

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:38:51*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/649
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/649.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_254/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_254_S335_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_254/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_254_S335_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:38:50 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	87,327,319
Mapped reads	82,496,998 / 94.47%
Unmapped reads	4,830,321 / 5.53%
Mapped paired reads	82,496,998 / 94.47%
Mapped reads, first in pair	41,332,570 / 47.33%
Mapped reads, second in pair	41,164,428 / 47.14%
Mapped reads, both in pair	80,873,205 / 92.61%
Mapped reads, singletons	1,623,793 / 1.86%
Read min/max/mean length	30 / 151 / 147.95
Duplicated reads (flagged)	12,303,099 / 14.09%
Clipped reads	19,221,097 / 22.01%

### 2.2. ACGT Content

Number/percentage of A's	3,504,451,992 / 30.81%
Number/percentage of C's	2,181,198,111 / 19.17%
Number/percentage of T's	3,512,972,005 / 30.88%
Number/percentage of G's	2,177,435,214 / 19.14%
Number/percentage of N's	43,520 / 0%
GC Percentage	38.31%

### 2.3. Coverage

Mean	36.5973
Standard Deviation	309.0877

## 2.4. Mapping Quality

Mean Mapping Quality	44.25
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## 2.5. Insert size

Mean	225,025.09
Standard Deviation	2,261,701.3
P25/Median/P75	307 / 408 / 534

## 2.6. Mismatches and indels

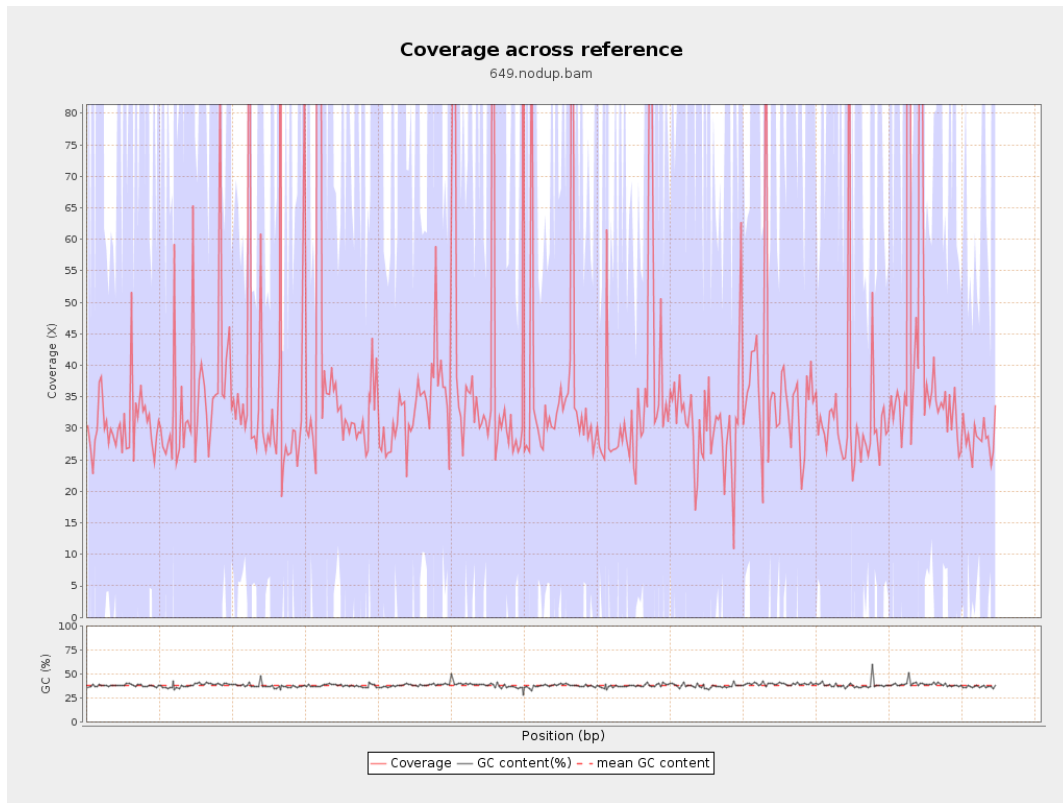
General error rate	2.27%
Mismatches	237,288,244
Insertions	7,709,735
Mapped reads with at least one insertion	8.4%
Deletions	7,730,614
Mapped reads with at least one deletion	8.31%
Homopolymer indels	56.09%

## 2.7. Chromosome stats

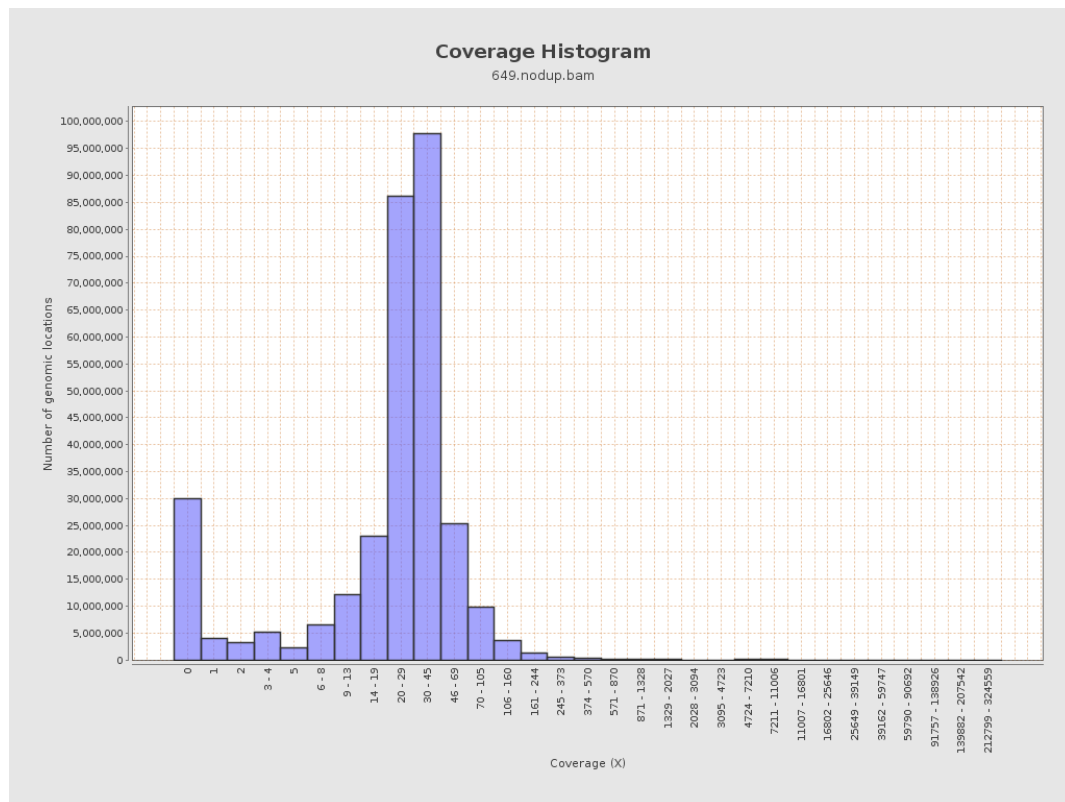
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	897481514	30.1935	113.8764

LT669789.1	36598175	1373314762	37.5241	336.6524
LT669790.1	30422129	1204906766	39.6063	303.0129
LT669791.1	52758100	1908385951	36.1724	304.1014
LT669792.1	28376109	1031491569	36.3507	325.7806
LT669793.1	33388210	1139021701	34.1145	210.2075
LT669794.1	50579949	1751112602	34.6207	274.1979
LT669795.1	49795044	2099548691	42.1638	431.5596

### 3. Results : Coverage across reference

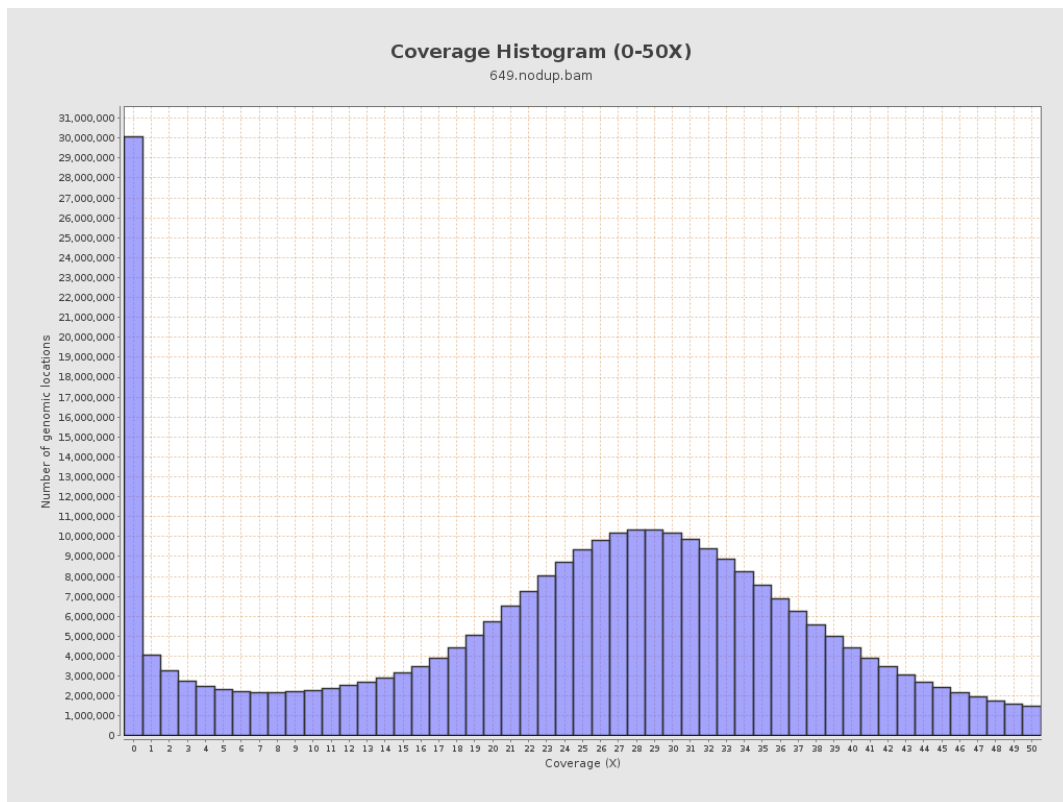


## 4. Results : Coverage Histogram

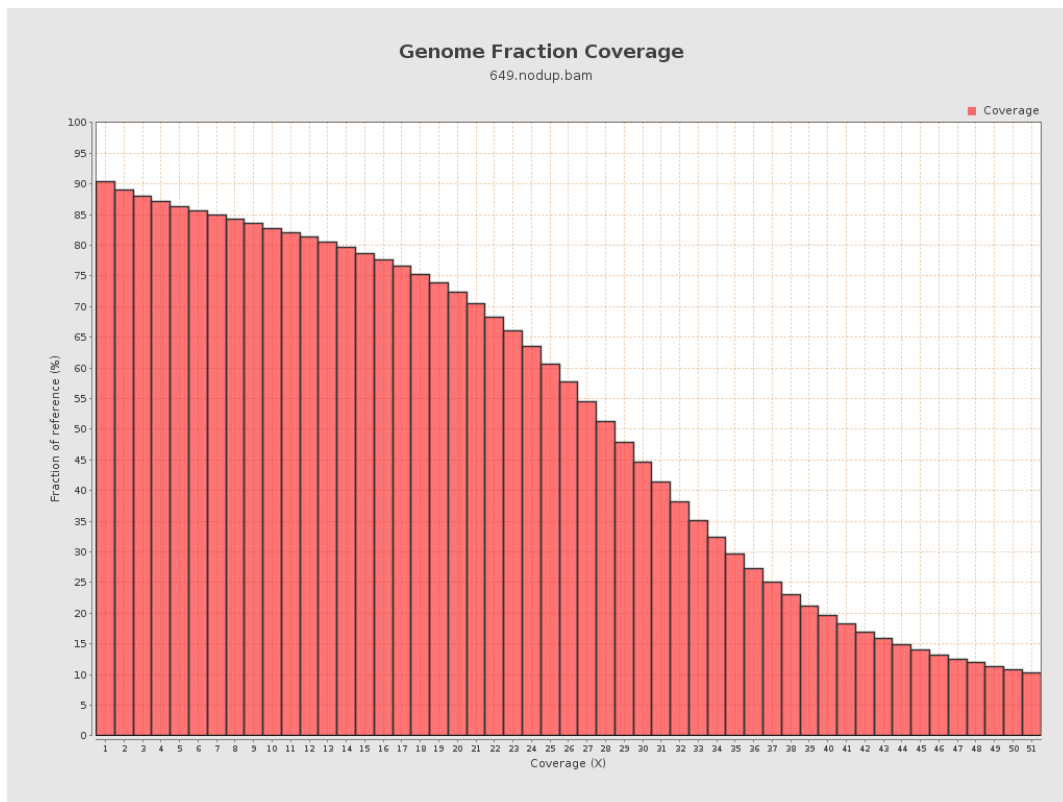




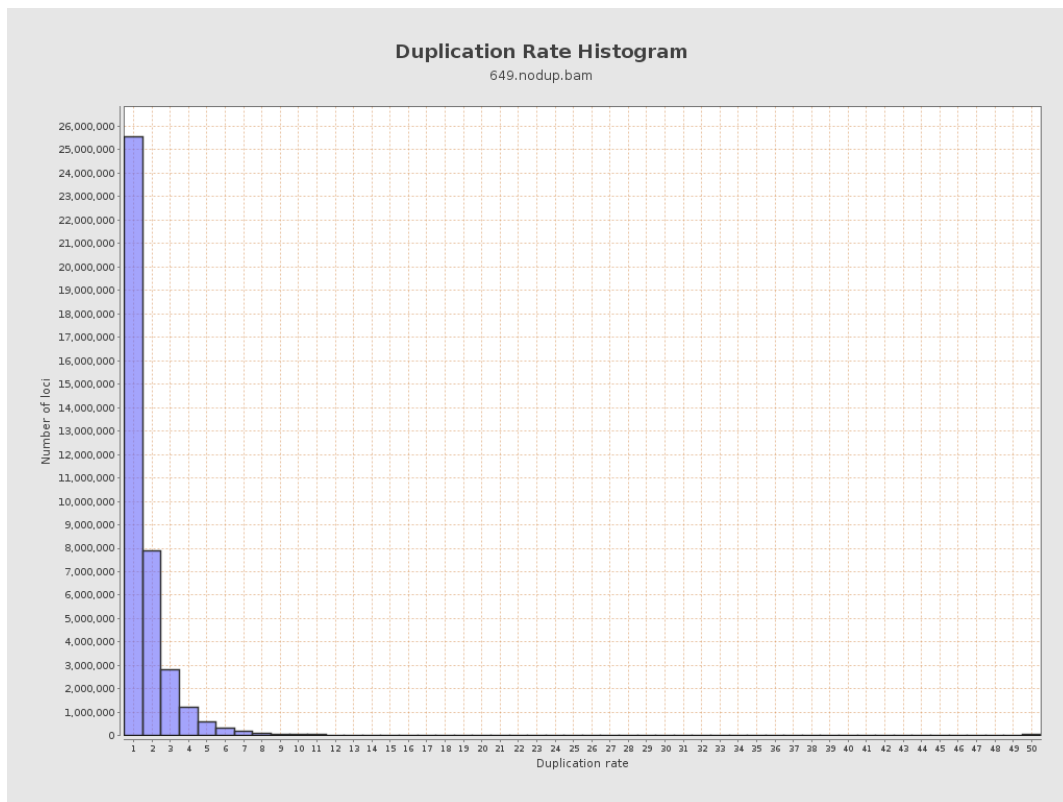
## 5. Results : Coverage Histogram (0-50X)



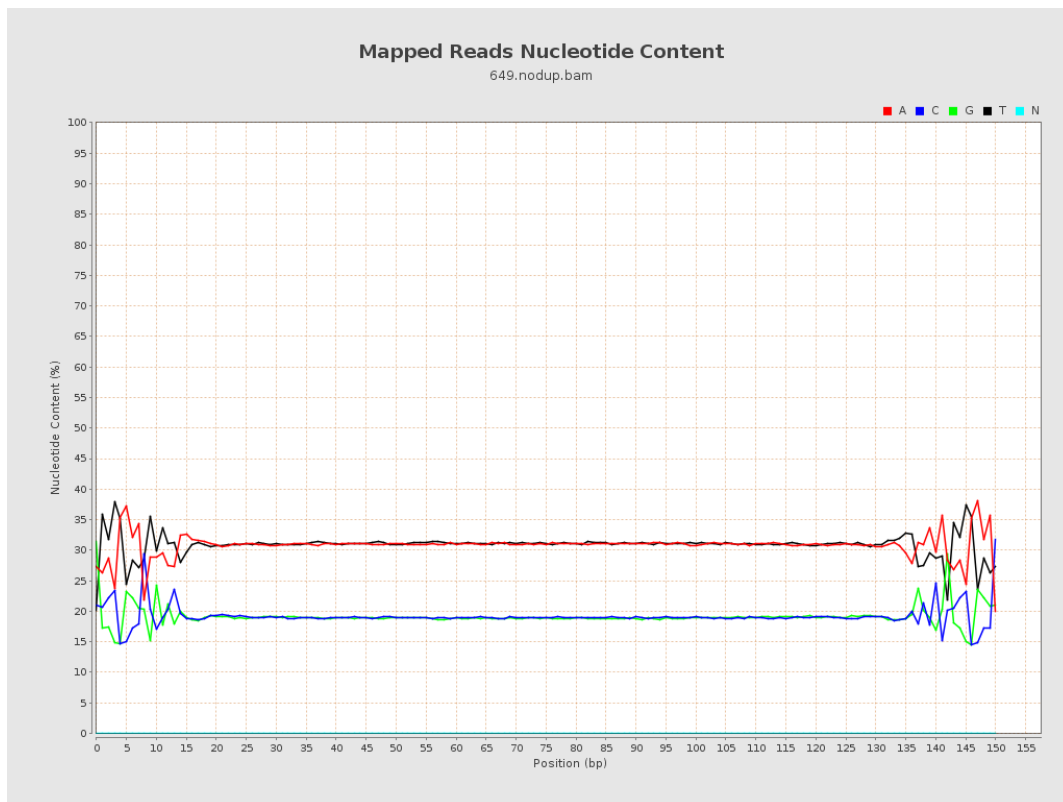
## 6. Results : Genome Fraction Coverage



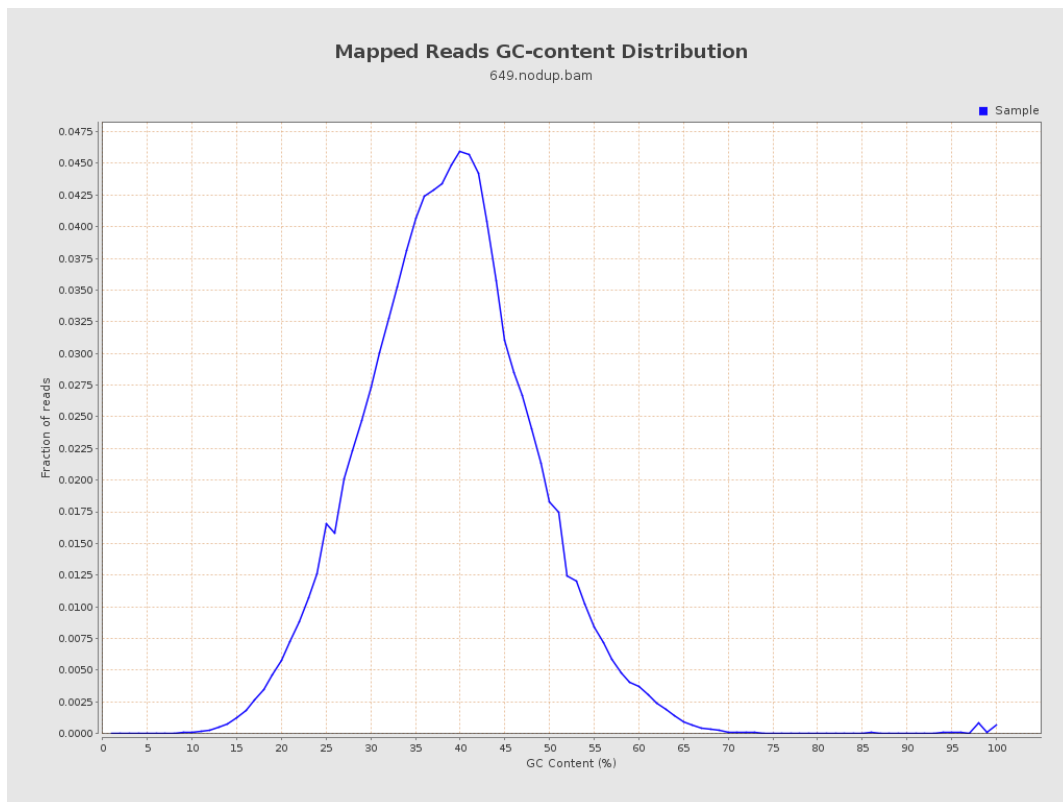
## 7. Results : Duplication Rate Histogram



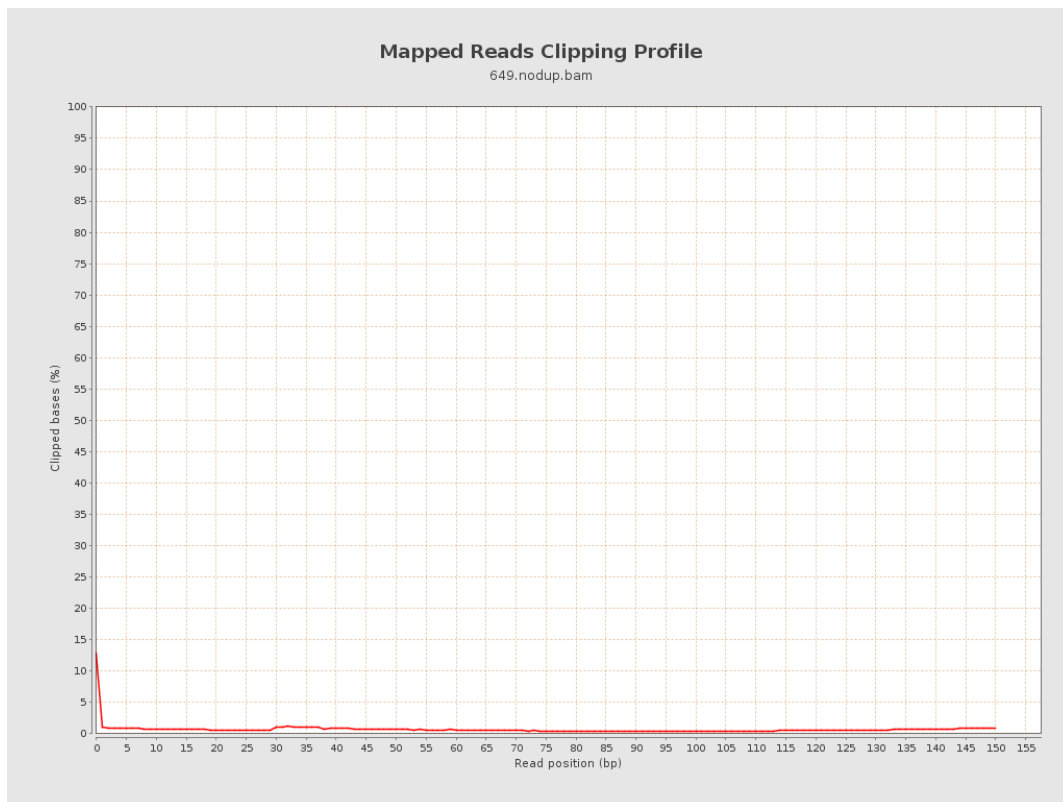
## 8. Results : Mapped Reads Nucleotide Content



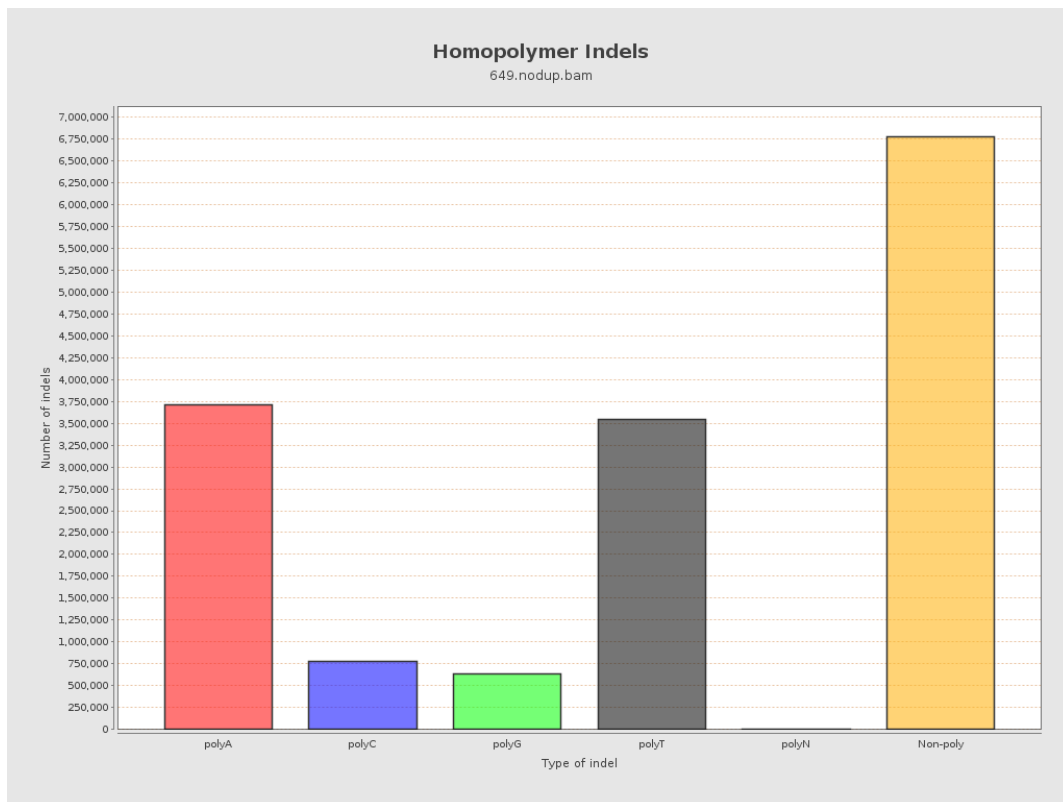
## 9. Results : Mapped Reads GC-content Distribution



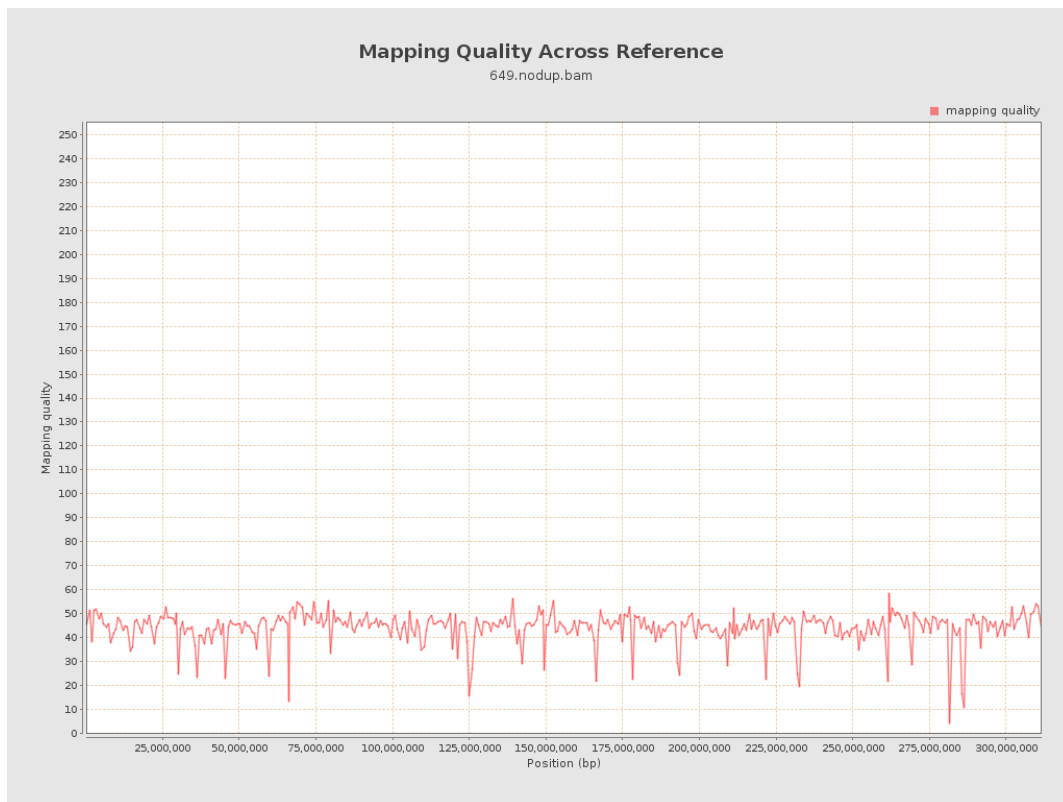
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

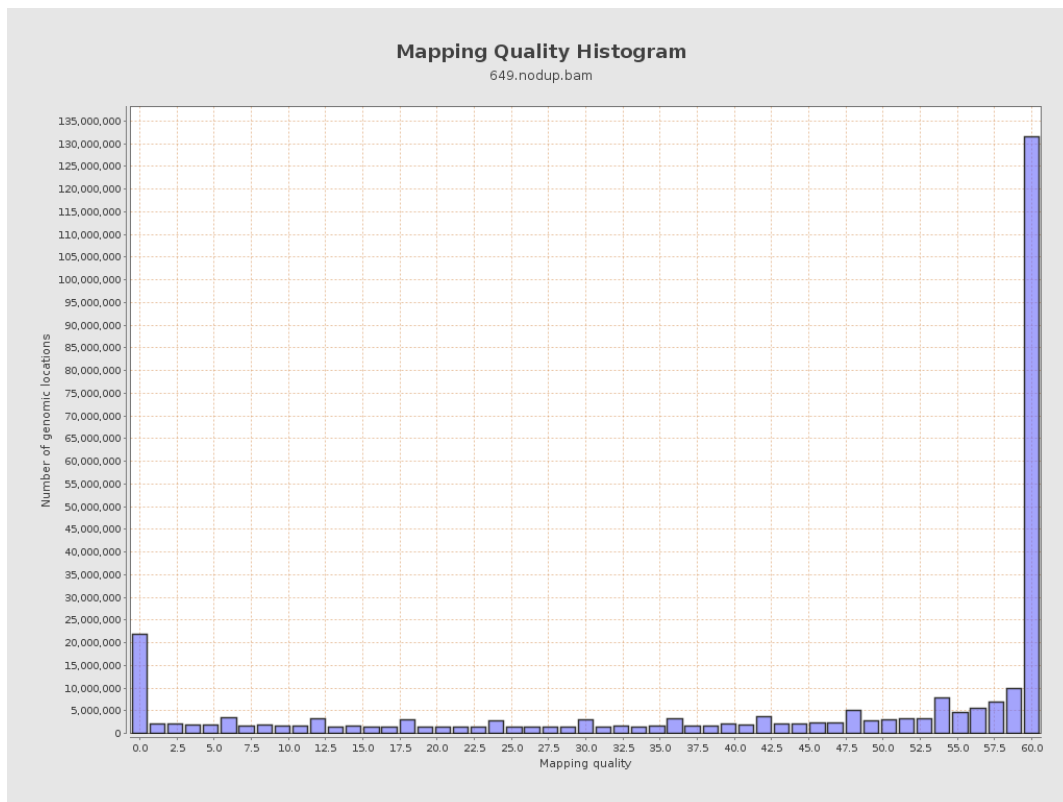


## 12. Results : Mapping Quality Across Reference

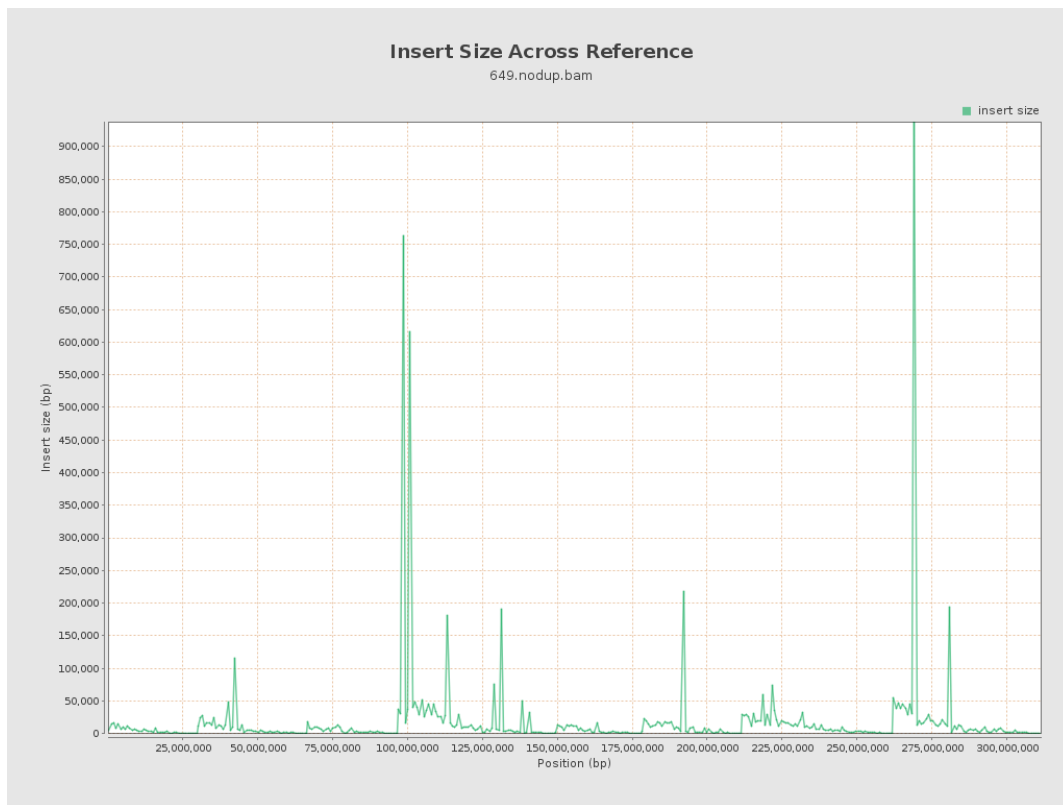




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

