 30.99%
Number/percentage of G's	1,892,527,613 / 19.03%
Number/percentage of N's	37,445 / 0%
GC Percentage	38.06%

### 2.3. Coverage

Mean	32
Standard Deviation	272.0375

## 2.4. Mapping Quality

Mean Mapping Quality	44.85
----------------------	-------

## 2.5. Insert size

Mean	226,048.17
Standard Deviation	2,278,015.4
P25/Median/P75	311 / 414 / 540

## 2.6. Mismatches and indels

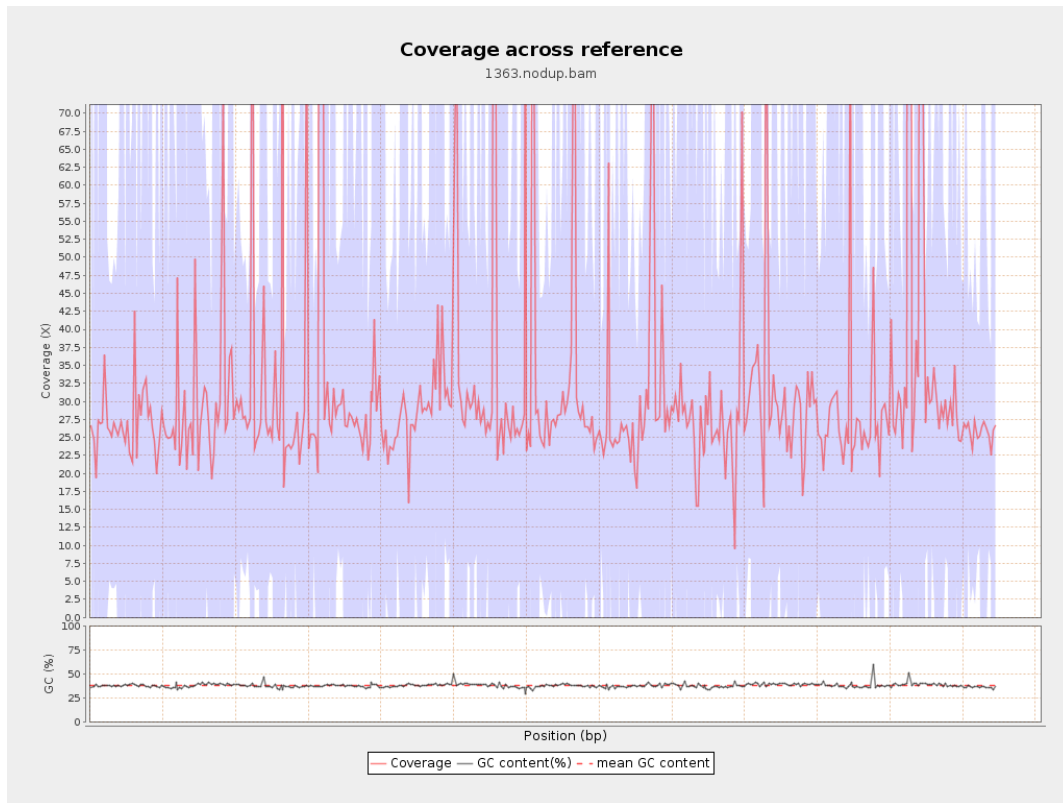
General error rate	2.26%
Mismatches	205,890,866
Insertions	6,780,781
Mapped reads with at least one insertion	8.38%
Deletions	6,718,771
Mapped reads with at least one deletion	8.25%
Homopolymer indels	57.16%

## 2.7. Chromosome stats

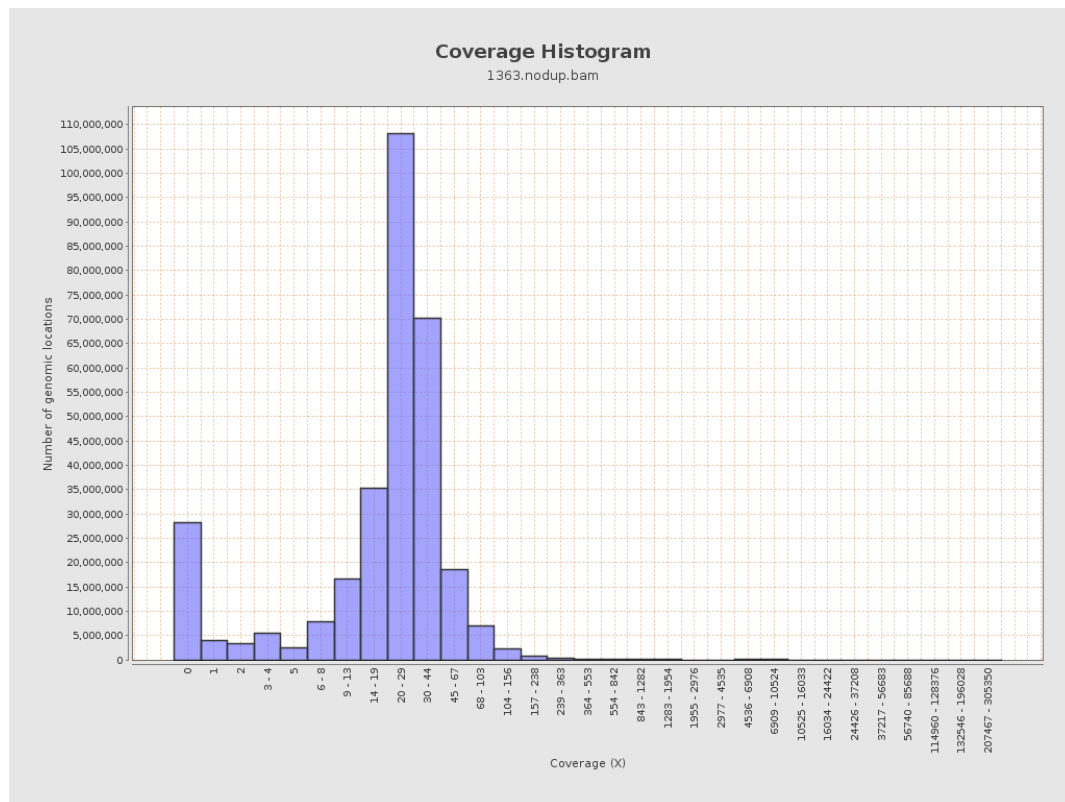
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	793817295	26.706	90.8386

LT669789.1	36598175	1160029045	31.6964	267.8721
LT669790.1	30422129	1101389103	36.2036	324.7106
LT669791.1	52758100	1657210135	31.4115	250.5767
LT669792.1	28376109	906743529	31.9545	263.5533
LT669793.1	33388210	985768967	29.5245	185.7506
LT669794.1	50579949	1512758680	29.9083	222.7517
LT669795.1	49795044	1854827674	37.2492	401.7074

### 3. Results : Coverage across reference

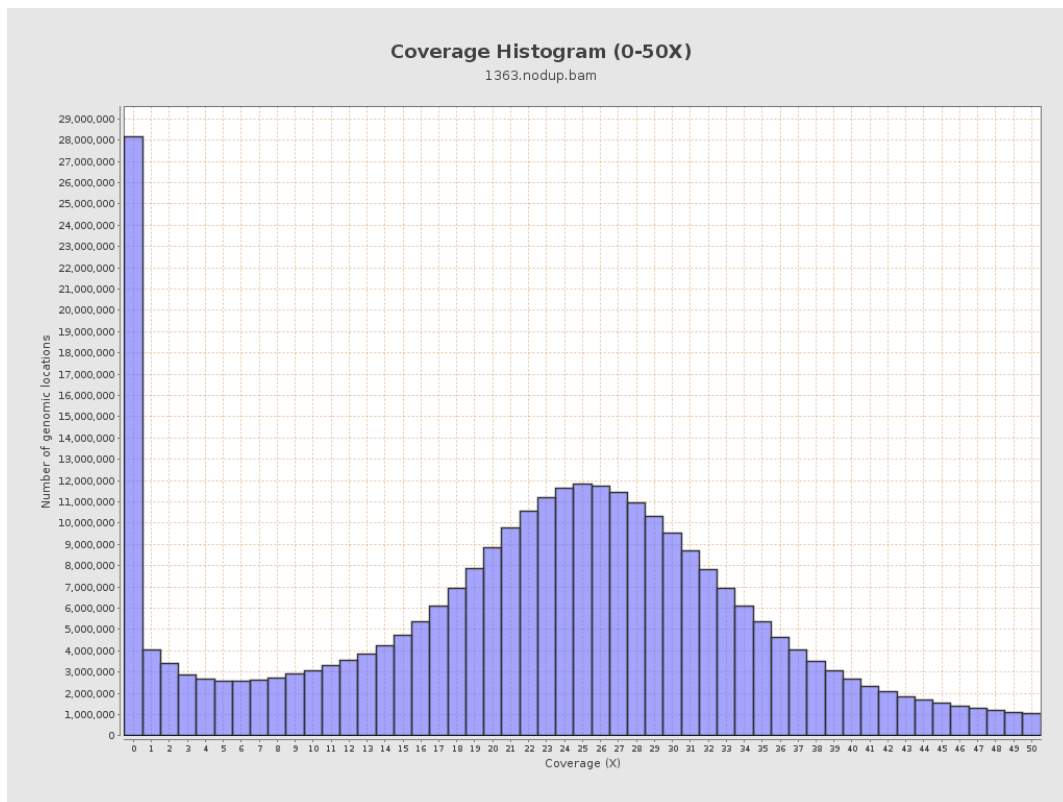


## 4. Results : Coverage Histogram

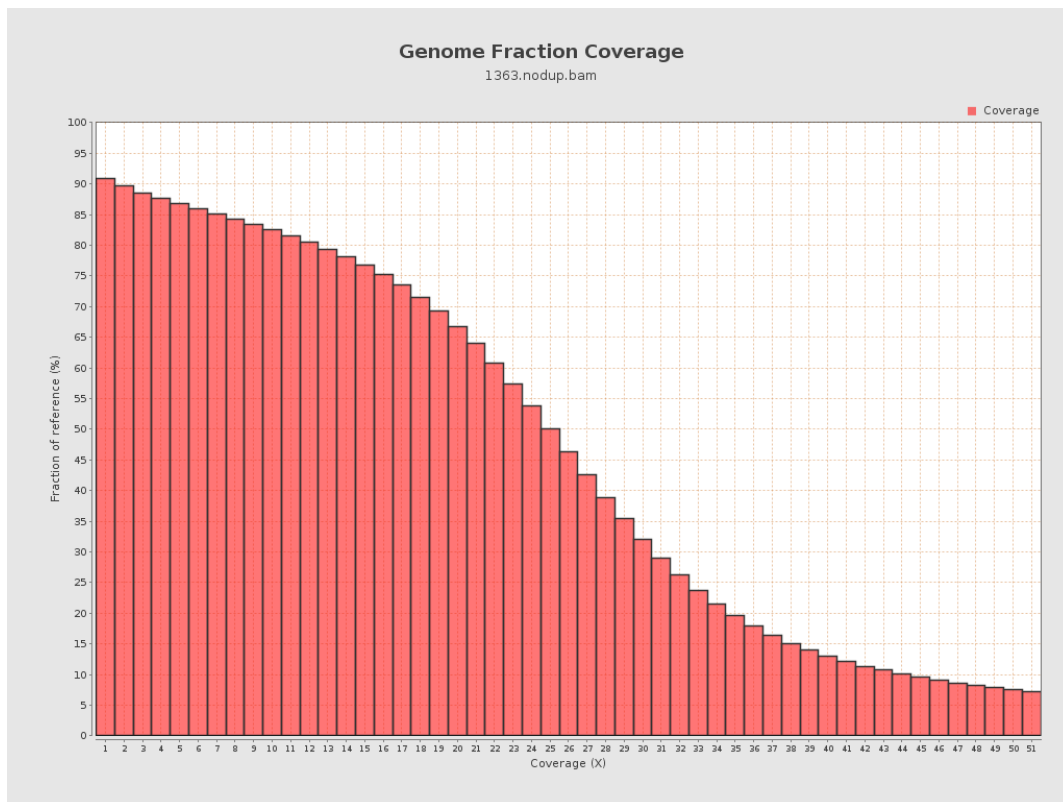




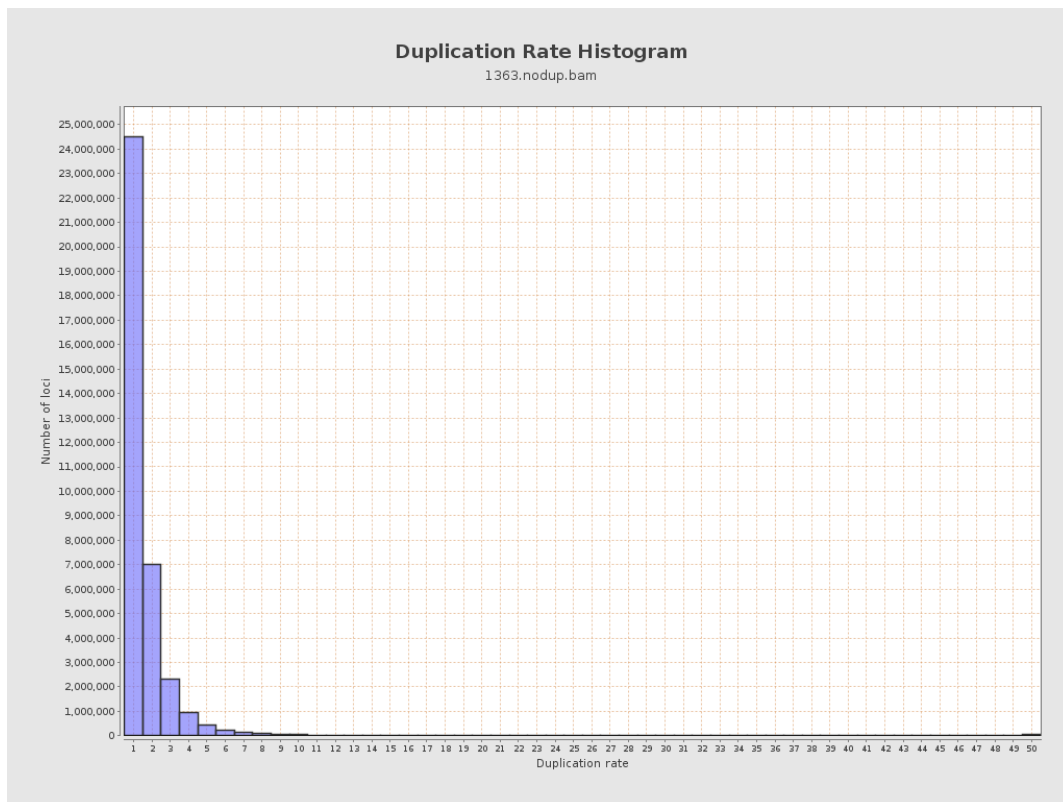
## 5. Results : Coverage Histogram (0-50X)



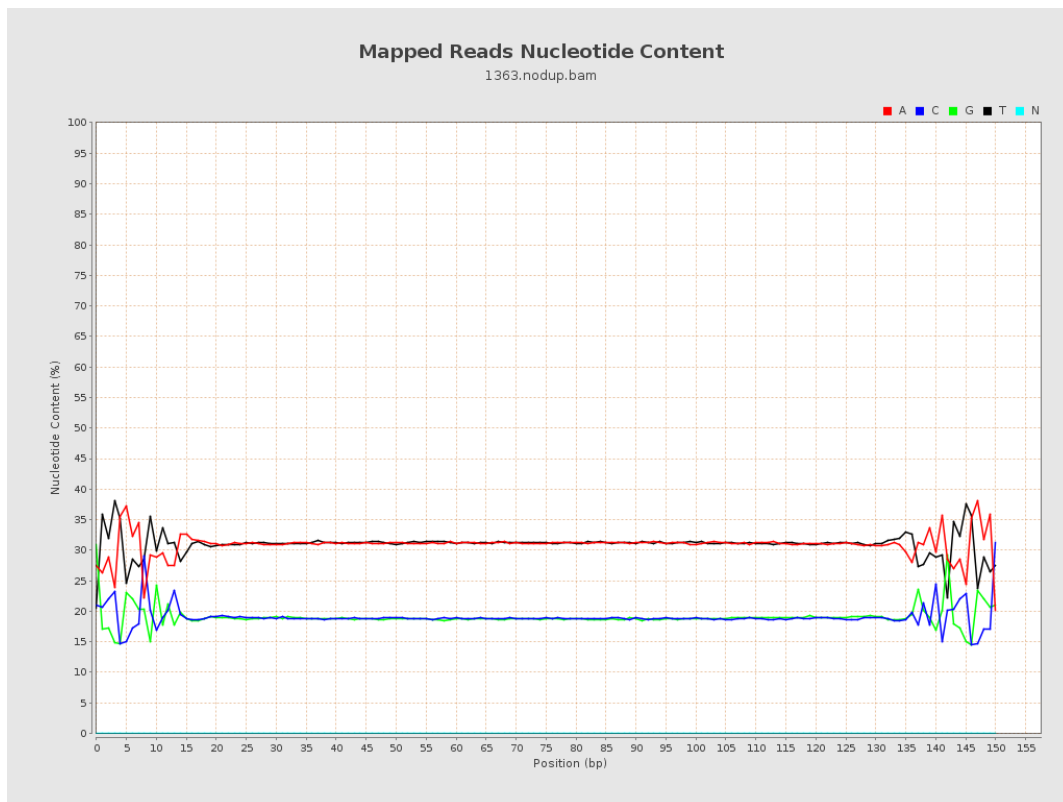
## 6. Results : Genome Fraction Coverage



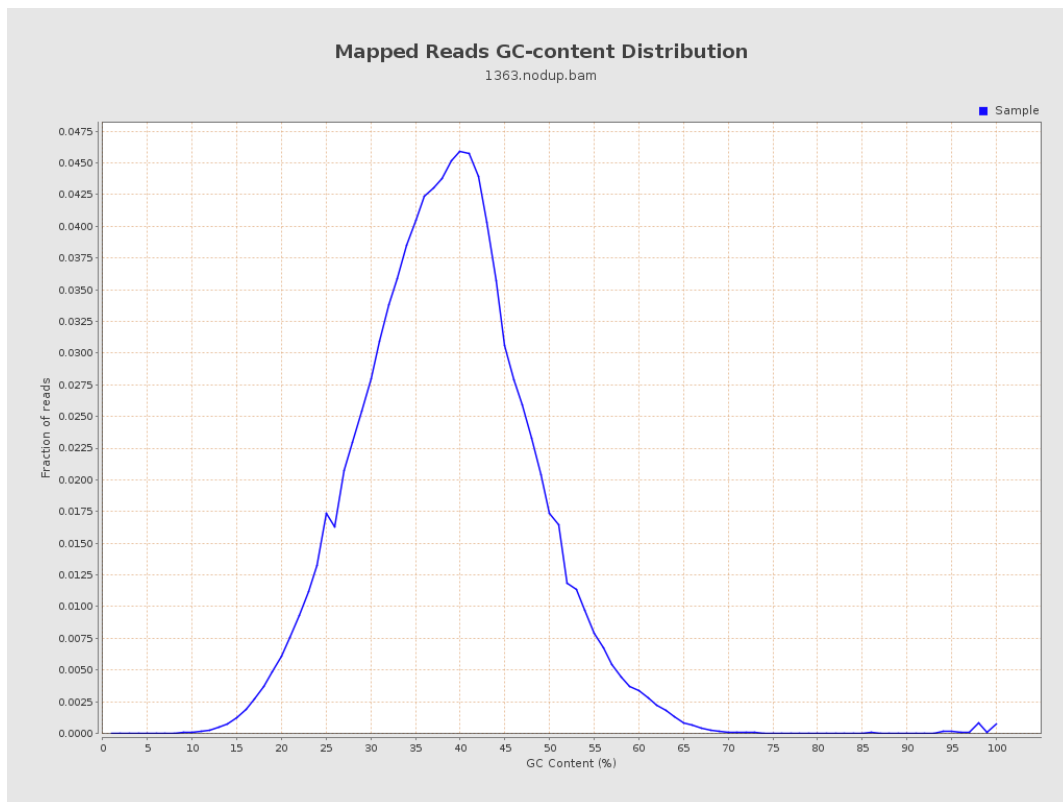
## 7. Results : Duplication Rate Histogram



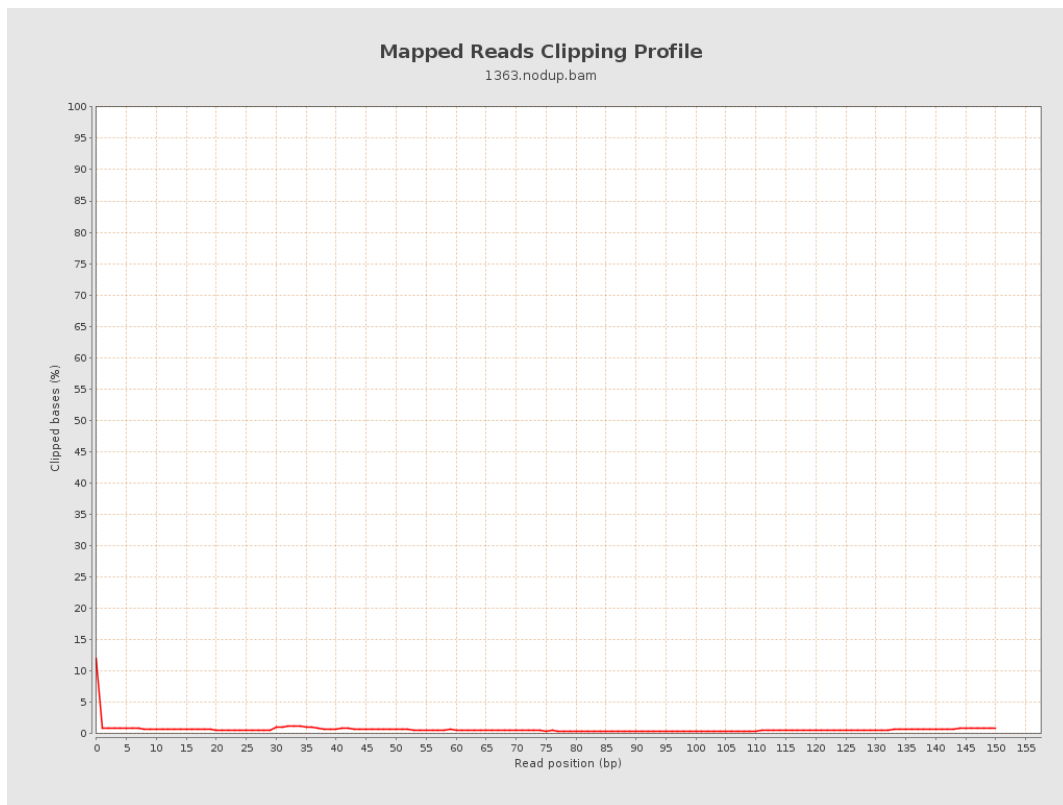
## 8. Results : Mapped Reads Nucleotide Content



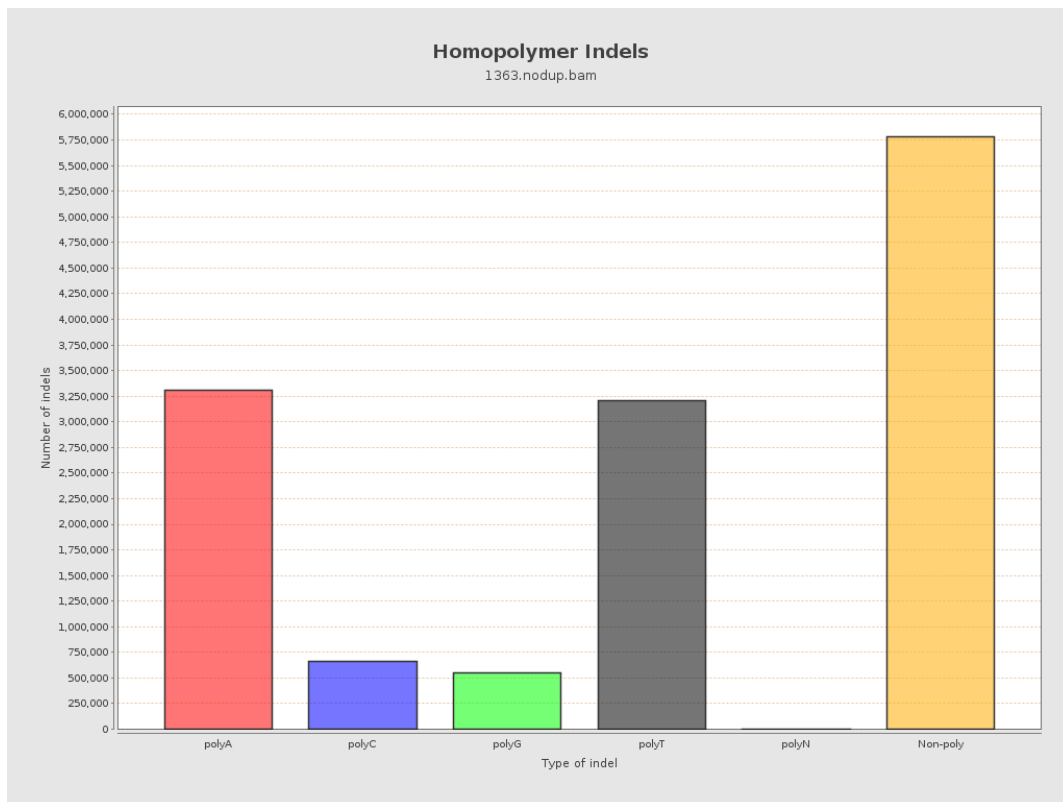
## 9. Results : Mapped Reads GC-content Distribution



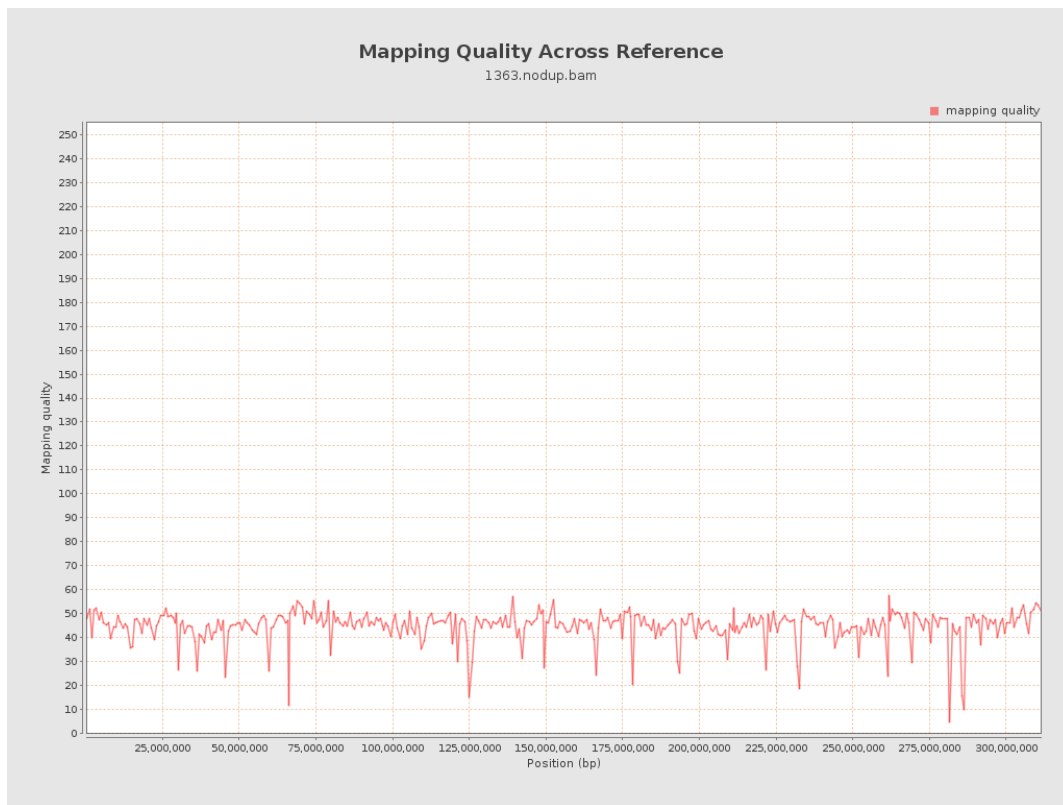
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

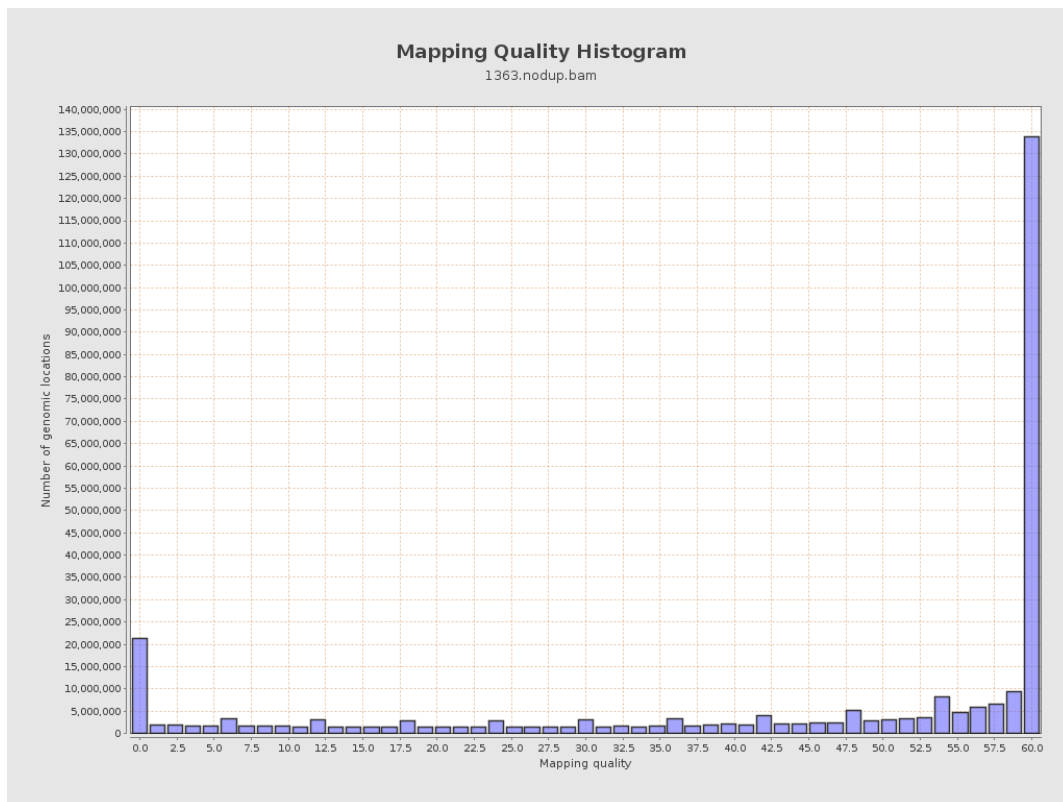


## 12. Results : Mapping Quality Across Reference

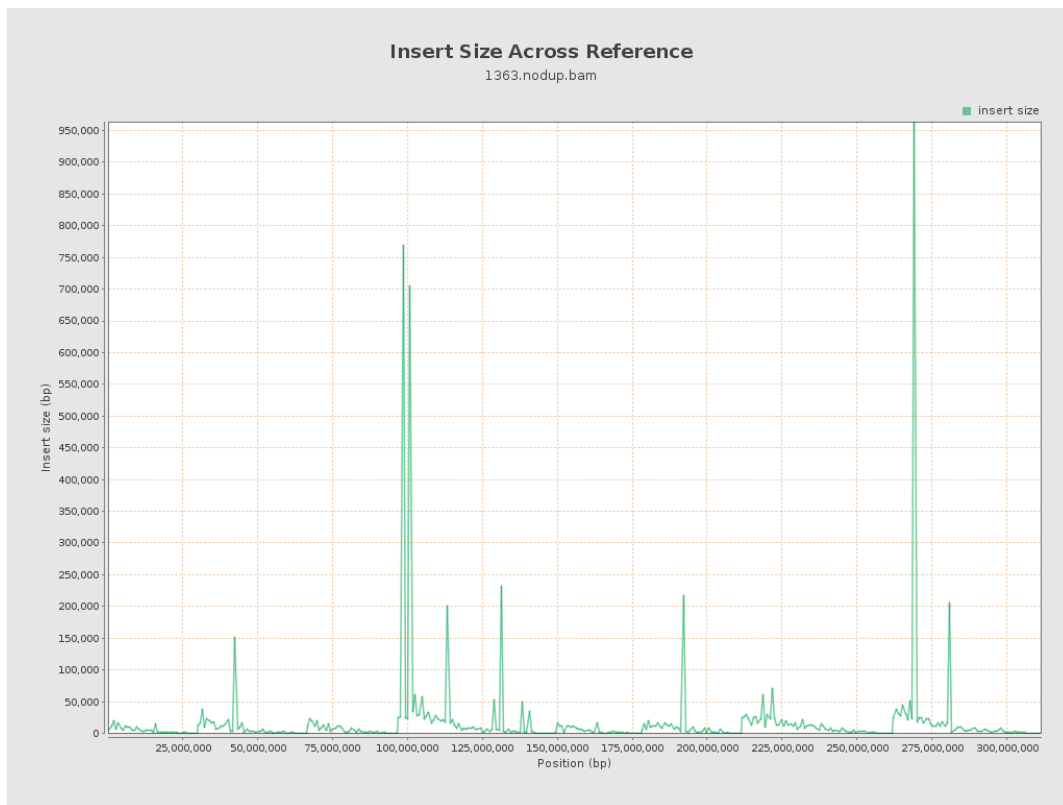




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

