

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:28:38*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/140
9
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1409 .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_133/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_133_S223_L002 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_133/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_133_S223_L002 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:28:38 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	61,024,098
Mapped reads	55,941,018 / 91.67%
Unmapped reads	5,083,080 / 8.33%
Mapped paired reads	55,941,018 / 91.67%
Mapped reads, first in pair	28,014,873 / 45.91%
Mapped reads, second in pair	27,926,145 / 45.76%
Mapped reads, both in pair	54,833,777 / 89.86%
Mapped reads, singletons	1,107,241 / 1.81%
Read min/max/mean length	30 / 151 / 148.13
Duplicated reads (flagged)	8,231,722 / 13.49%
Clipped reads	12,391,640 / 20.31%

### 2.2. ACGT Content

Number/percentage of A's	2,387,945,485 / 30.76%
Number/percentage of C's	1,493,401,182 / 19.24%
Number/percentage of T's	2,389,753,965 / 30.79%
Number/percentage of G's	1,491,098,177 / 19.21%
Number/percentage of N's	33,889 / 0%
GC Percentage	38.45%

### 2.3. Coverage

Mean	24.9744
Standard Deviation	193.7997

## 2.4. Mapping Quality

Mean Mapping Quality	43.72
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## 2.5. Insert size

Mean	234,607.62
Standard Deviation	2,286,584.4
P25/Median/P75	320 / 420 / 551

## 2.6. Mismatches and indels

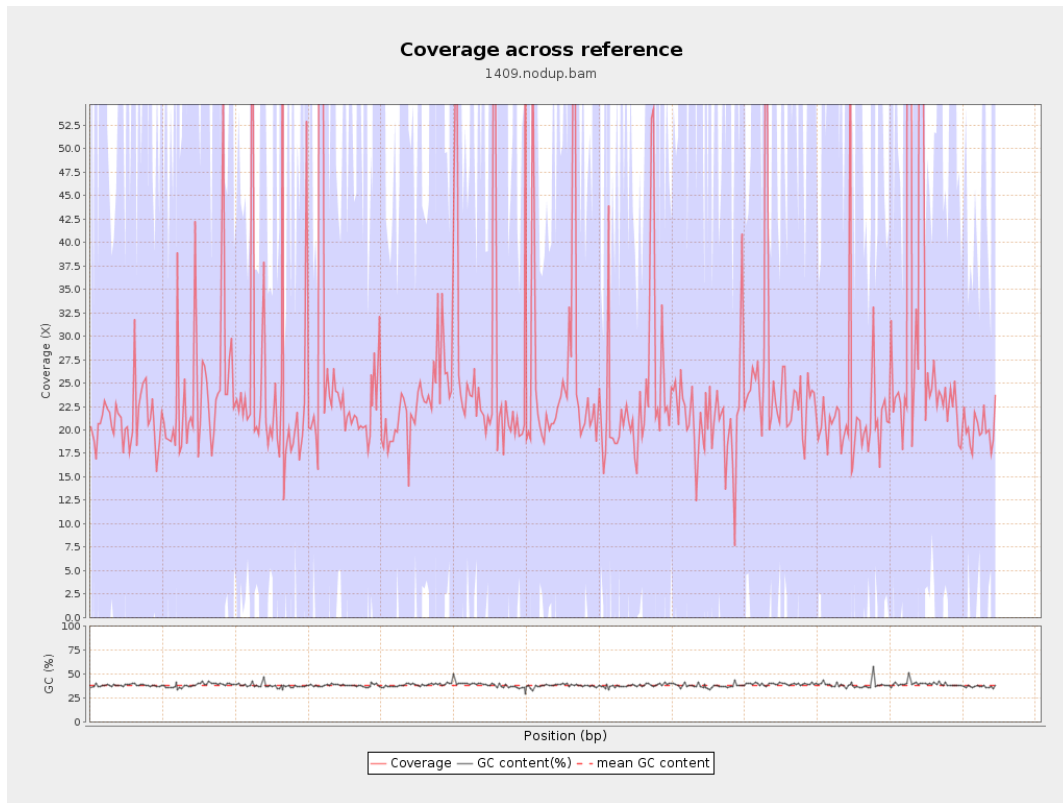
General error rate	2.31%
Mismatches	164,566,432
Insertions	5,288,070
Mapped reads with at least one insertion	8.49%
Deletions	5,439,451
Mapped reads with at least one deletion	8.63%
Homopolymer indels	56.02%

## 2.7. Chromosome stats

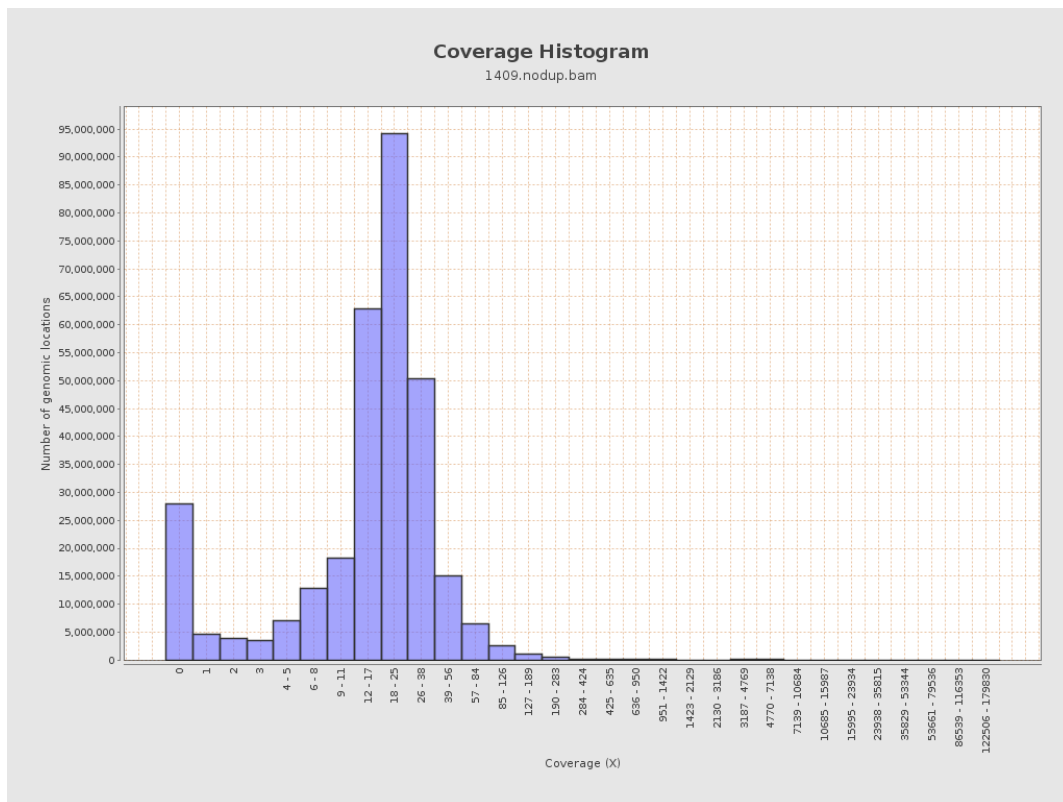
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	619552149	20.8433	56.2816

LT669789.1	36598175	924553612	25.2623	196.9937
LT669790.1	30422129	810788009	26.6513	185.977
LT669791.1	52758100	1292490632	24.4984	164.9706
LT669792.1	28376109	702553147	24.7586	224.2436
LT669793.1	33388210	771526503	23.1078	126.4451
LT669794.1	50579949	1197501164	23.6754	157.7983
LT669795.1	49795044	1464115372	29.4028	299.9592

### 3. Results : Coverage across reference

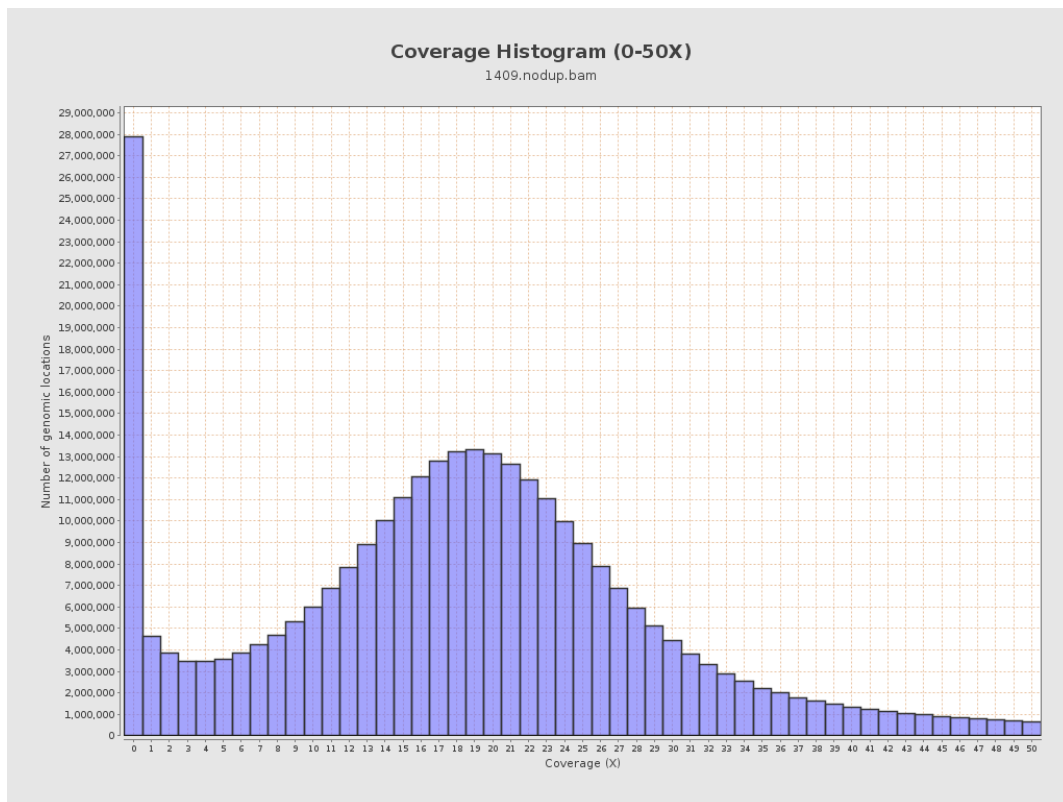


## 4. Results : Coverage Histogram

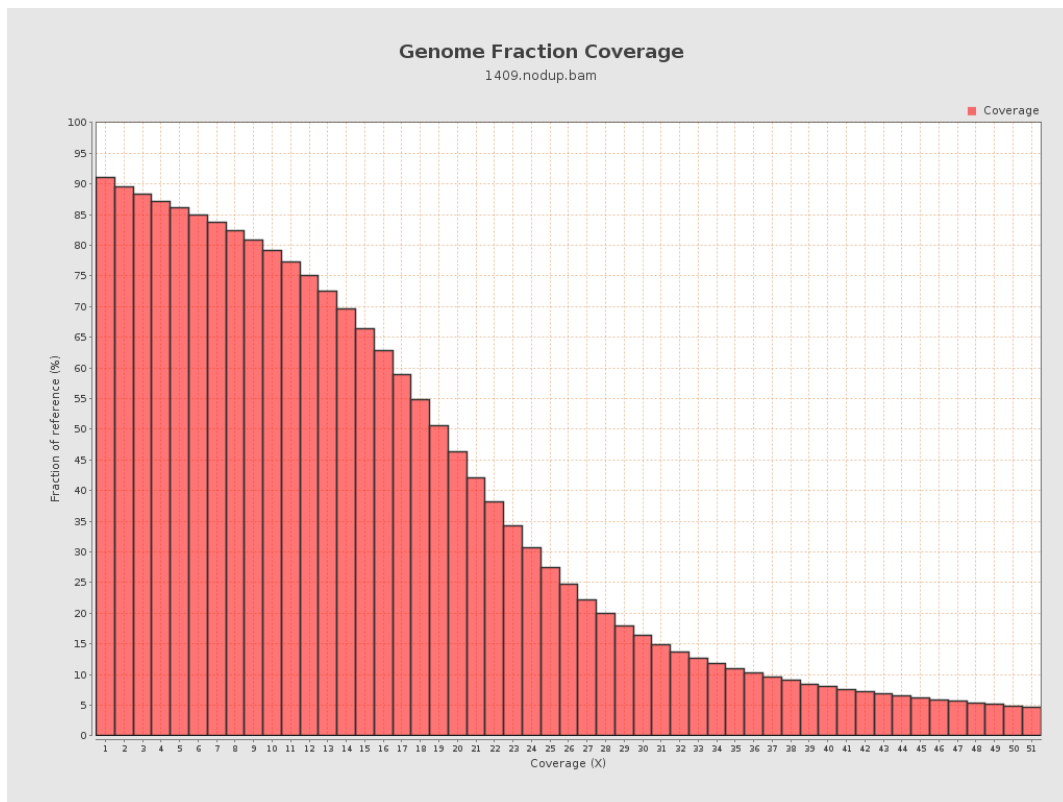




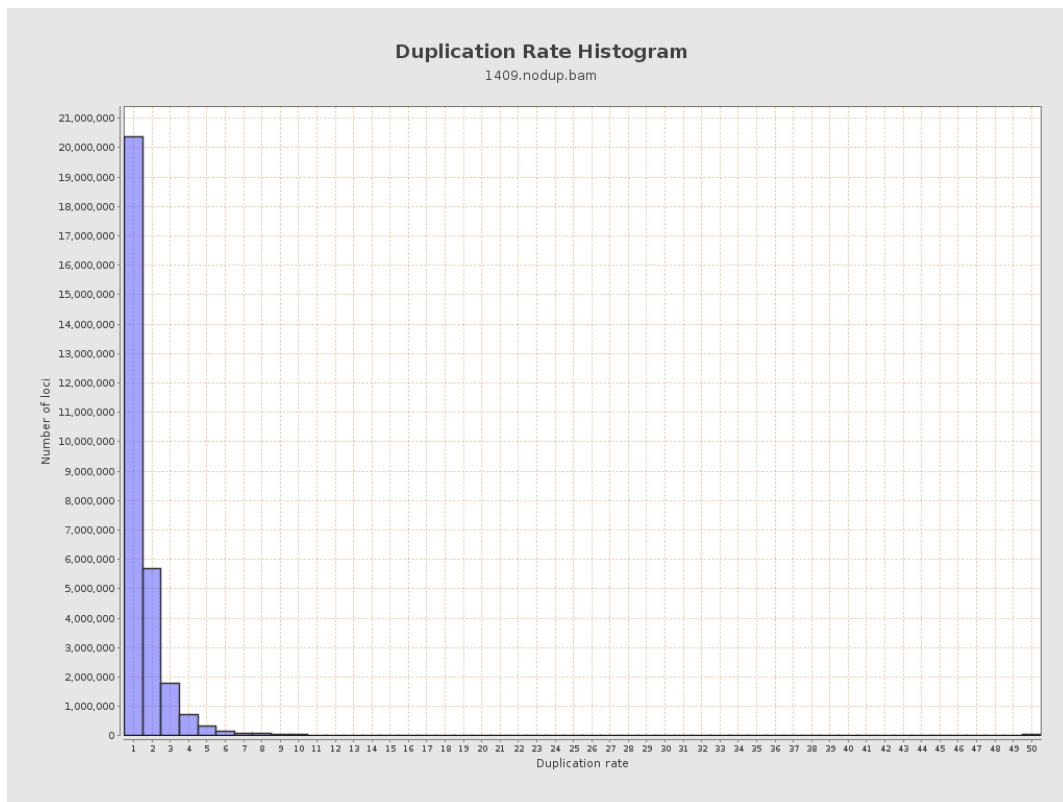
## 5. Results : Coverage Histogram (0-50X)



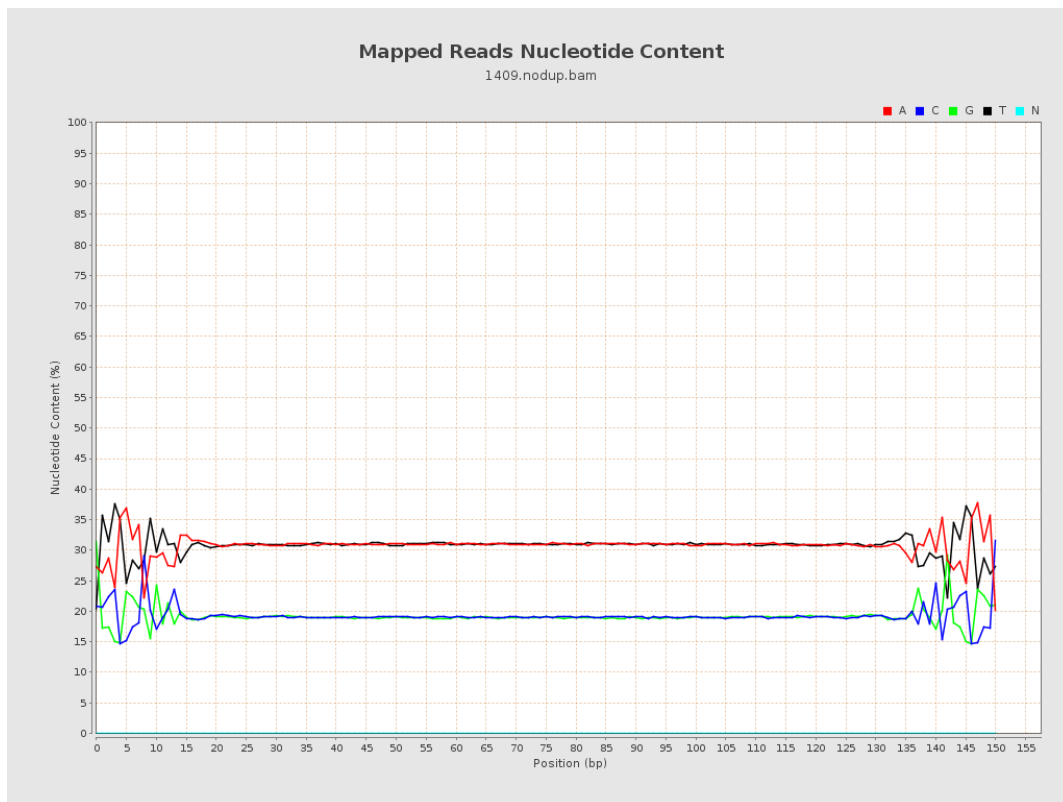
## 6. Results : Genome Fraction Coverage



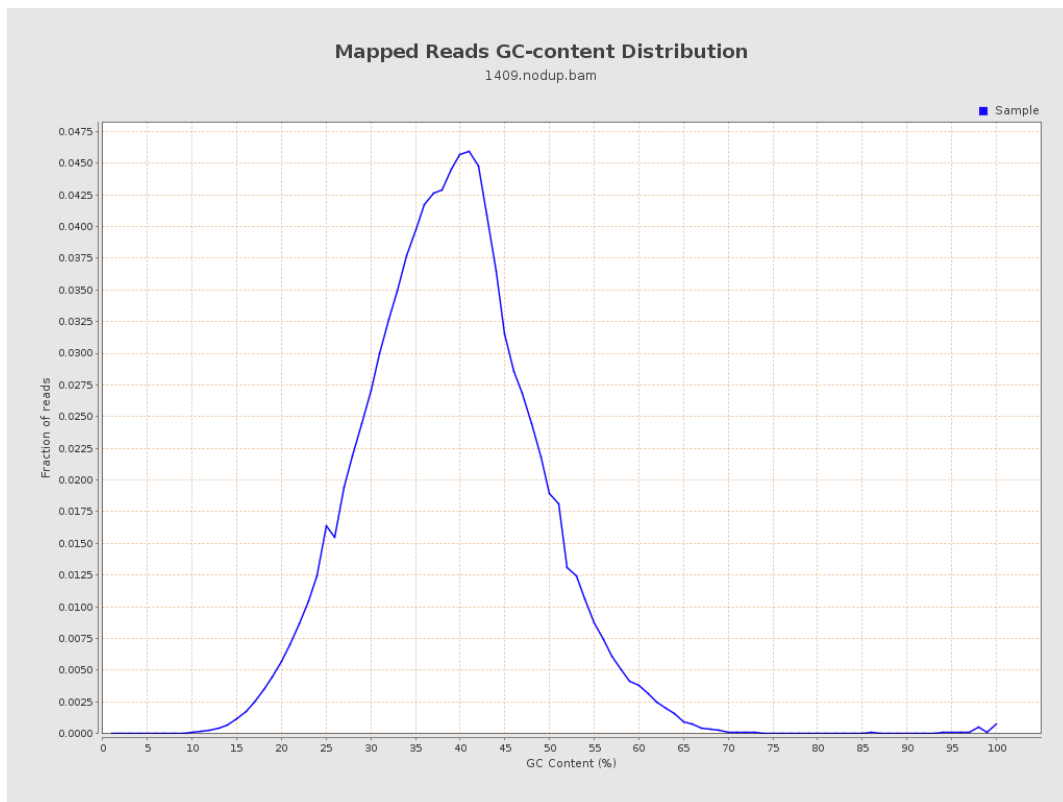
## 7. Results : Duplication Rate Histogram



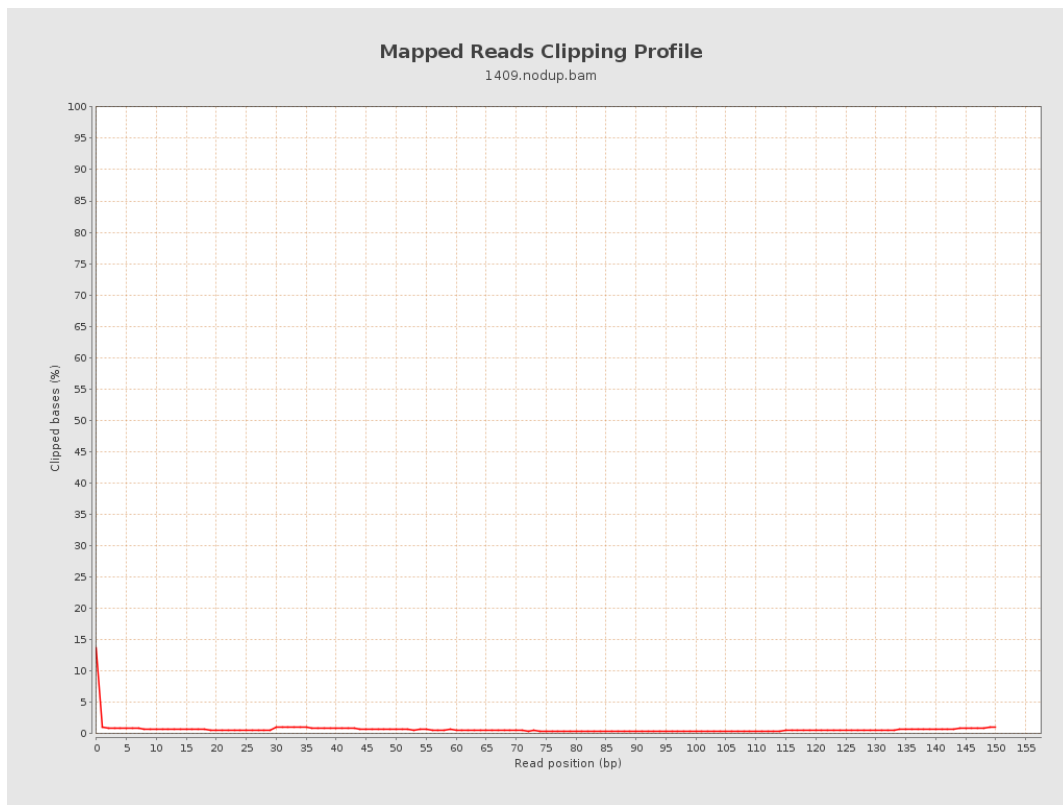
## 8. Results : Mapped Reads Nucleotide Content



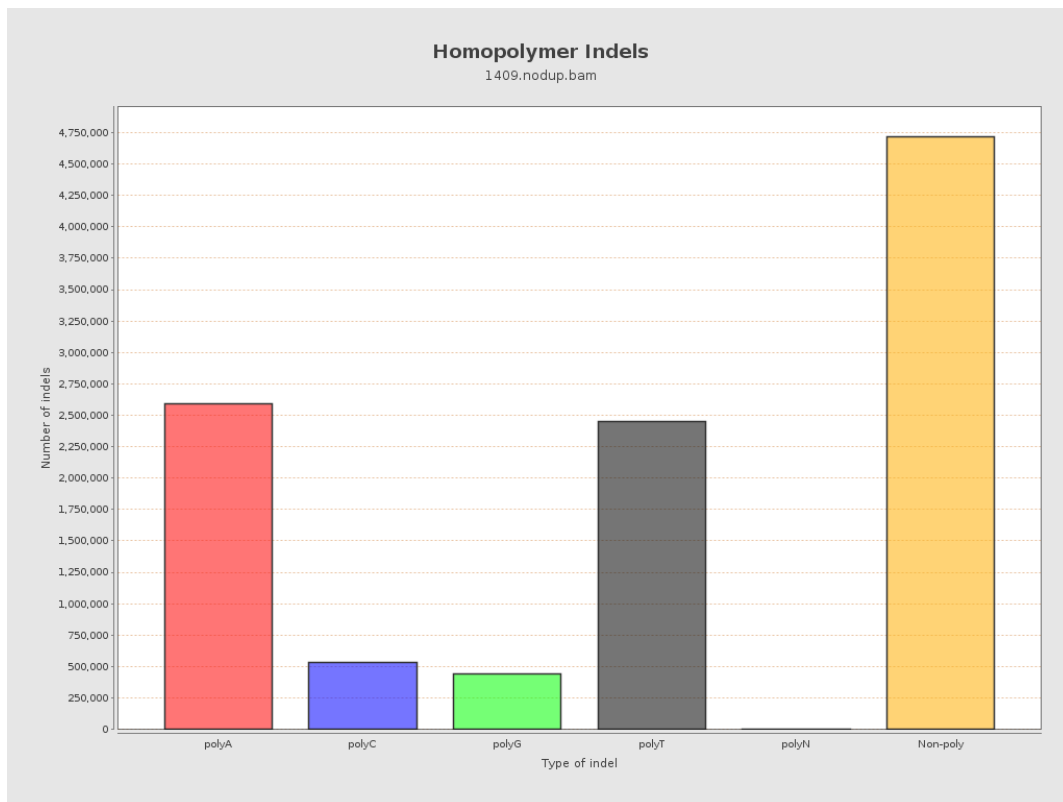
## 9. Results : Mapped Reads GC-content Distribution



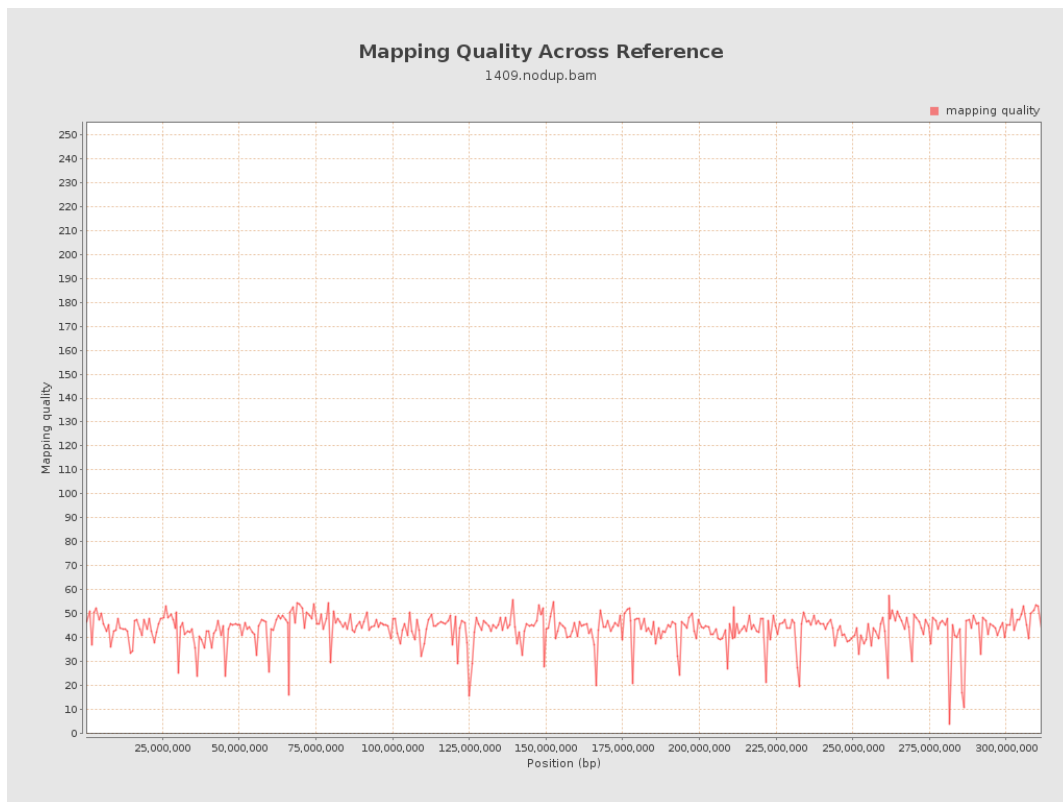
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

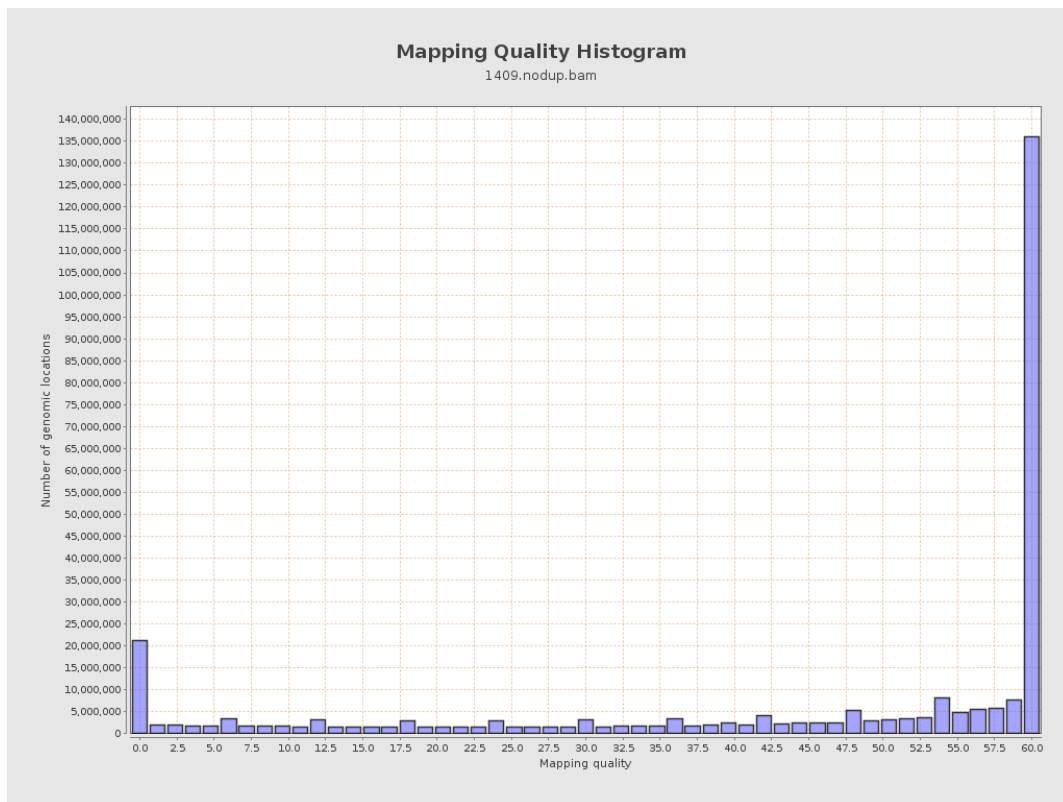


## 12. Results : Mapping Quality Across Reference

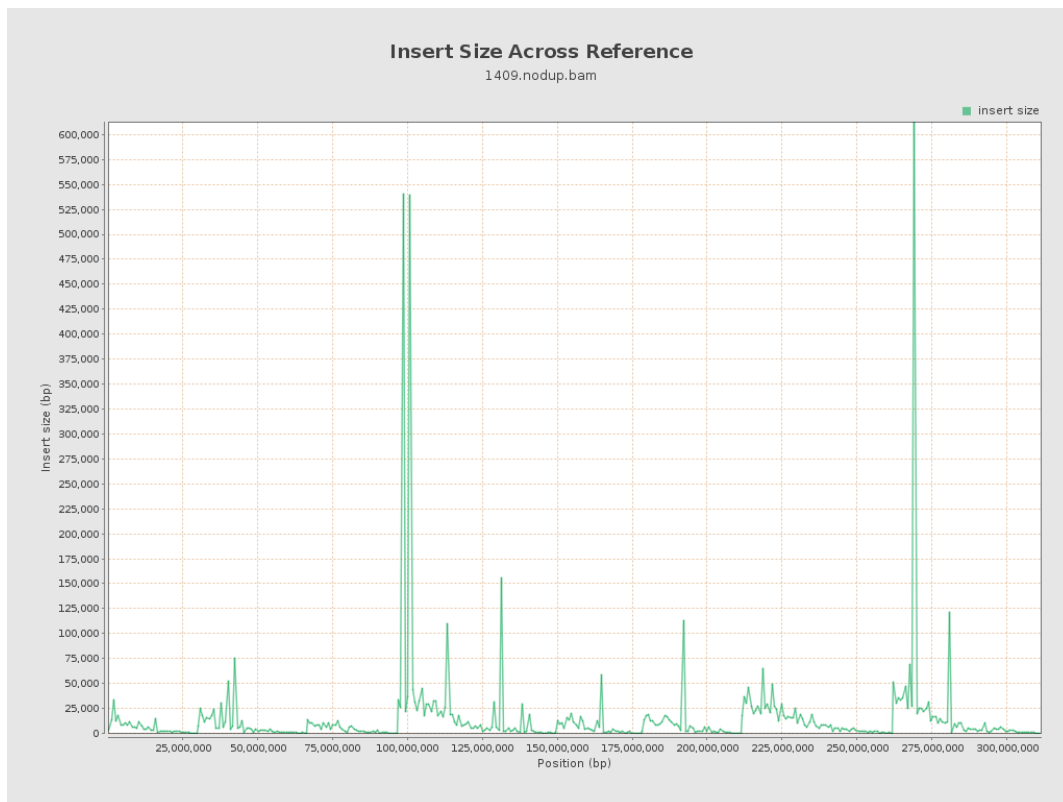




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

