

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:35:43*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/117
1
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1171 .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_437/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_437_S412_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_437/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_437_S412_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:42 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	80,061,312
Mapped reads	72,230,604 / 90.22%
Unmapped reads	7,830,708 / 9.78%
Mapped paired reads	72,230,604 / 90.22%
Mapped reads, first in pair	36,168,804 / 45.18%
Mapped reads, second in pair	36,061,800 / 45.04%
Mapped reads, both in pair	70,847,468 / 88.49%
Mapped reads, singletons	1,383,136 / 1.73%
Read min/max/mean length	30 / 151 / 148.4
Duplicated reads (flagged)	12,059,099 / 15.06%
Clipped reads	15,019,068 / 18.76%

### 2.2. ACGT Content

Number/percentage of A's	3,118,270,256 / 30.91%
Number/percentage of C's	1,930,055,357 / 19.13%
Number/percentage of T's	3,120,901,926 / 30.94%
Number/percentage of G's	1,919,314,027 / 19.02%
Number/percentage of N's	34,290 / 0%
GC Percentage	38.16%

### 2.3. Coverage

Mean	32.4542
Standard Deviation	239.5385

## 2.4. Mapping Quality

Mean Mapping Quality	44.35
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## 2.5. Insert size

Mean	228,223.27
Standard Deviation	2,264,517.93
P25/Median/P75	353 / 458 / 595

## 2.6. Mismatches and indels

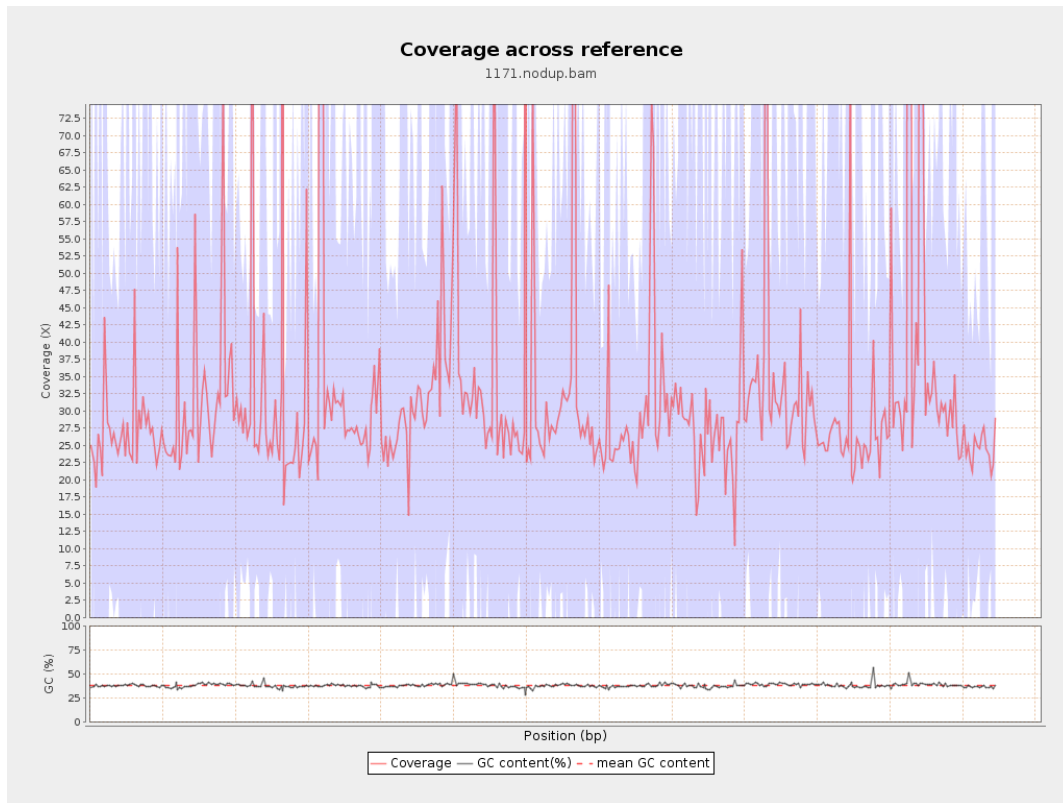
General error rate	2.22%
Mismatches	205,755,487
Insertions	6,601,421
Mapped reads with at least one insertion	8.23%
Deletions	6,742,707
Mapped reads with at least one deletion	8.31%
Homopolymer indels	56.73%

## 2.7. Chromosome stats

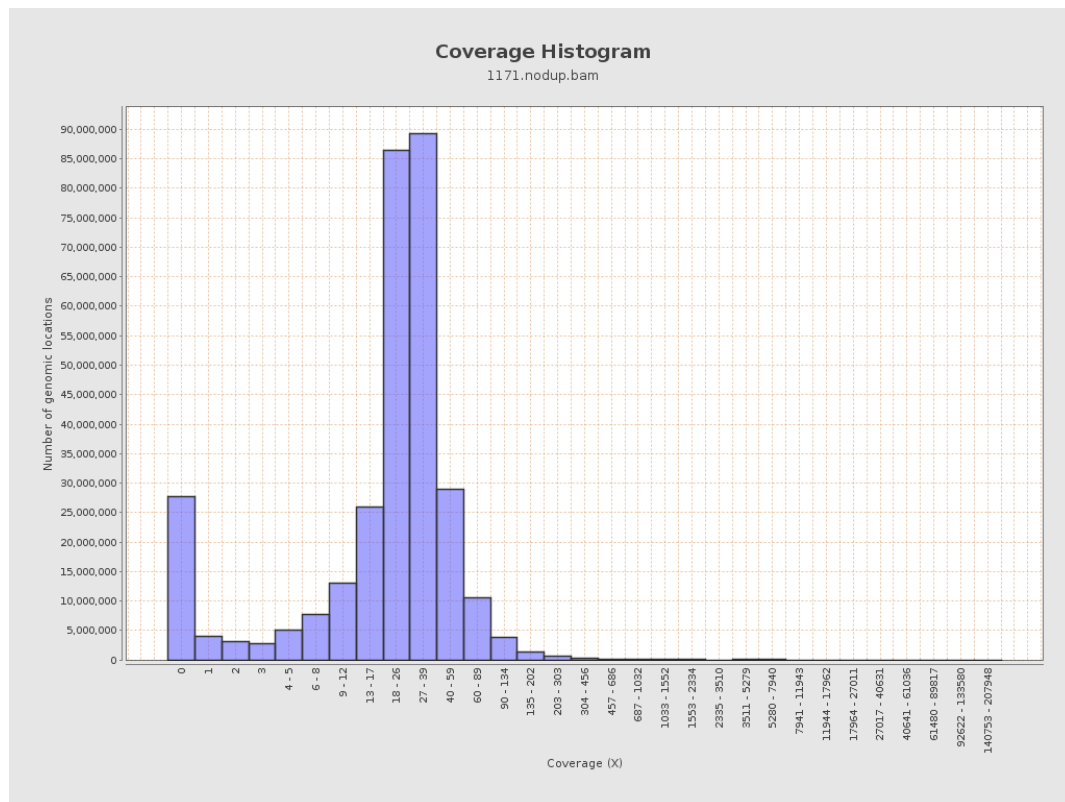
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	786903647	26.4734	60.884

LT669789.1	36598175	1211096442	33.0917	253.4792
LT669790.1	30422129	1022961942	33.6256	231.9154
LT669791.1	52758100	1710200460	32.4159	191.8063
LT669792.1	28376109	913381583	32.1884	304.5148
LT669793.1	33388210	983706898	29.4627	120.9397
LT669794.1	50579949	1577369037	31.1857	214.371
LT669795.1	49795044	1908459326	38.3263	358.38

### 3. Results : Coverage across reference

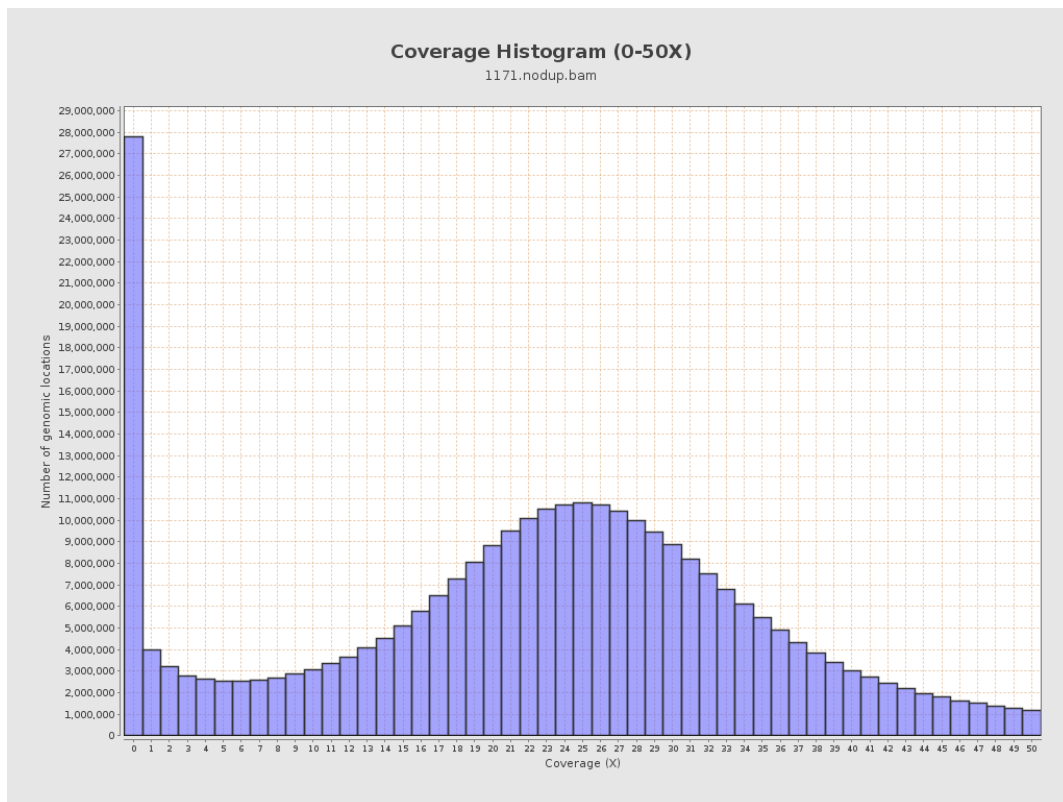


## 4. Results : Coverage Histogram

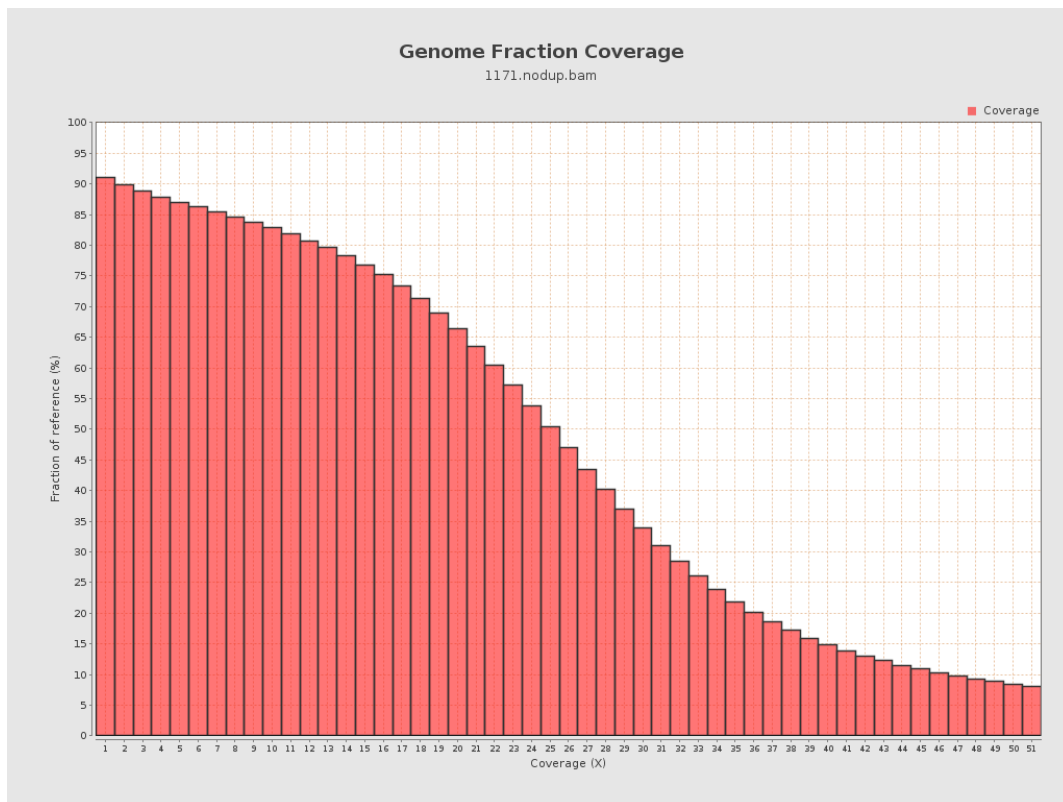




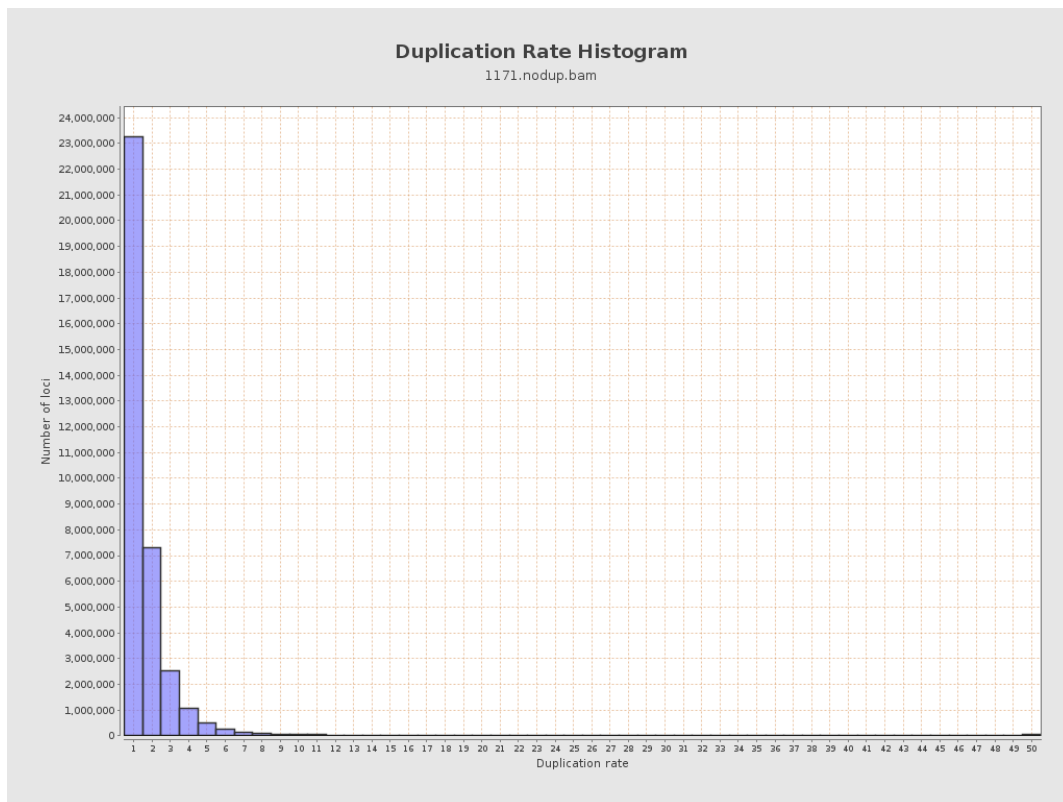
## 5. Results : Coverage Histogram (0-50X)



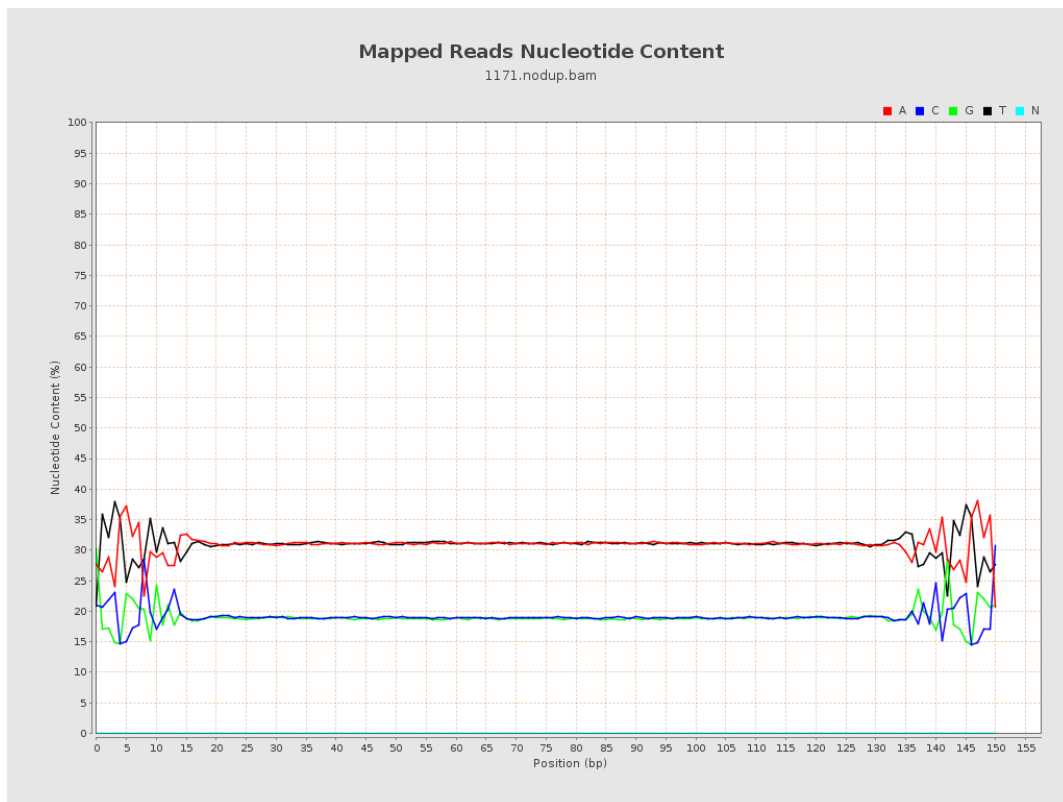
## 6. Results : Genome Fraction Coverage



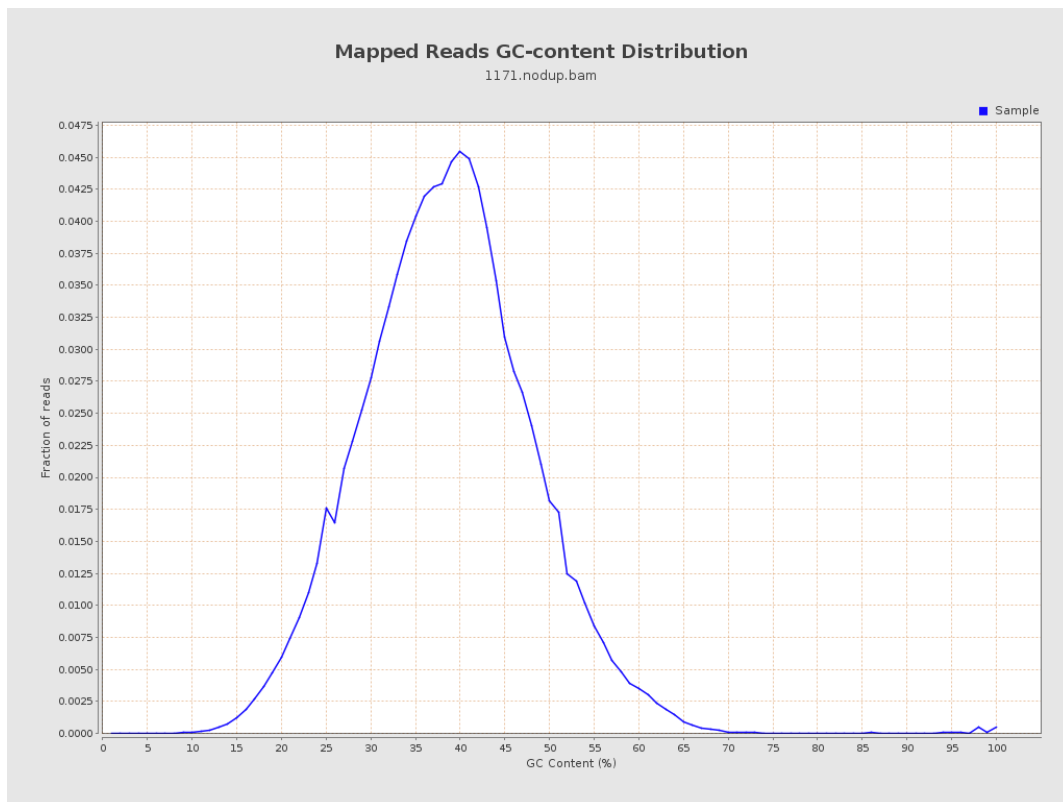
## 7. Results : Duplication Rate Histogram



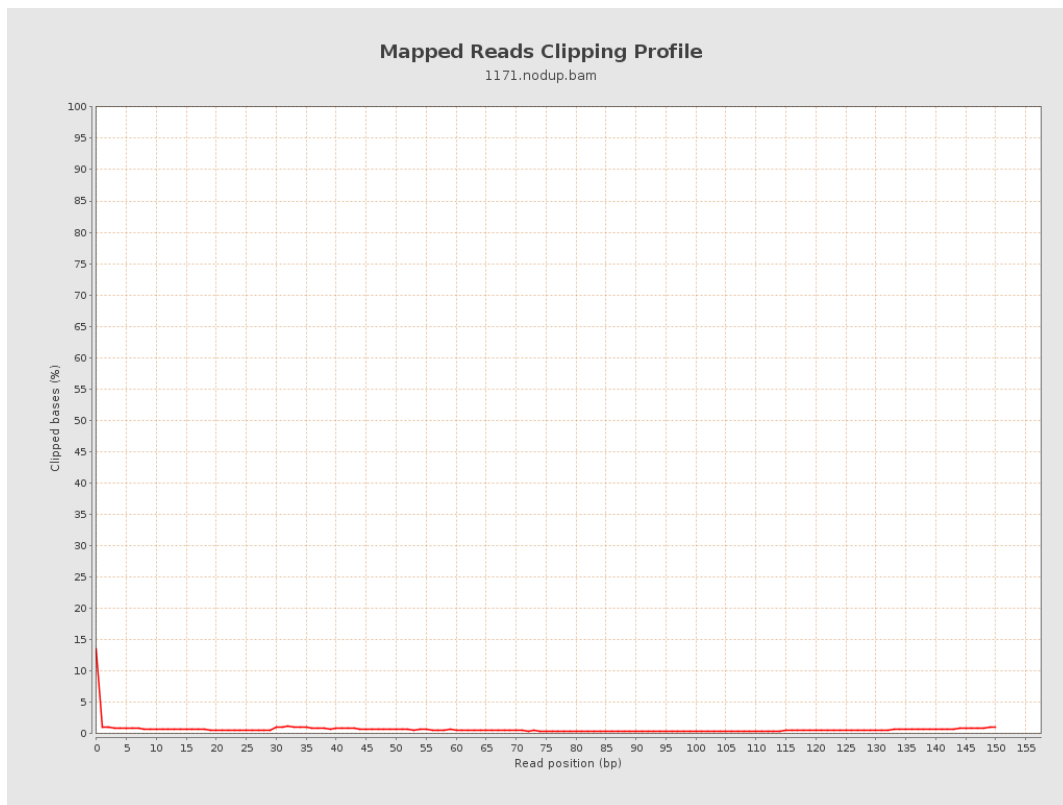
## 8. Results : Mapped Reads Nucleotide Content



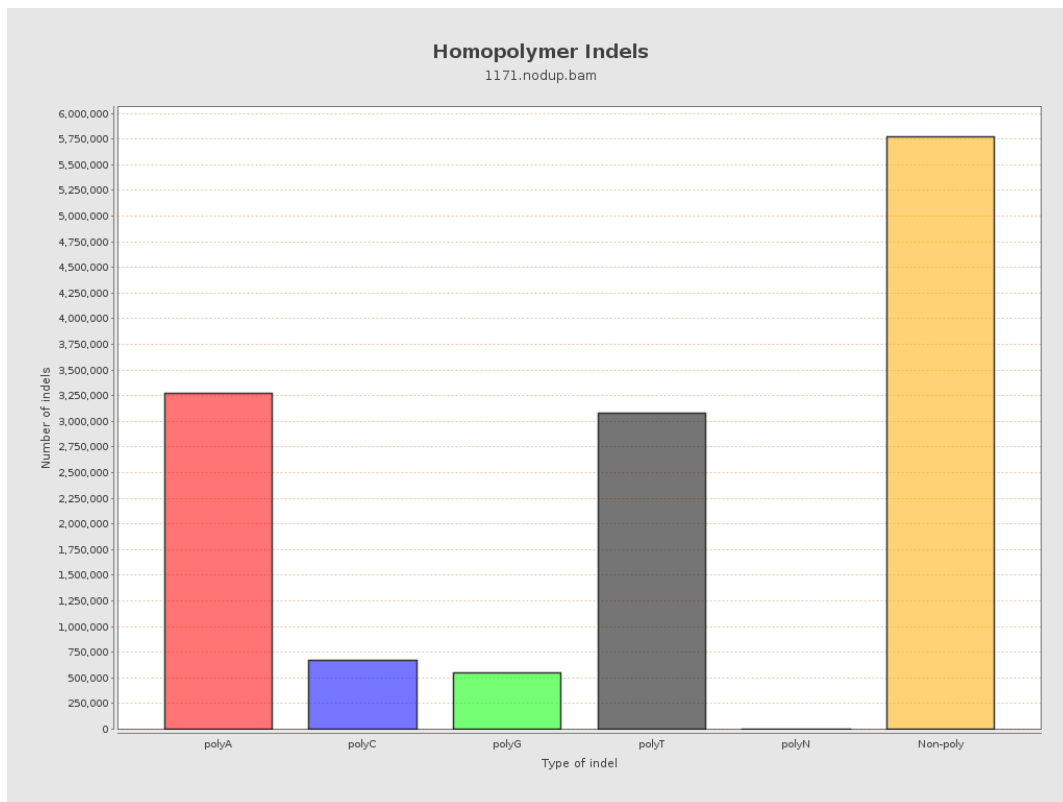
## 9. Results : Mapped Reads GC-content Distribution



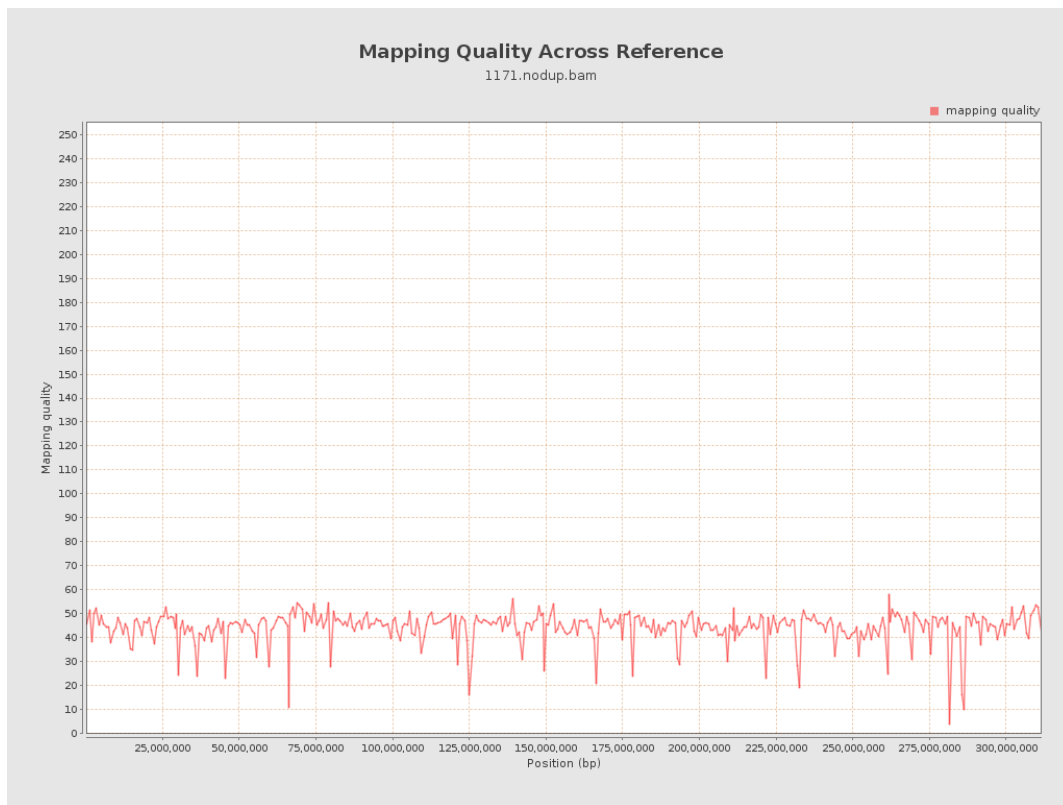
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

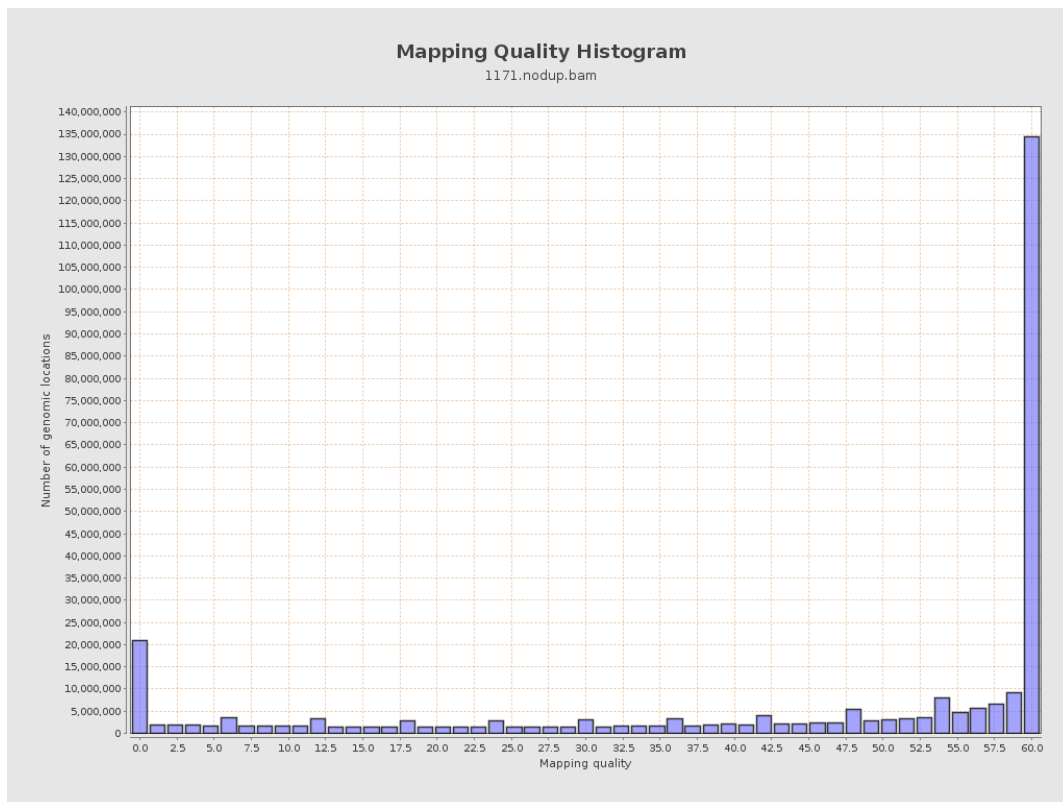


## 12. Results : Mapping Quality Across Reference

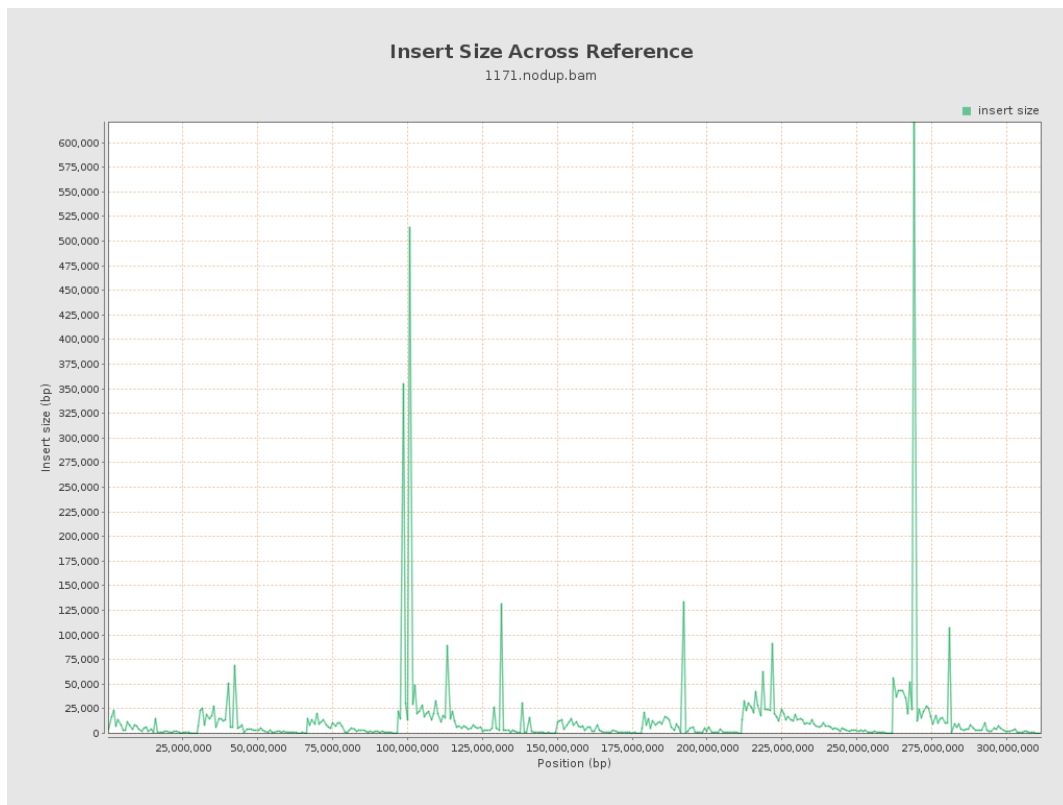




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

