

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:35:30*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/101
6
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1016 .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_546/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_546_S113_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_546/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_546_S113_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:28 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	76,087,015
Mapped reads	72,312,609 / 95.04%
Unmapped reads	3,774,406 / 4.96%
Mapped paired reads	72,312,609 / 95.04%
Mapped reads, first in pair	36,244,251 / 47.64%
Mapped reads, second in pair	36,068,358 / 47.4%
Mapped reads, both in pair	71,041,819 / 93.37%
Mapped reads, singletons	1,270,790 / 1.67%
Read min/max/mean length	30 / 151 / 148.12
Duplicated reads (flagged)	11,114,155 / 14.61%
Clipped reads	16,669,857 / 21.91%

### 2.2. ACGT Content

Number/percentage of A's	3,098,724,912 / 30.92%
Number/percentage of C's	1,915,273,254 / 19.11%
Number/percentage of T's	3,095,979,008 / 30.9%
Number/percentage of G's	1,910,265,189 / 19.06%
Number/percentage of N's	72,993 / 0%
GC Percentage	38.18%

### 2.3. Coverage

Mean	32.2348
Standard Deviation	249.1501

## 2.4. Mapping Quality

Mean Mapping Quality	43.99
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## 2.5. Insert size

Mean	209,108.54
Standard Deviation	2,160,055.07
P25/Median/P75	298 / 392 / 510

## 2.6. Mismatches and indels

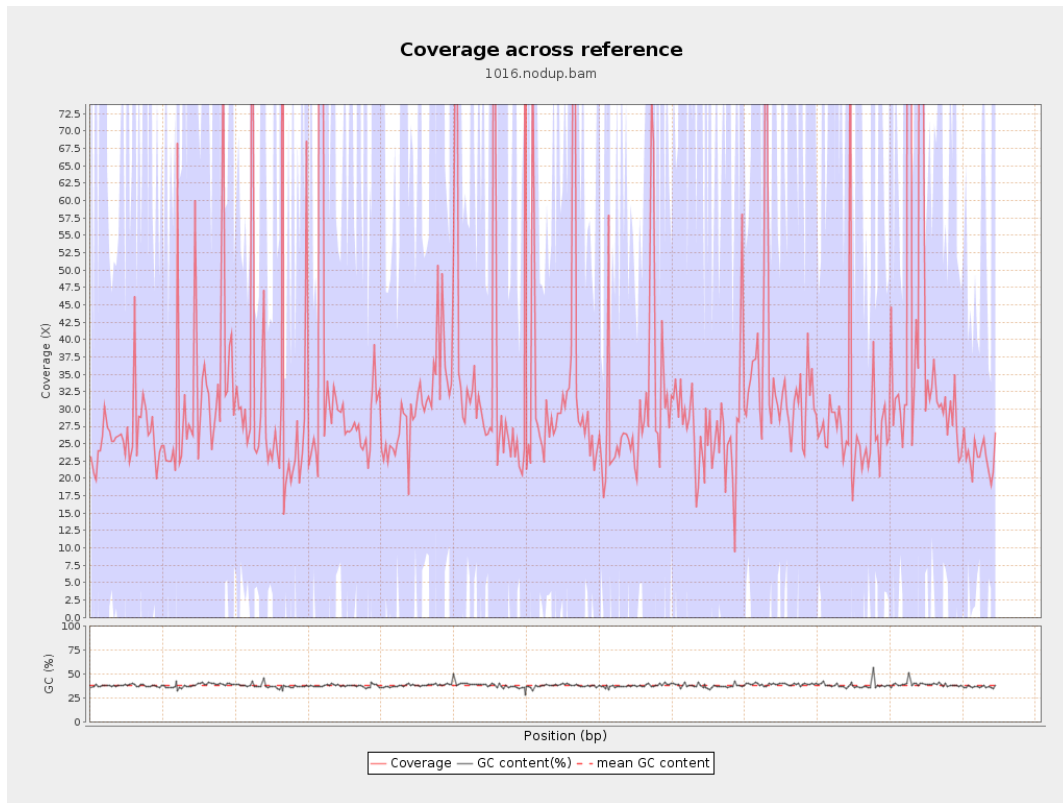
General error rate	2.46%
Mismatches	228,684,502
Insertions	6,630,550
Mapped reads with at least one insertion	8.26%
Deletions	6,831,828
Mapped reads with at least one deletion	8.42%
Homopolymer indels	56.61%

## 2.7. Chromosome stats

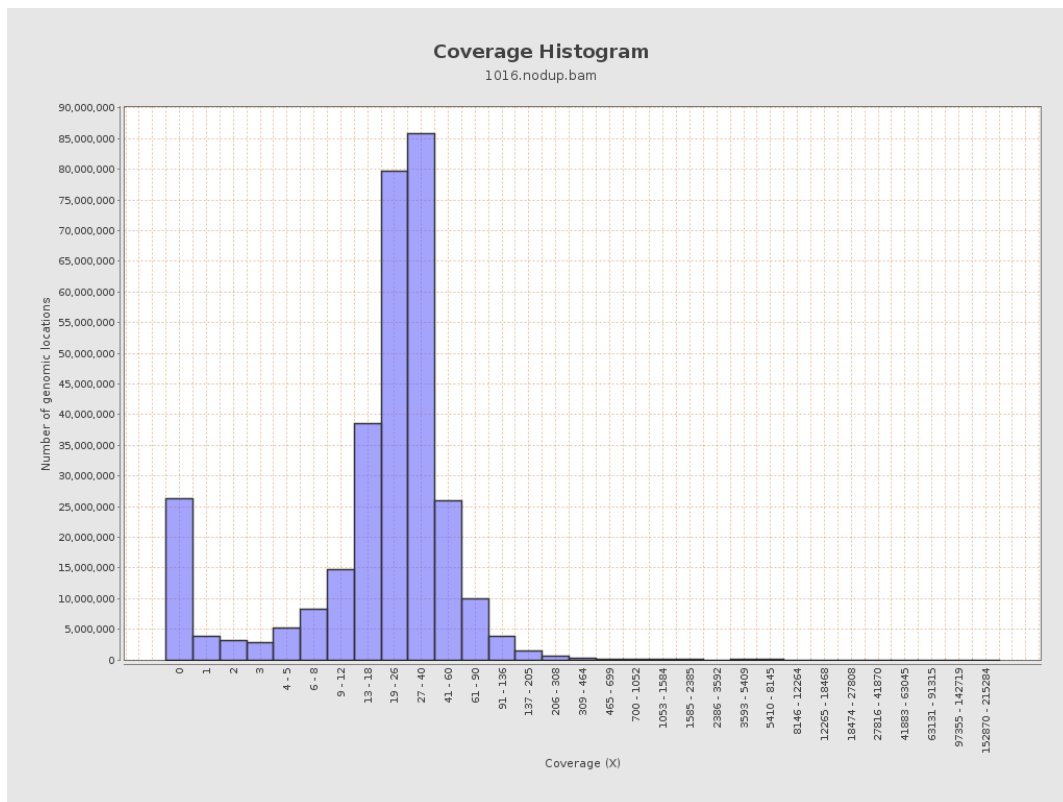
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	762834968	25.6636	73.2688

LT669789.1	36598175	1236378956	33.7825	279.317
LT669790.1	30422129	1020533100	33.5457	260.1621
LT669791.1	52758100	1692640669	32.083	215.665
LT669792.1	28376109	896801318	31.6041	274.8232
LT669793.1	33388210	986684724	29.5519	133.8505
LT669794.1	50579949	1608411689	31.7994	242.33
LT669795.1	49795044	1841440012	36.9804	350.094

### 3. Results : Coverage across reference

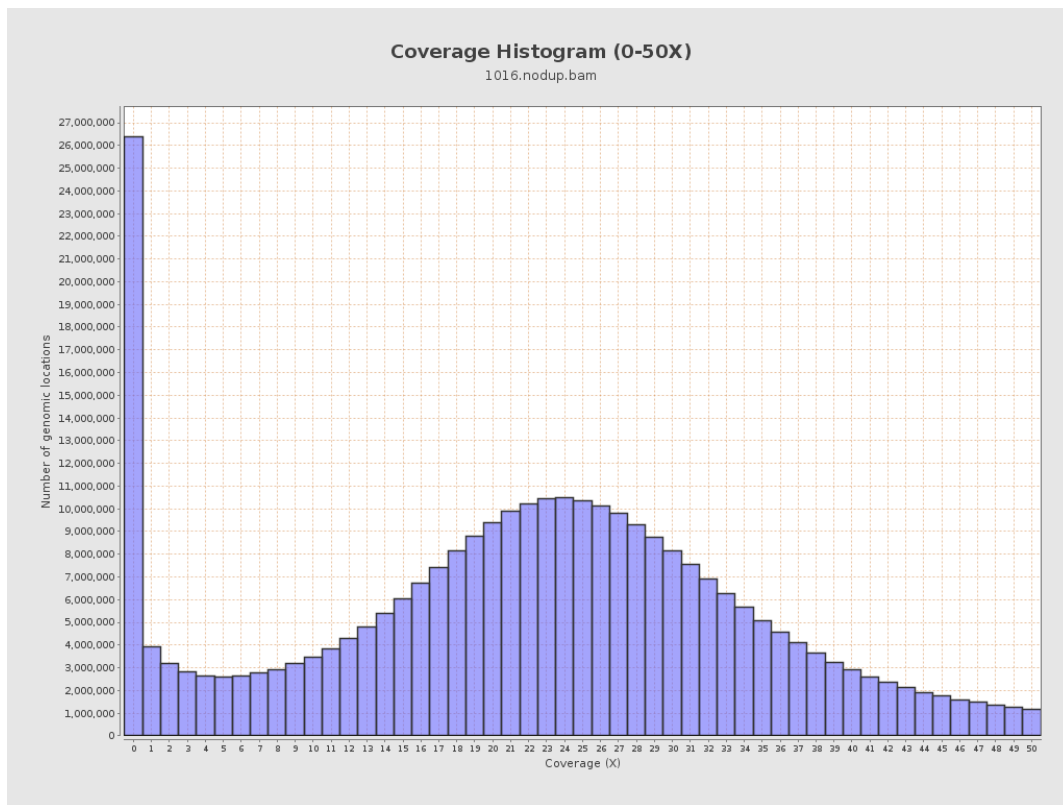


## 4. Results : Coverage Histogram

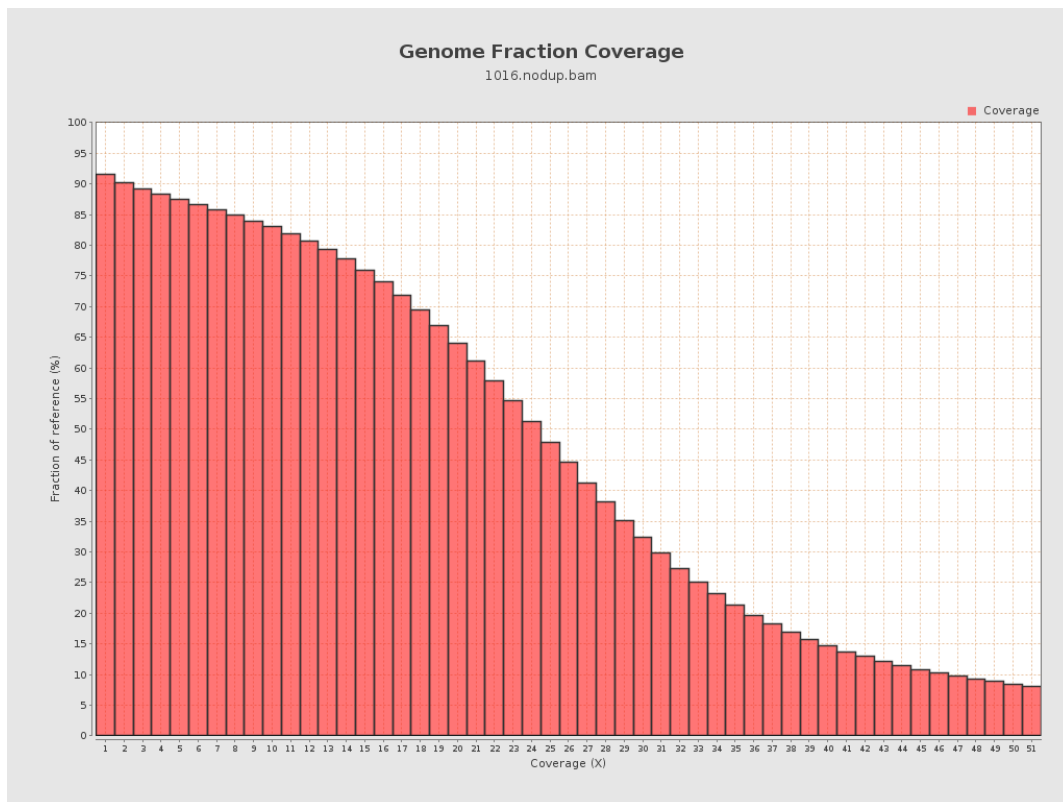




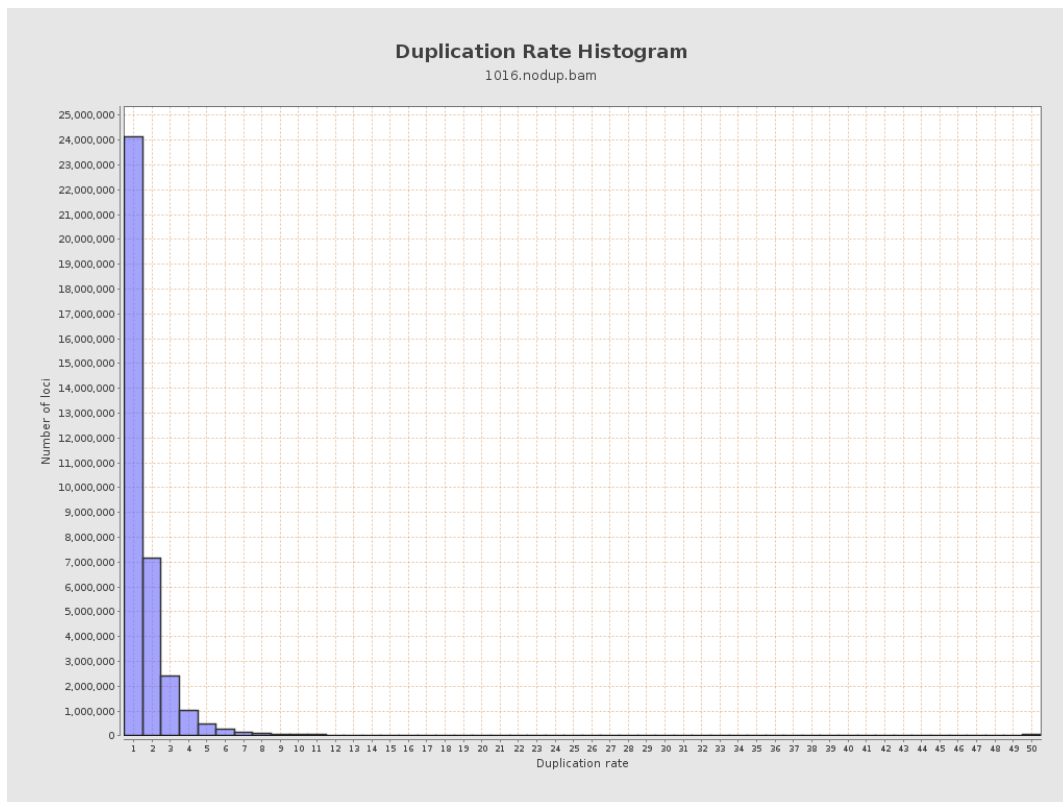
## 5. Results : Coverage Histogram (0-50X)



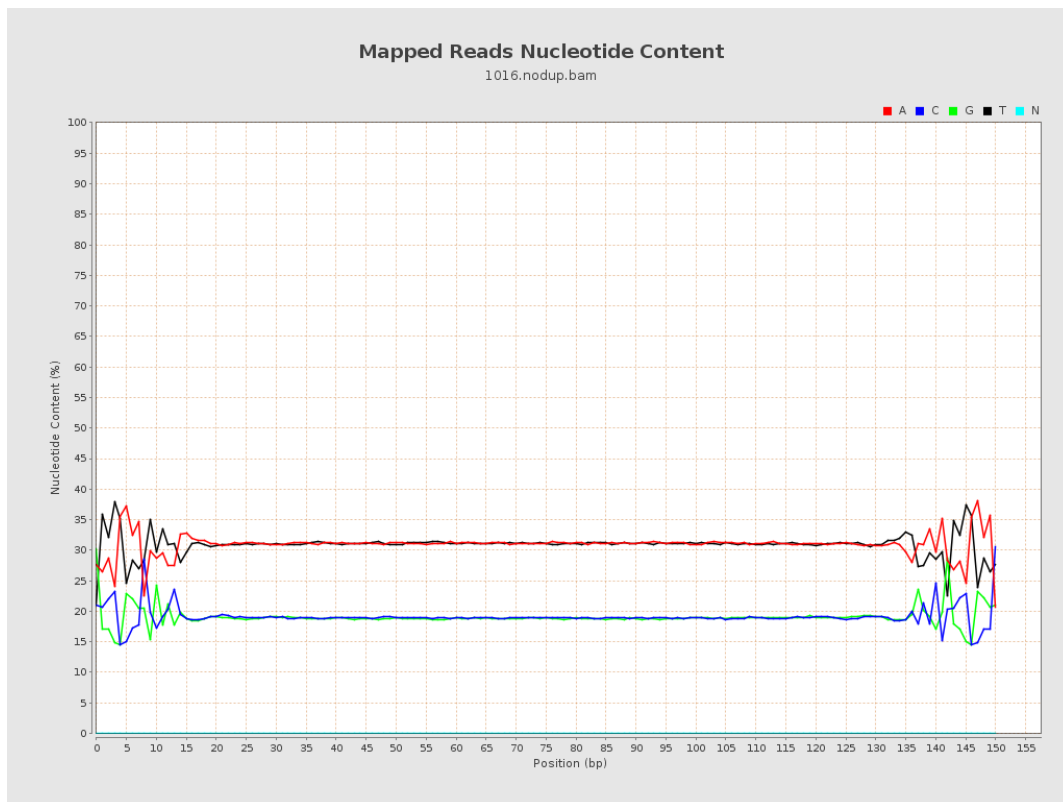
## 6. Results : Genome Fraction Coverage



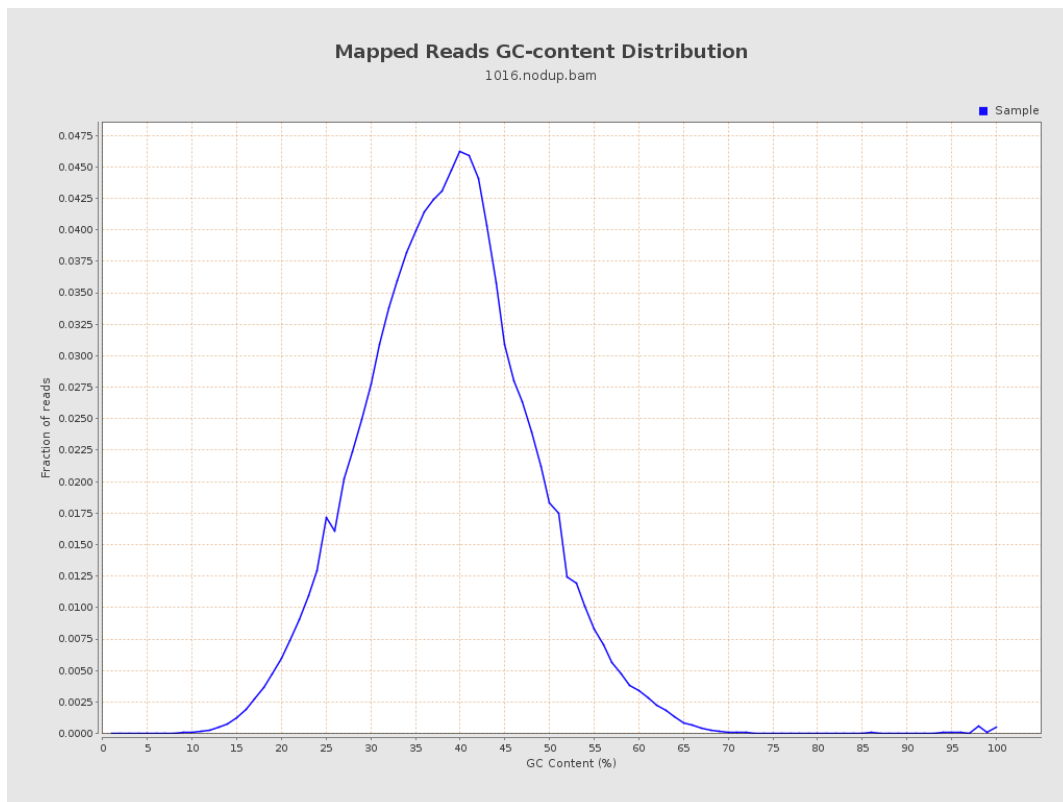
## 7. Results : Duplication Rate Histogram



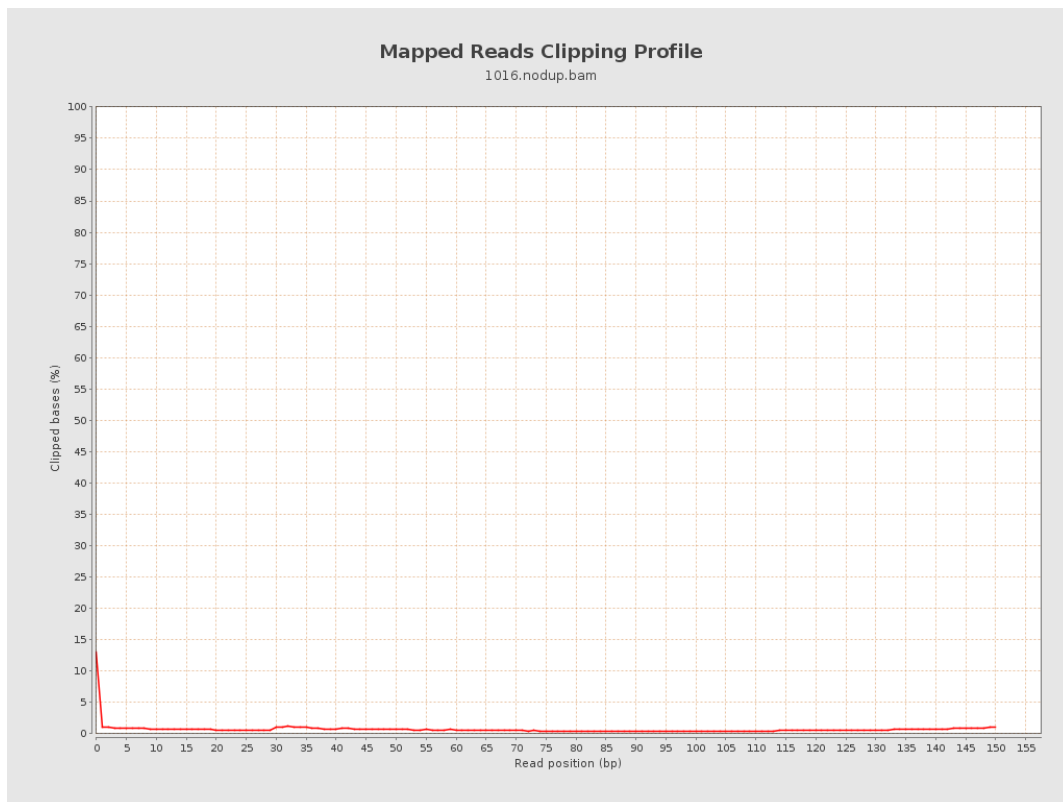
## 8. Results : Mapped Reads Nucleotide Content



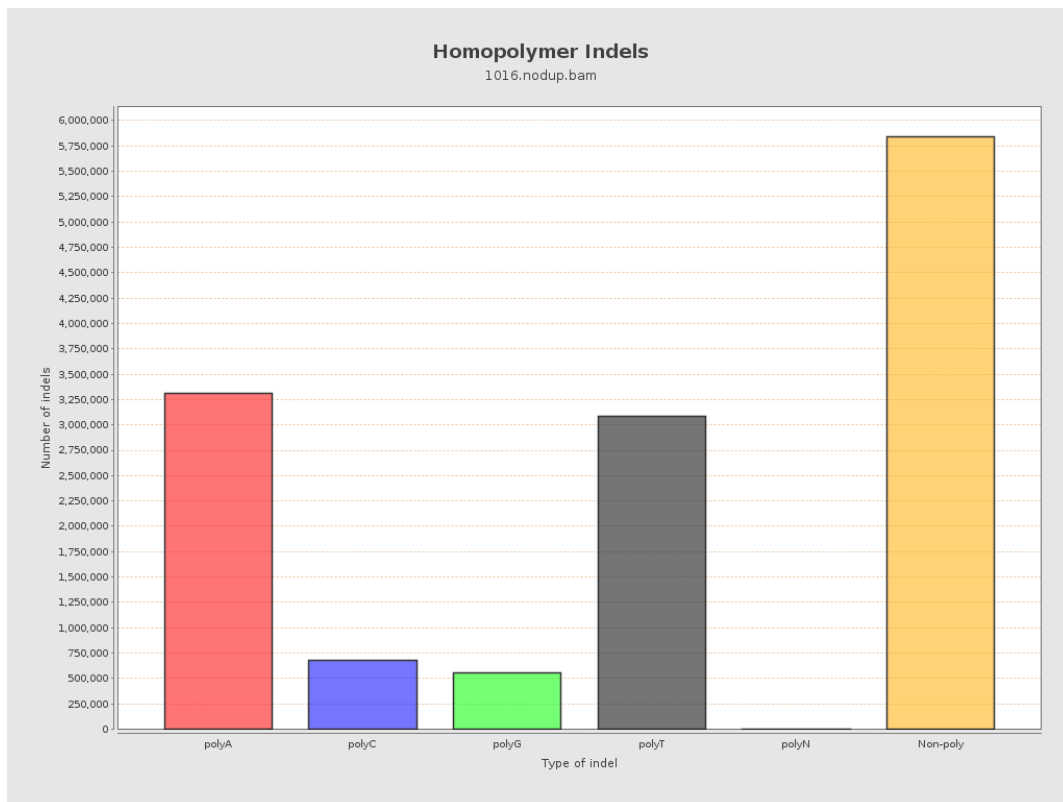
## 9. Results : Mapped Reads GC-content Distribution



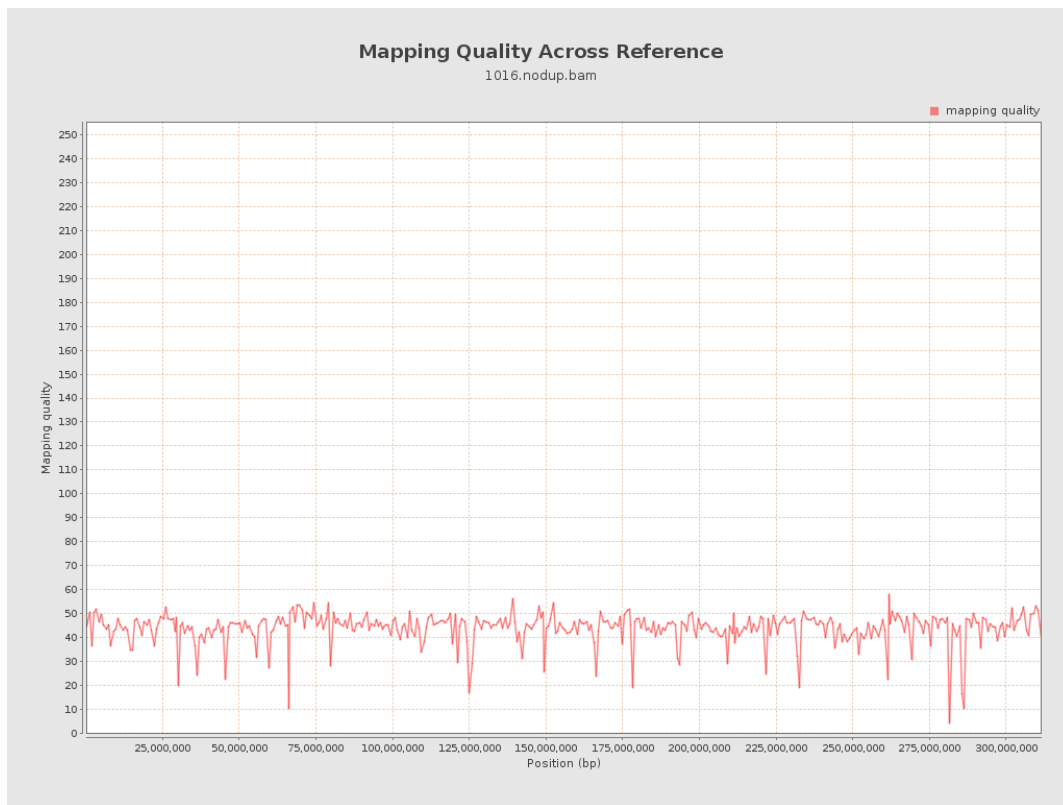
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

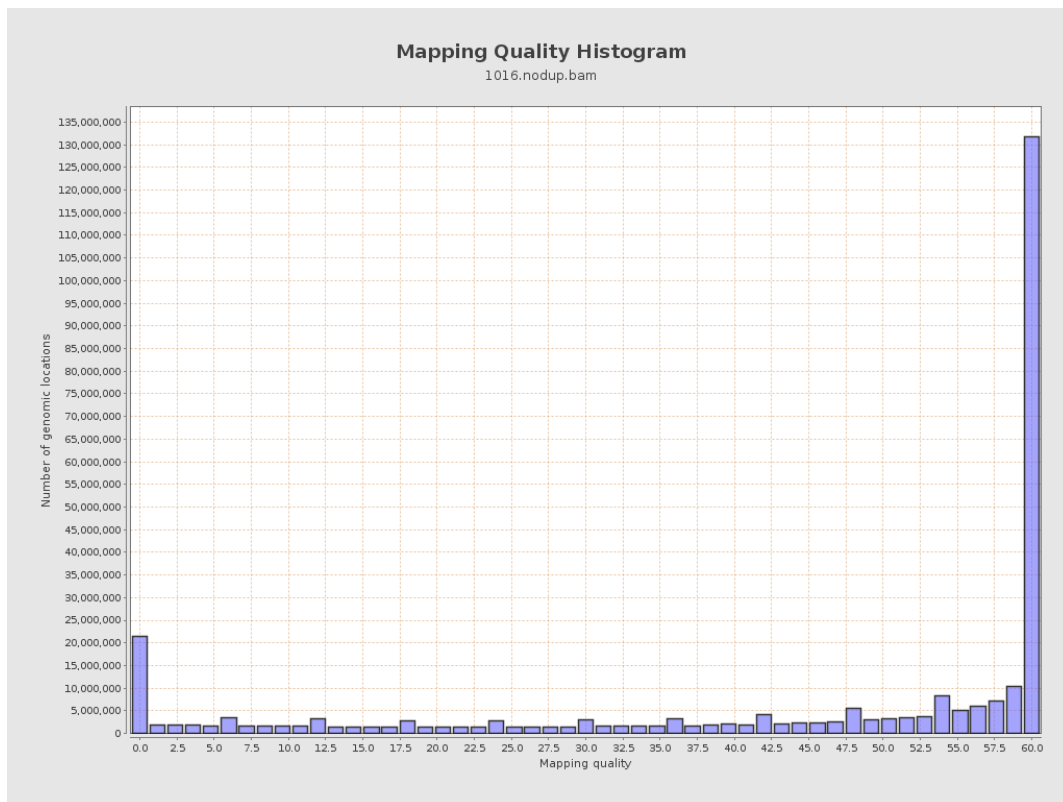


## 12. Results : Mapping Quality Across Reference

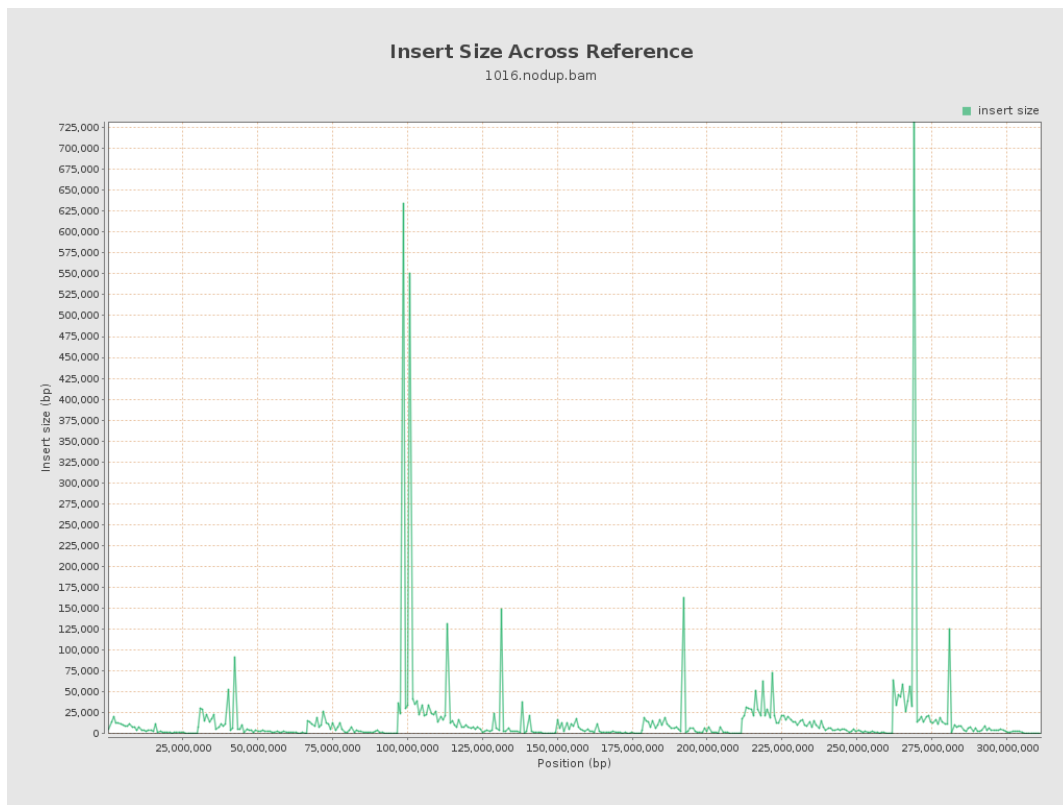




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

