

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:37:55*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/516
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/516 .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/awdata/P26207/P26207_420/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_420_S395_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_420/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_420_S395_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:37:54 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	85,531,784
Mapped reads	78,458,701 / 91.73%
Unmapped reads	7,073,083 / 8.27%
Mapped paired reads	78,458,701 / 91.73%
Mapped reads, first in pair	39,296,193 / 45.94%
Mapped reads, second in pair	39,162,508 / 45.79%
Mapped reads, both in pair	76,079,158 / 88.95%
Mapped reads, singletons	2,379,543 / 2.78%
Read min/max/mean length	30 / 151 / 148.19
Duplicated reads (flagged)	14,991,550 / 17.53%
Clipped reads	17,821,472 / 20.84%

### 2.2. ACGT Content

Number/percentage of A's	3,345,496,873 / 30.94%
Number/percentage of C's	2,063,734,548 / 19.08%
Number/percentage of T's	3,347,728,046 / 30.96%
Number/percentage of G's	2,057,296,090 / 19.02%
Number/percentage of N's	37,802 / 0%
GC Percentage	38.11%

### 2.3. Coverage

Mean	34.7877
Standard Deviation	331.6434

## 2.4. Mapping Quality

Mean Mapping Quality	44.57
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## 2.5. Insert size

Mean	253,142.49
Standard Deviation	2,415,571.34
P25/Median/P75	347 / 452 / 587

## 2.6. Mismatches and indels

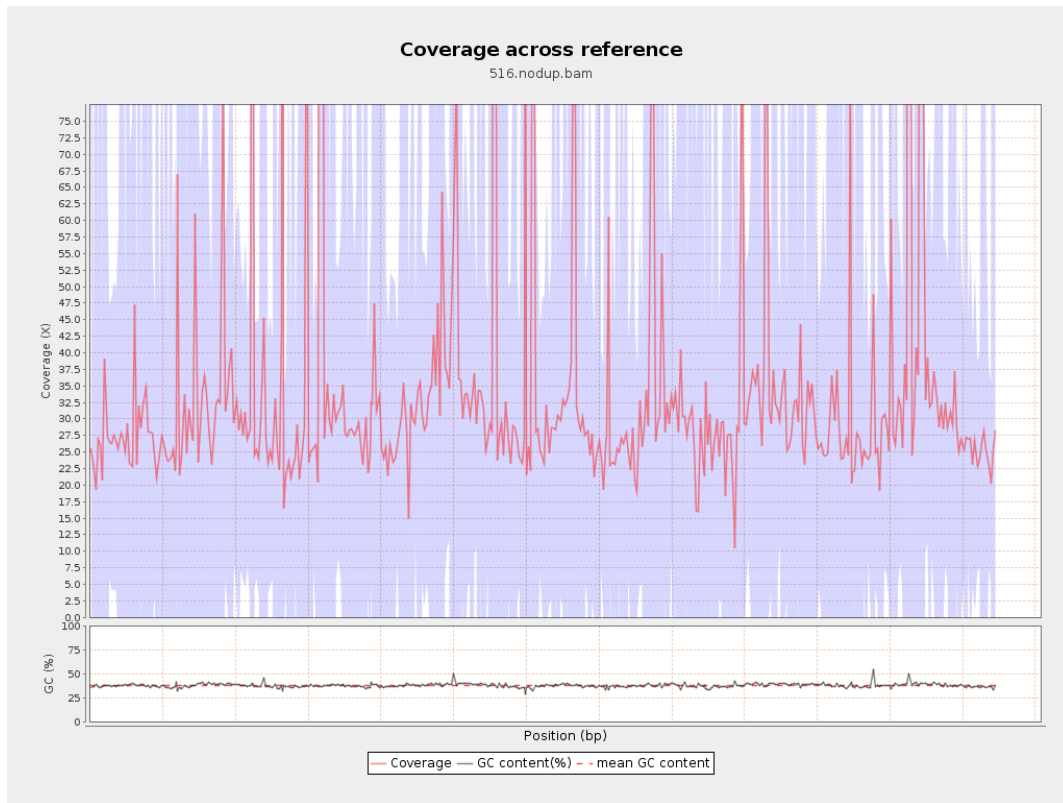
General error rate	2.3%
Mismatches	227,026,848
Insertions	7,679,270
Mapped reads with at least one insertion	8.74%
Deletions	7,323,157
Mapped reads with at least one deletion	8.3%
Homopolymer indels	57.86%

## 2.7. Chromosome stats

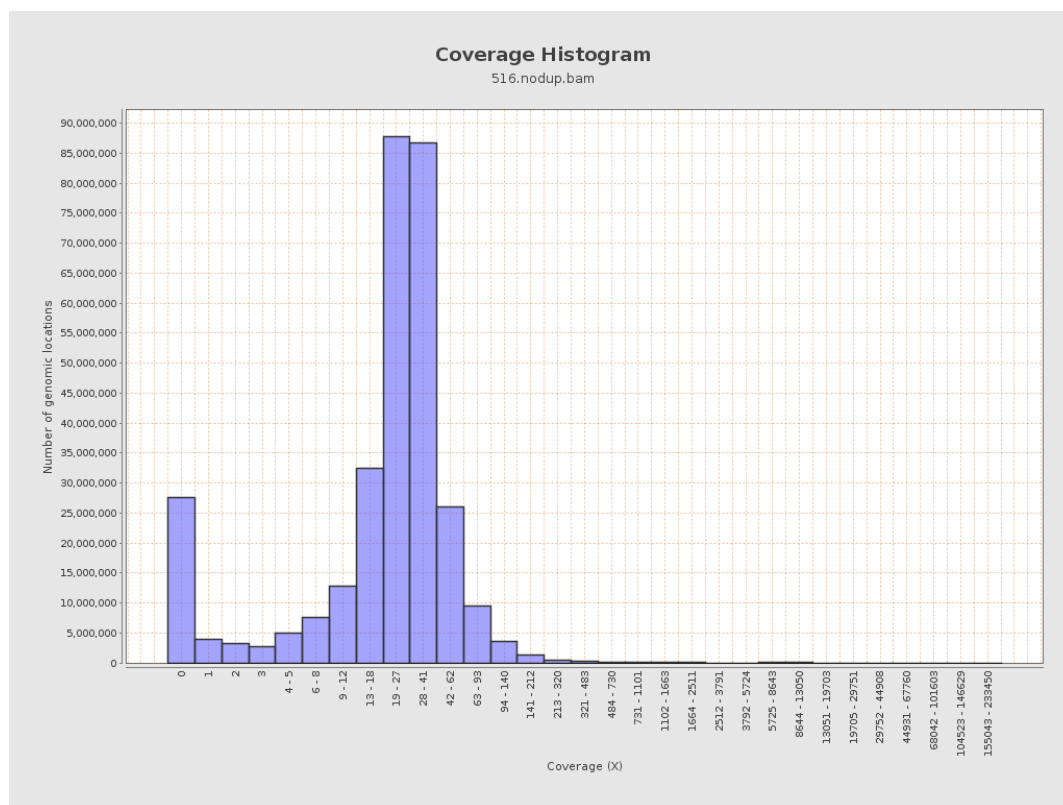
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	798785695	26.8731	117.5416

LT669789.1	36598175	1291946542	35.3008	345.1039
LT669790.1	30422129	1246852212	40.985	463.6245
LT669791.1	52758100	1841192063	34.8988	337.2809
LT669792.1	28376109	970464389	34.2001	338.3373
LT669793.1	33388210	1048968735	31.4173	219.2851
LT669794.1	50579949	1656768889	32.7554	265.4829
LT669795.1	49795044	1986341248	39.8903	414.1973

### 3. Results : Coverage across reference

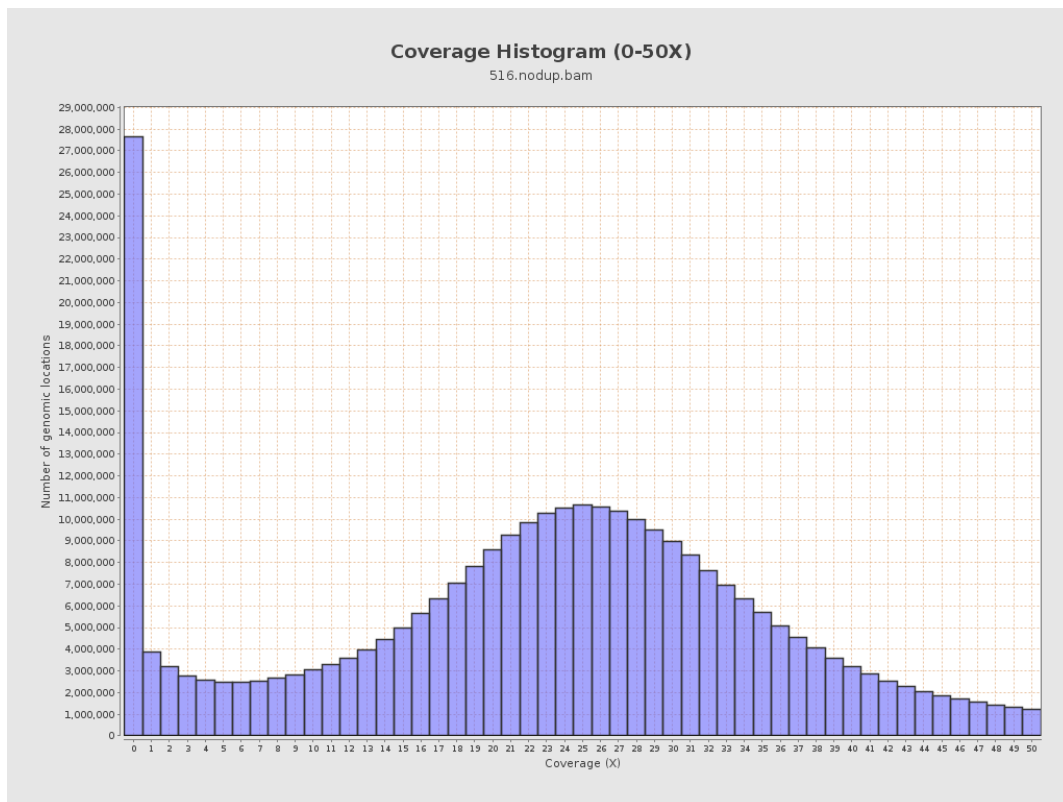


## 4. Results : Coverage Histogram

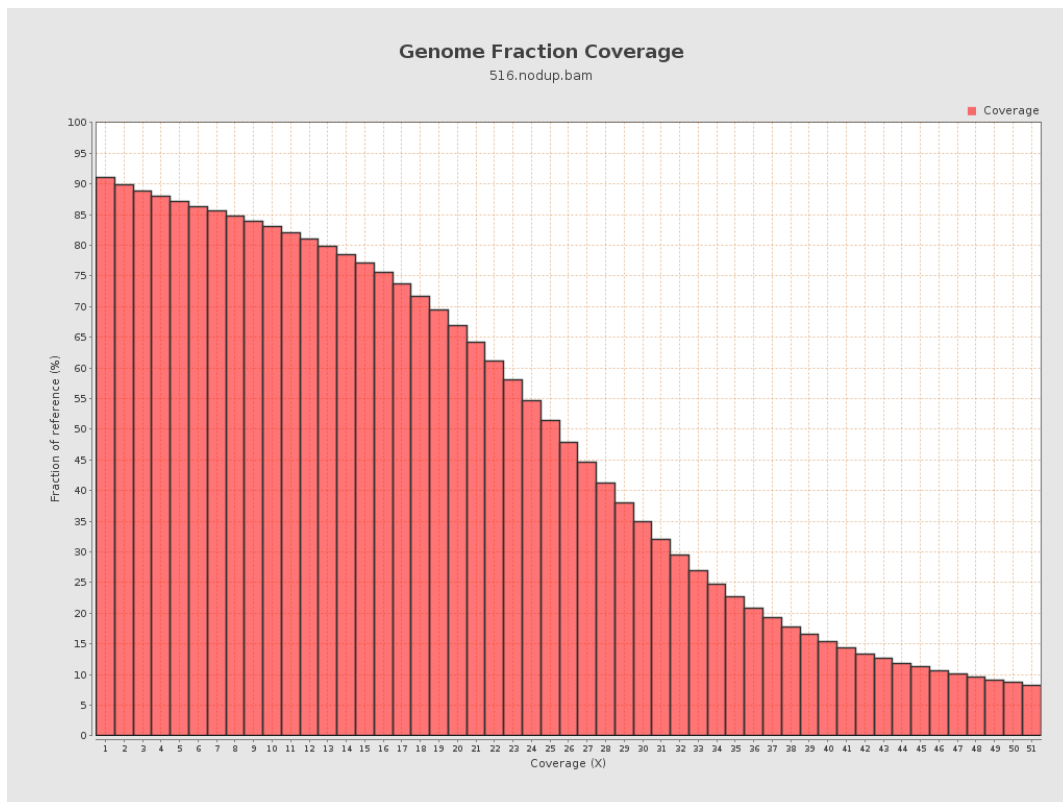




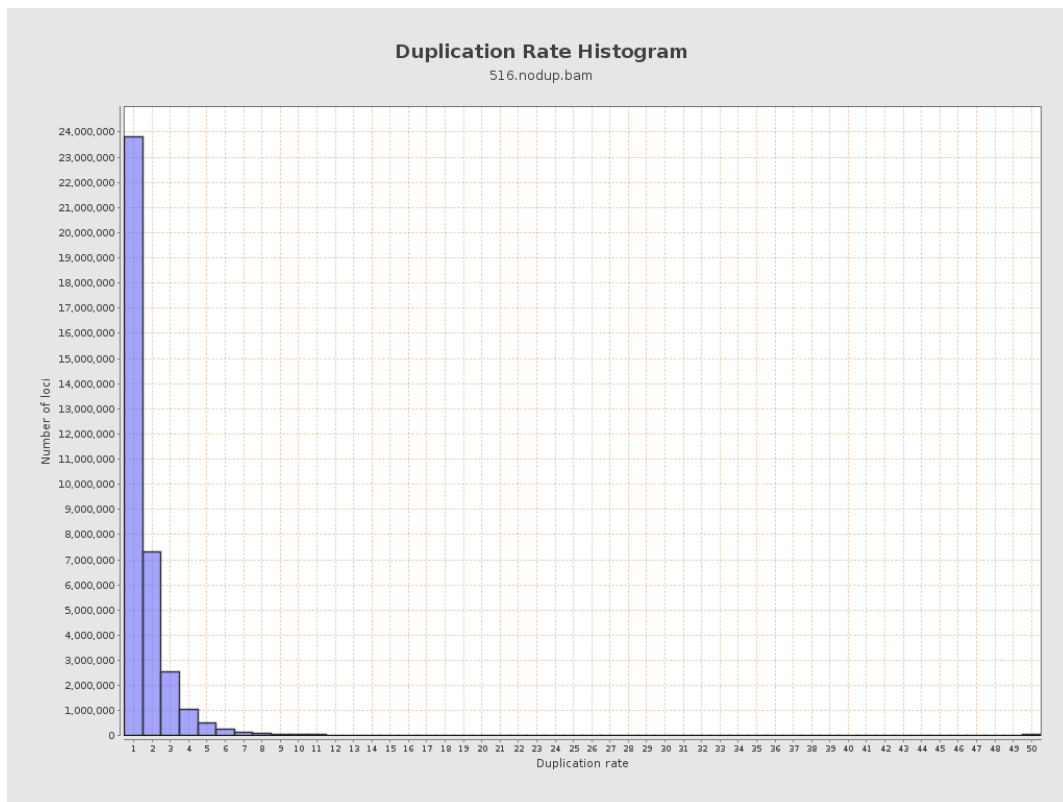
## 5. Results : Coverage Histogram (0-50X)



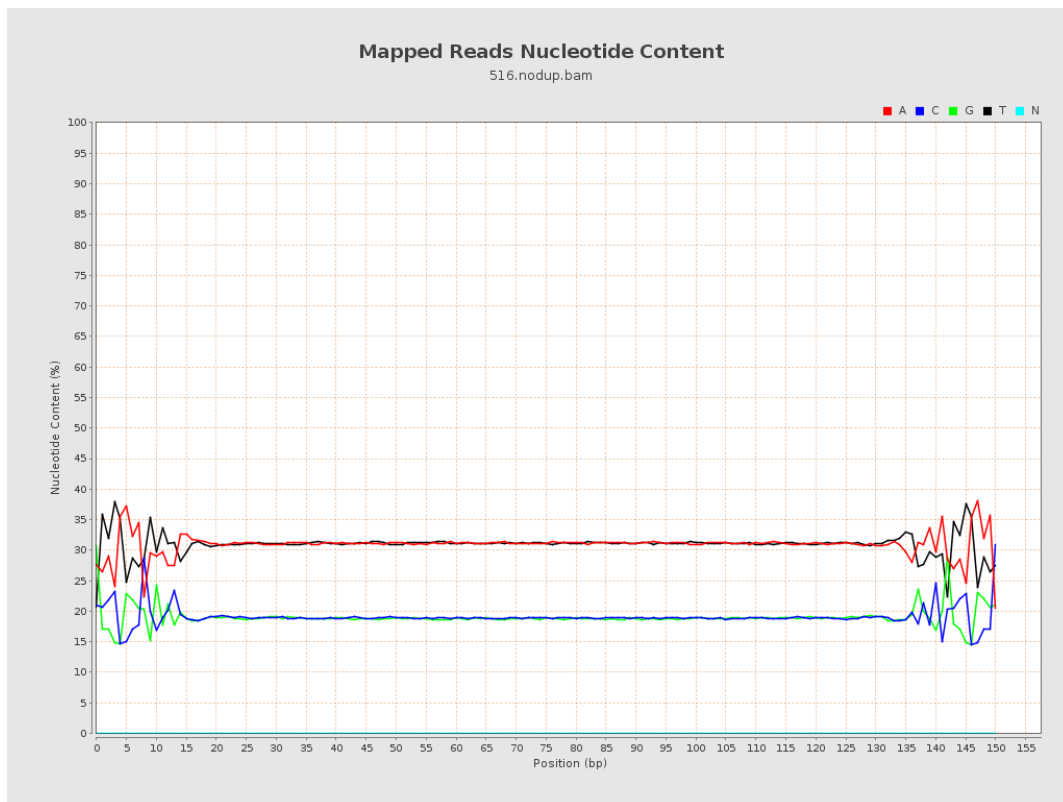
## 6. Results : Genome Fraction Coverage



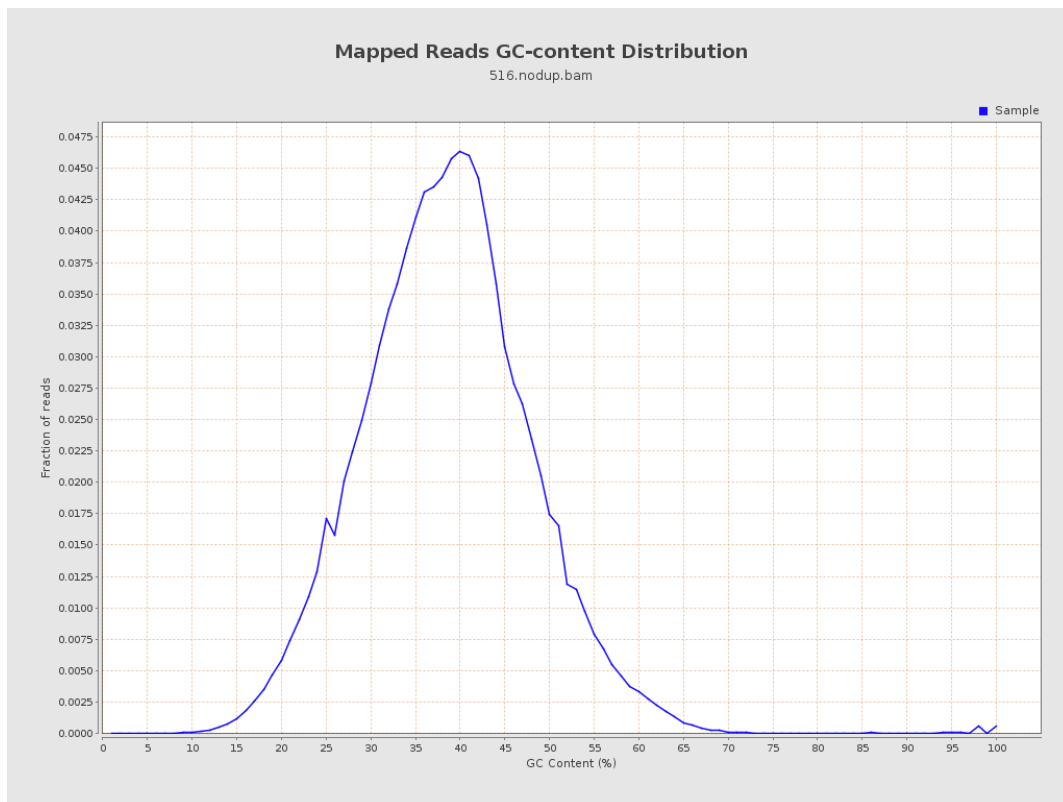
## 7. Results : Duplication Rate Histogram



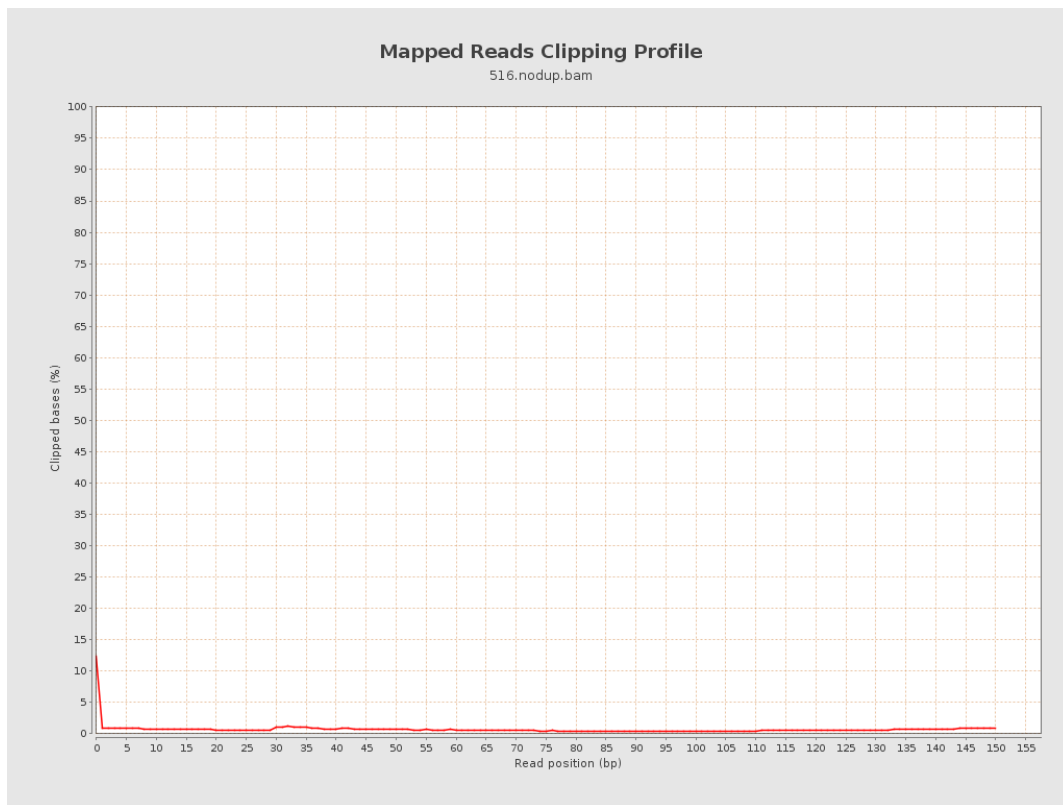
## 8. Results : Mapped Reads Nucleotide Content



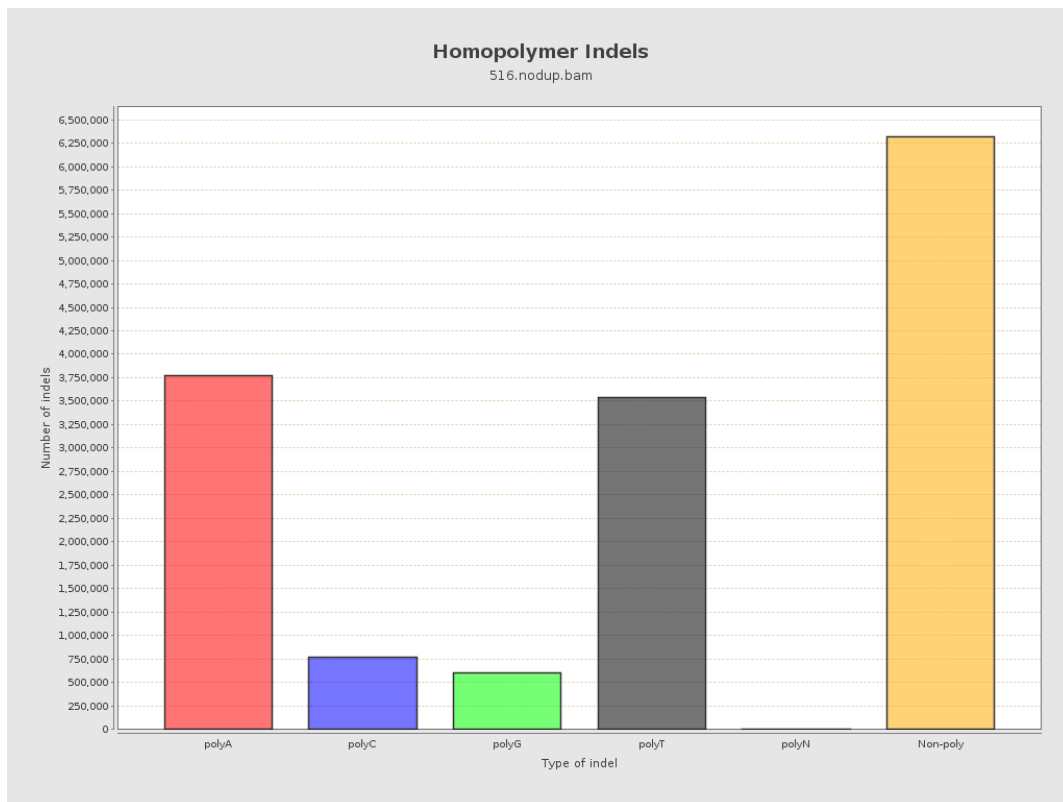
## 9. Results : Mapped Reads GC-content Distribution



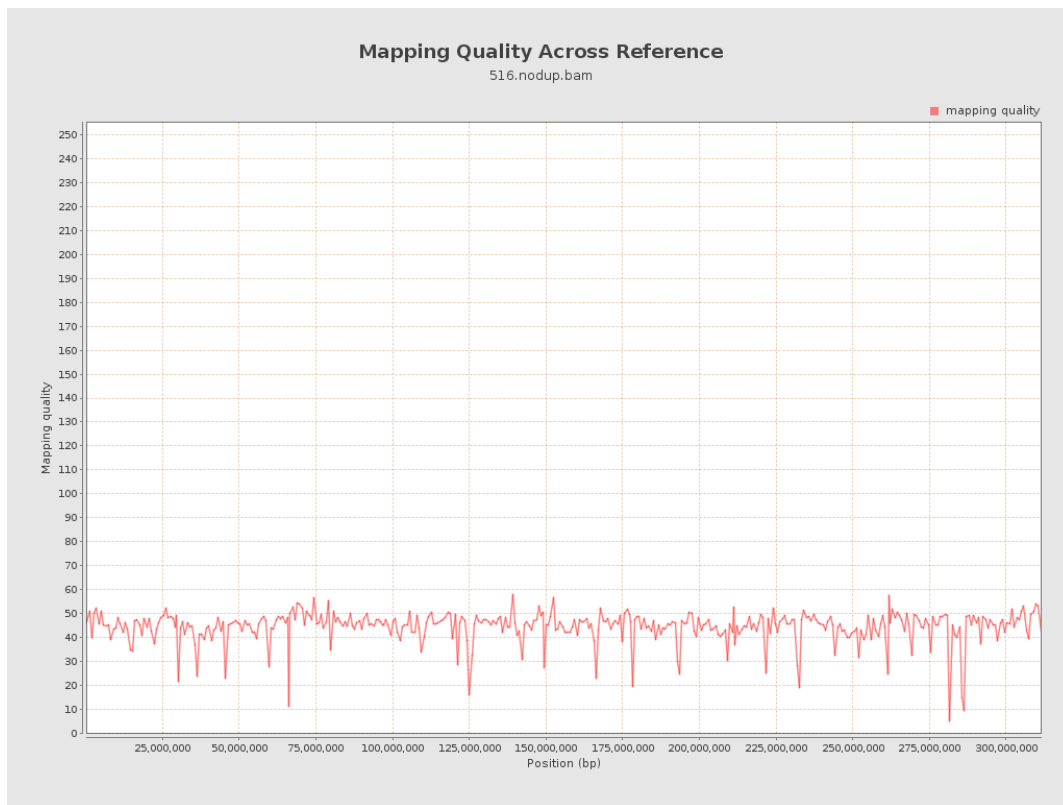
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

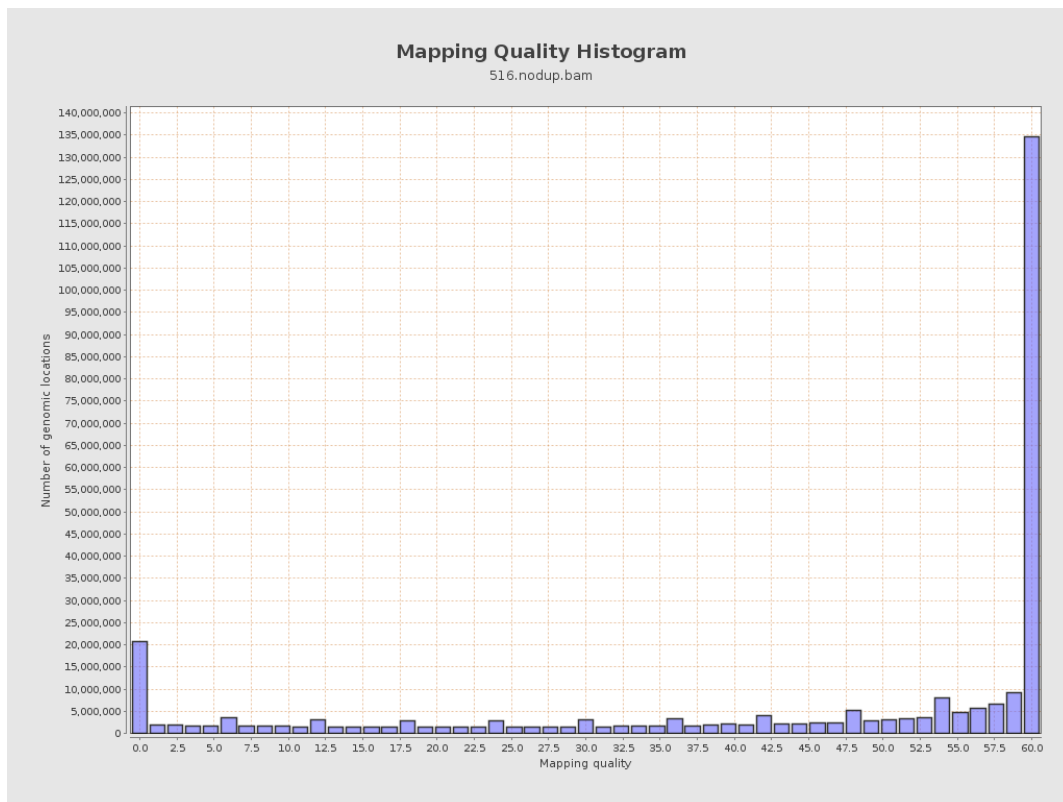


## 12. Results : Mapping Quality Across Reference

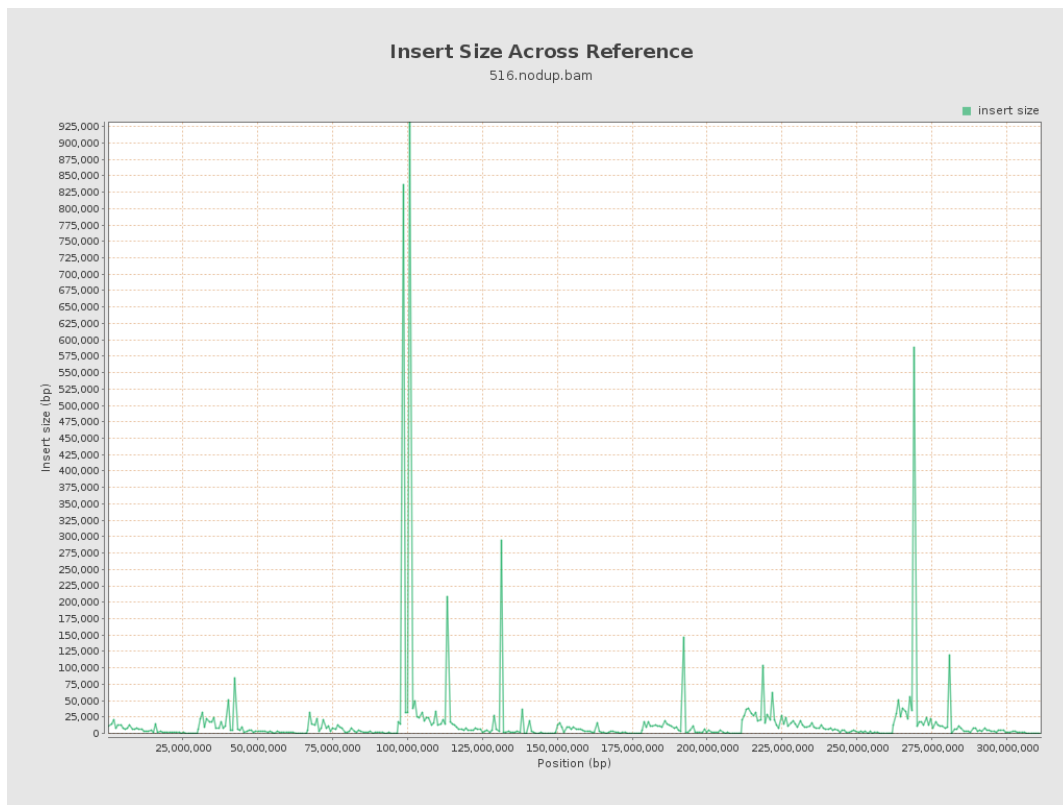




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

