

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:28:41*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/910
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/910.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_167/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_167_S257_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_167/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_167_S257_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:28:40 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	60,260,400
Mapped reads	56,353,809 / 93.52%
Unmapped reads	3,906,591 / 6.48%
Mapped paired reads	56,353,809 / 93.52%
Mapped reads, first in pair	28,213,386 / 46.82%
Mapped reads, second in pair	28,140,423 / 46.7%
Mapped reads, both in pair	55,093,468 / 91.43%
Mapped reads, singletons	1,260,341 / 2.09%
Read min/max/mean length	30 / 151 / 148.06
Duplicated reads (flagged)	9,414,521 / 15.62%
Clipped reads	12,854,512 / 21.33%

### 2.2. ACGT Content

Number/percentage of A's	2,402,176,987 / 30.8%
Number/percentage of C's	1,497,979,803 / 19.21%
Number/percentage of T's	2,402,710,563 / 30.8%
Number/percentage of G's	1,496,922,353 / 19.19%
Number/percentage of N's	32,068 / 0%
GC Percentage	38.4%

### 2.3. Coverage

Mean	25.0953
Standard Deviation	219.2782

## 2.4. Mapping Quality

Mean Mapping Quality	43.74
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## 2.5. Insert size

Mean	239,082.36
Standard Deviation	2,315,613.32
P25/Median/P75	323 / 422 / 555

## 2.6. Mismatches and indels

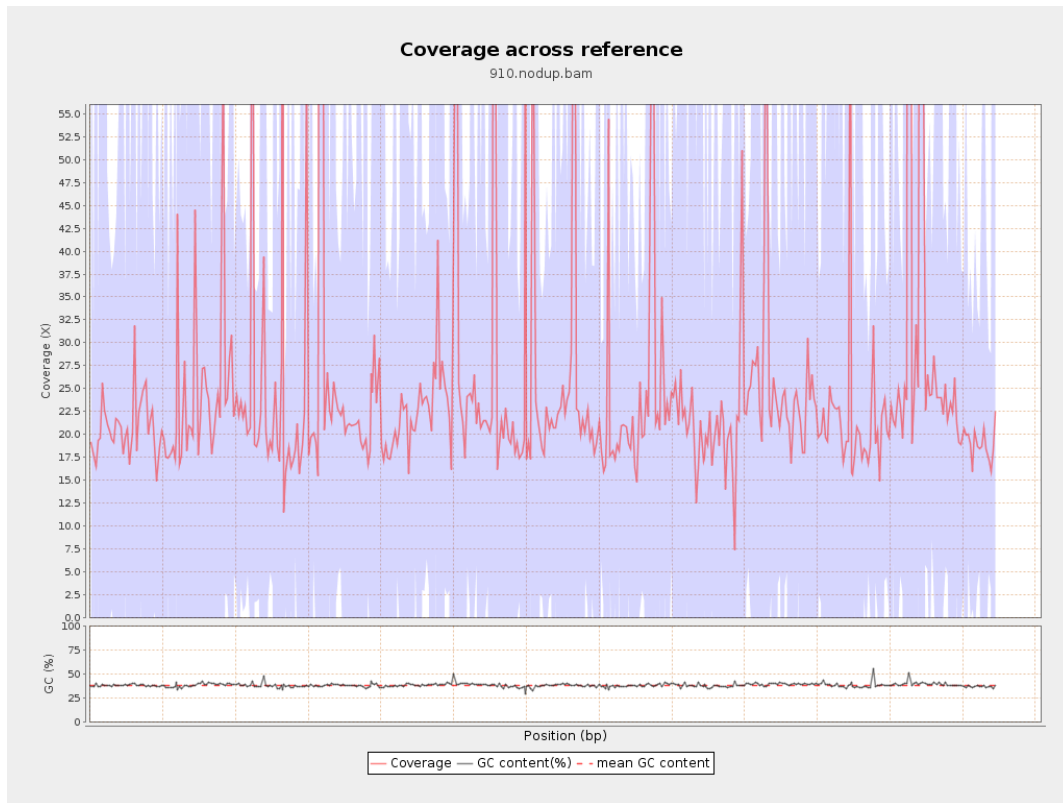
General error rate	2.41%
Mismatches	172,936,765
Insertions	5,438,210
Mapped reads with at least one insertion	8.65%
Deletions	5,538,448
Mapped reads with at least one deletion	8.72%
Homopolymer indels	56.22%

## 2.7. Chromosome stats

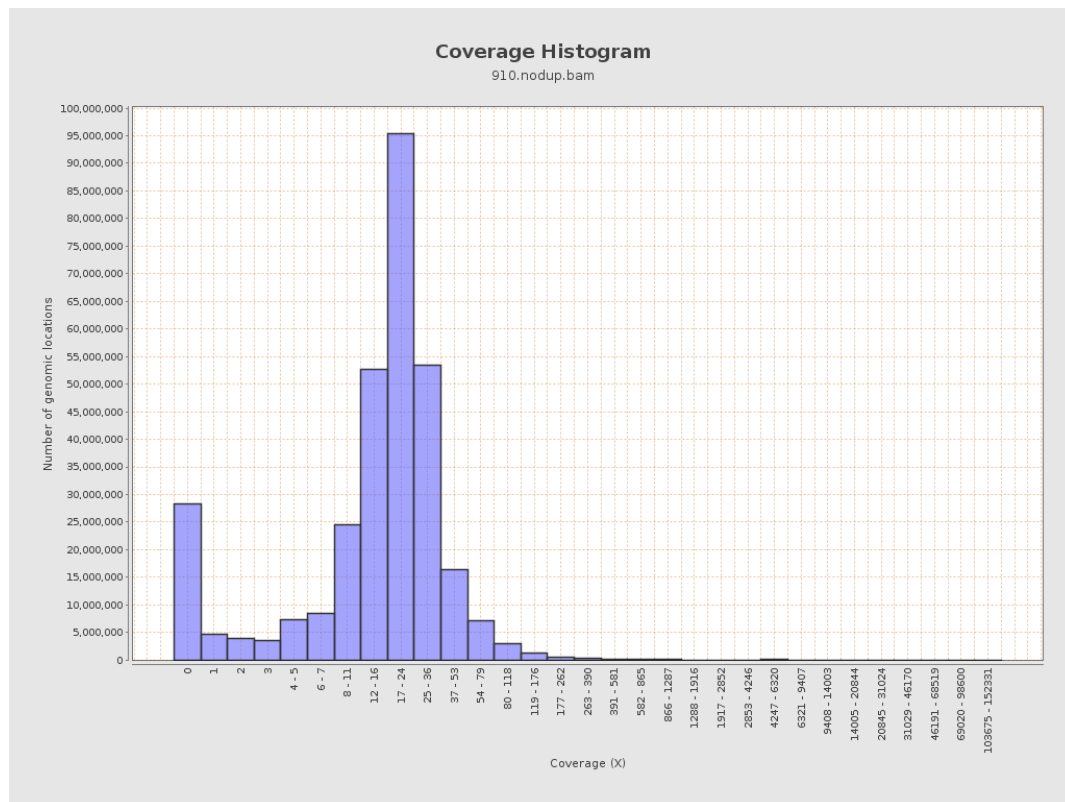
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	603466716	20.3021	78.9624

LT669789.1	36598175	945388936	25.8316	228.993
LT669790.1	30422129	828705618	27.2402	235.7461
LT669791.1	52758100	1297286281	24.5893	213.9473
LT669792.1	28376109	702320264	24.7504	234.5465
LT669793.1	33388210	789379243	23.6425	147.366
LT669794.1	50579949	1225699950	24.2329	207.2263
LT669795.1	49795044	1428493397	28.6875	294.3651

### 3. Results : Coverage across reference

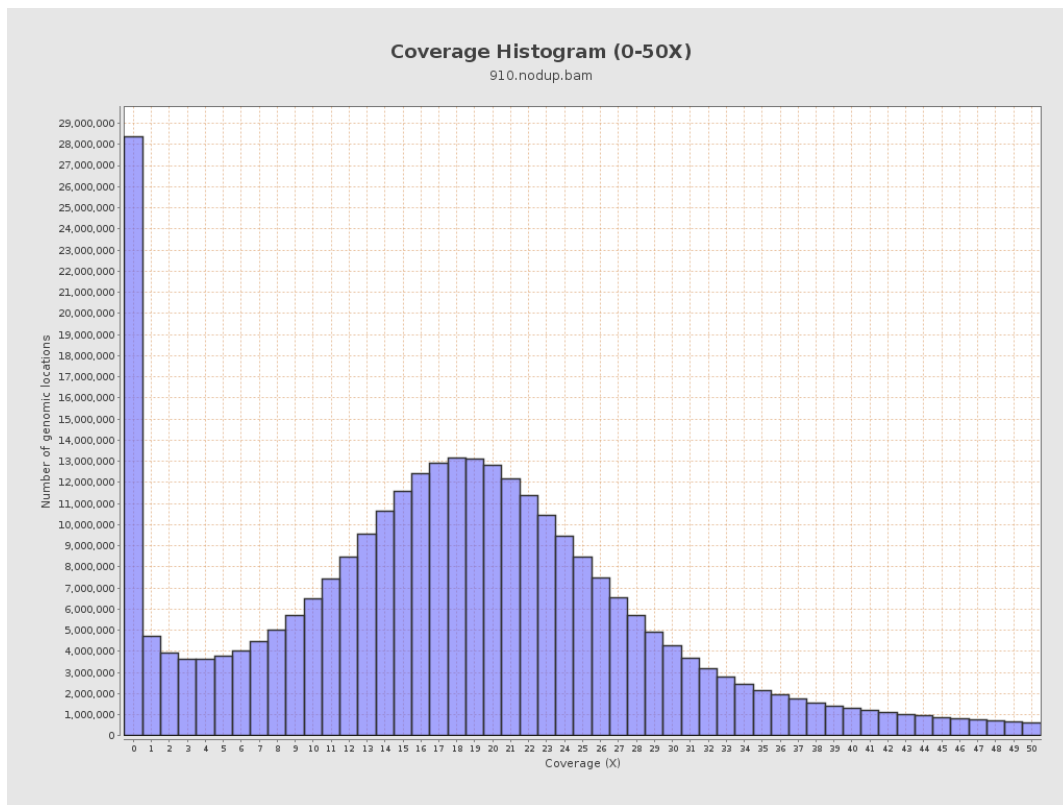


## 4. Results : Coverage Histogram

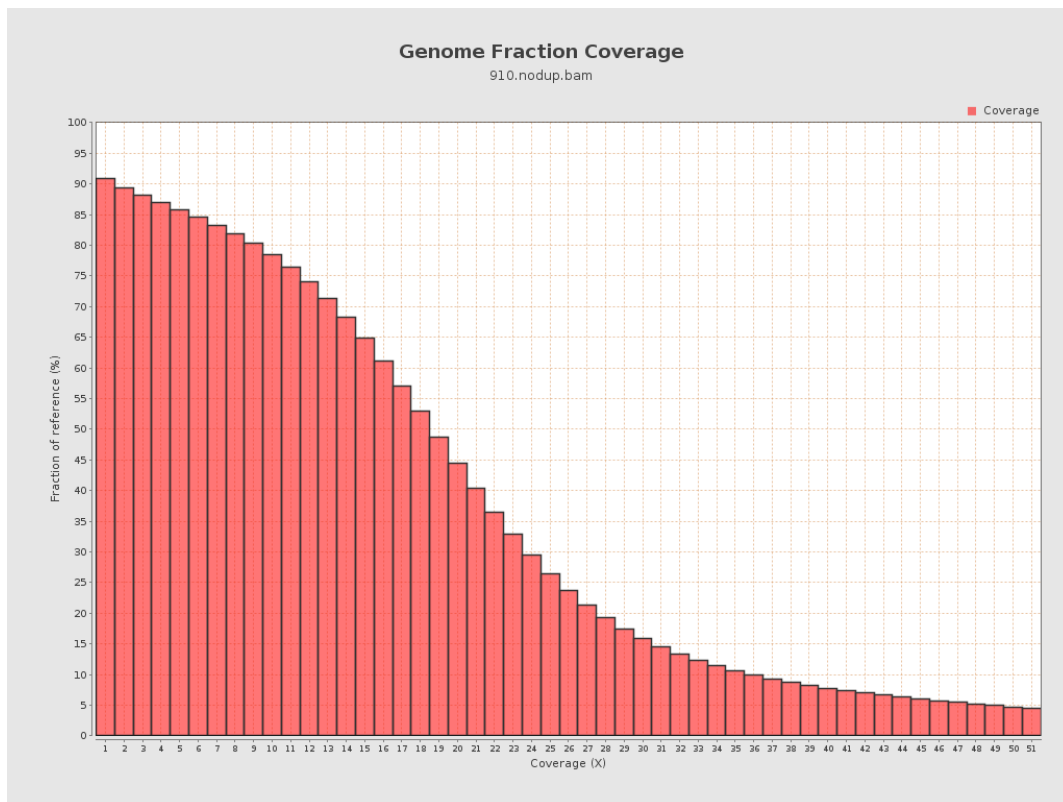




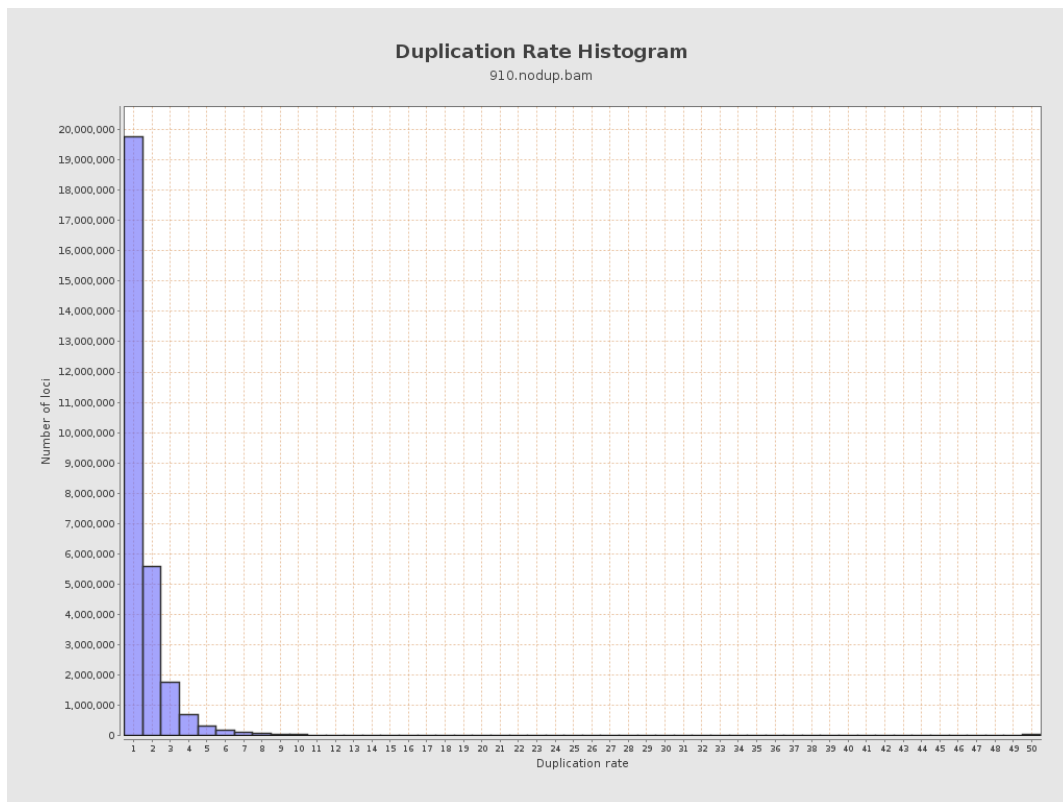
## 5. Results : Coverage Histogram (0-50X)



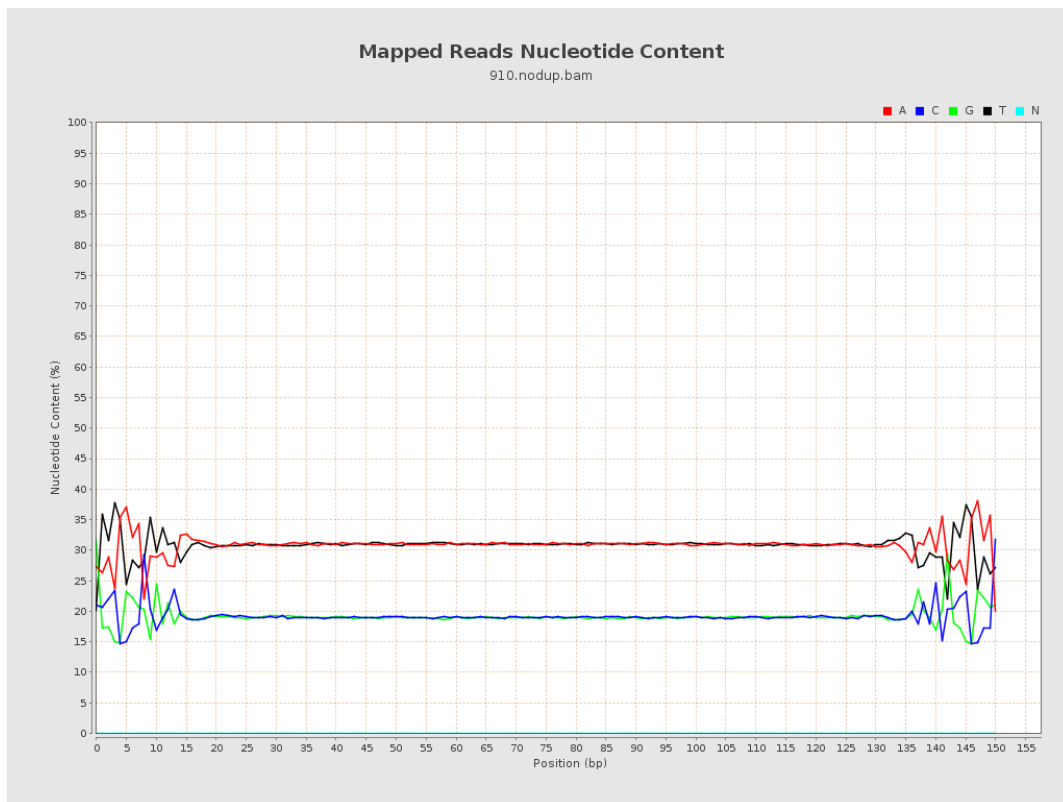
## 6. Results : Genome Fraction Coverage



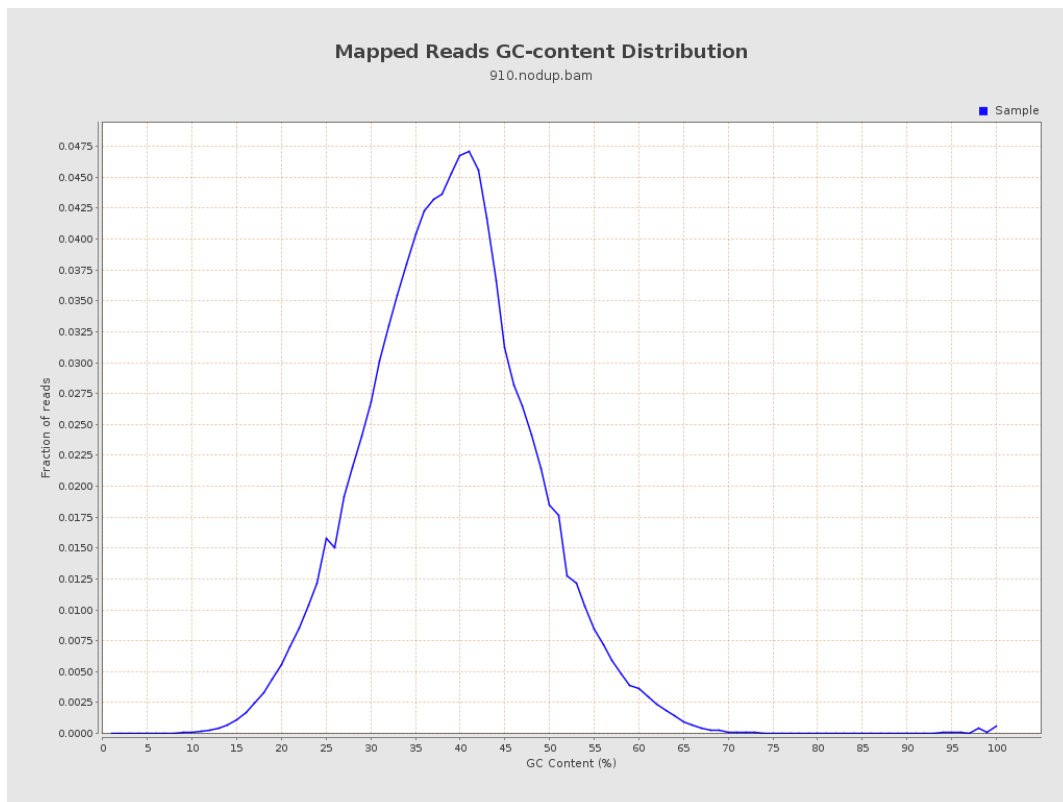
## 7. Results : Duplication Rate Histogram



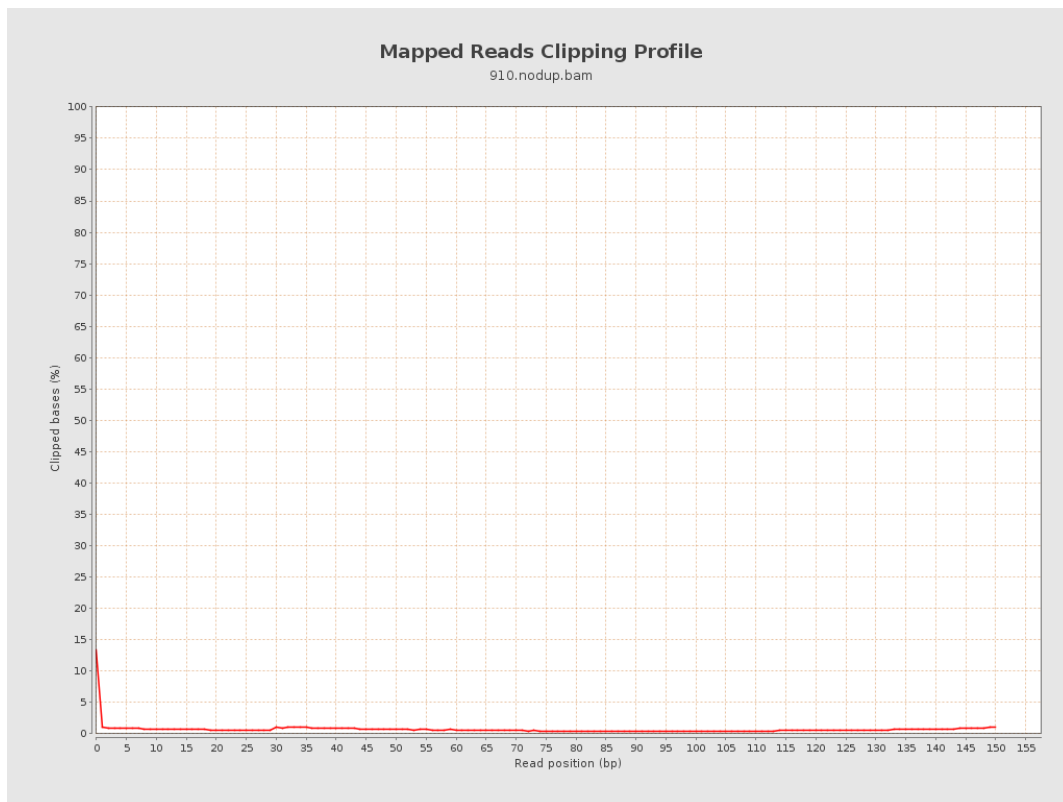
## 8. Results : Mapped Reads Nucleotide Content



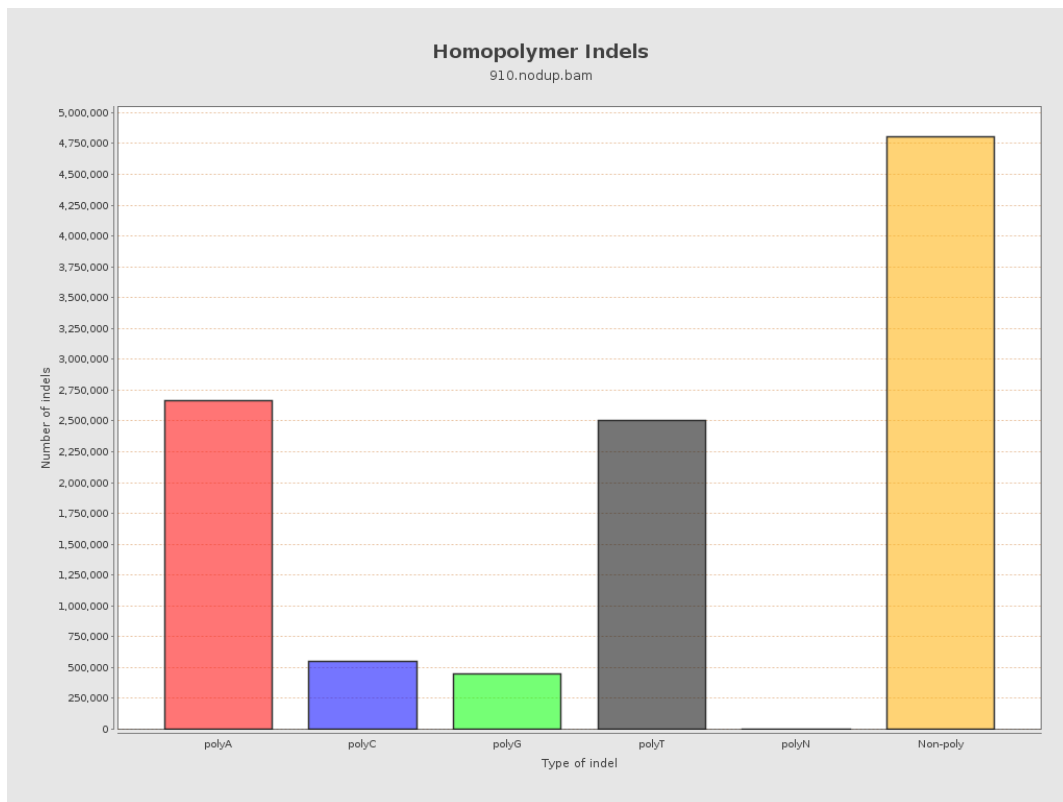
## 9. Results : Mapped Reads GC-content Distribution



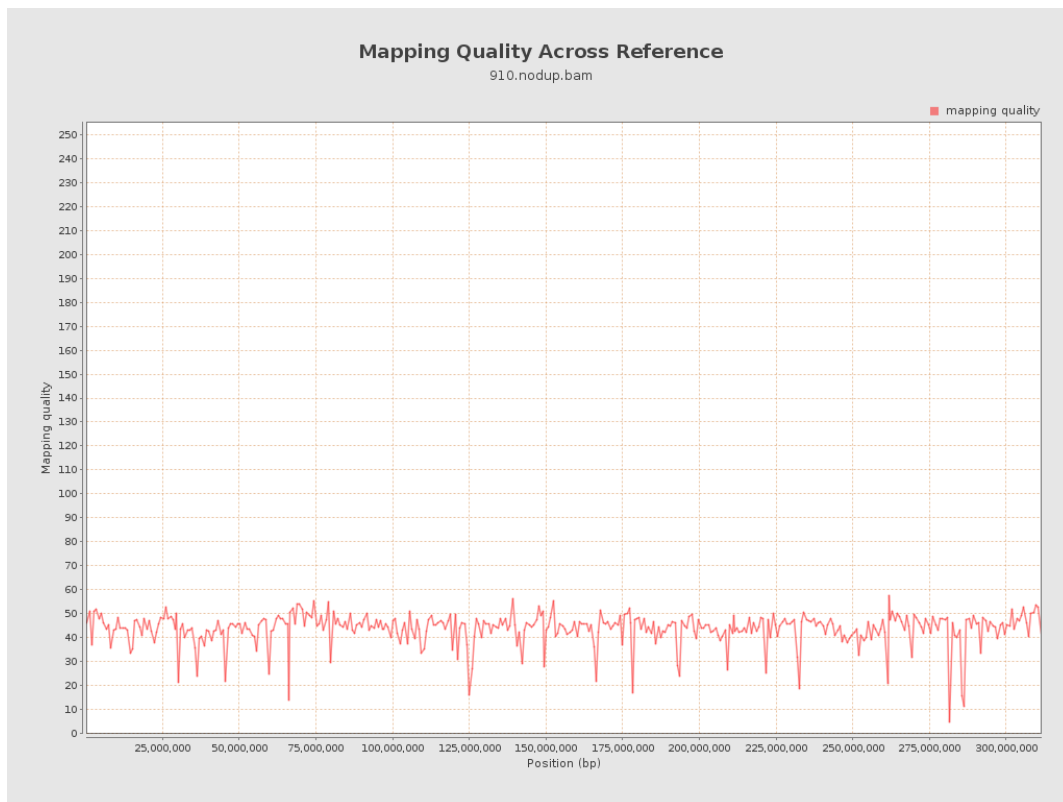
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

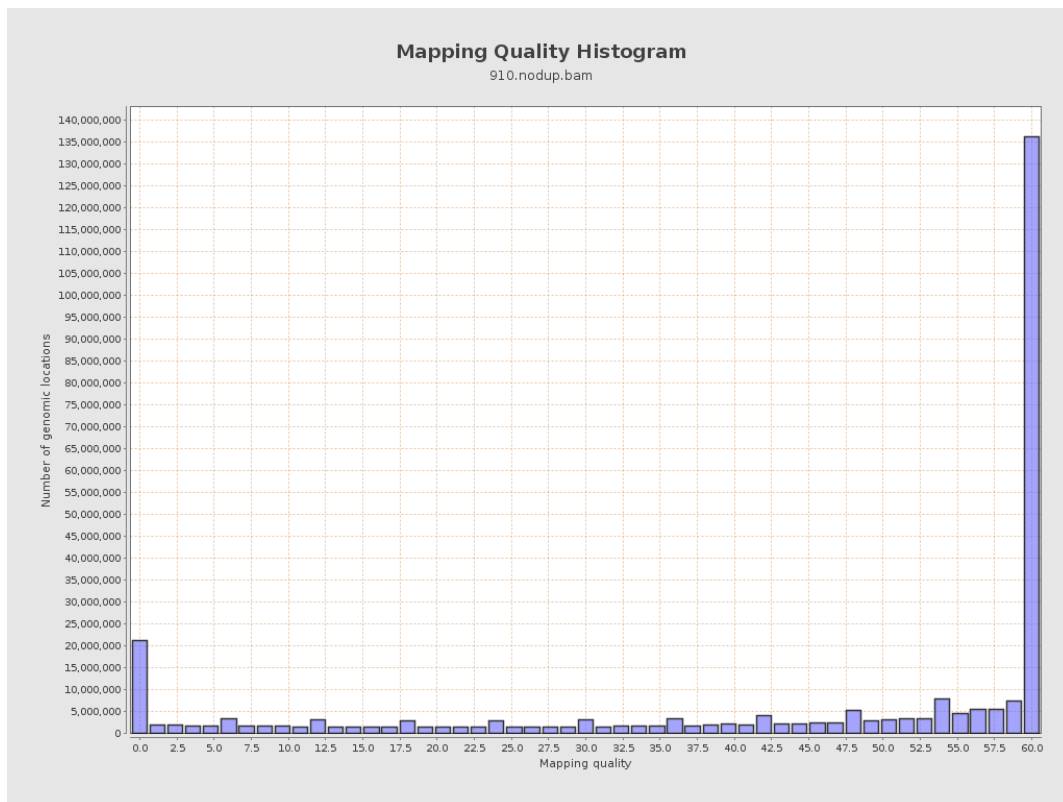


## 12. Results : Mapping Quality Across Reference

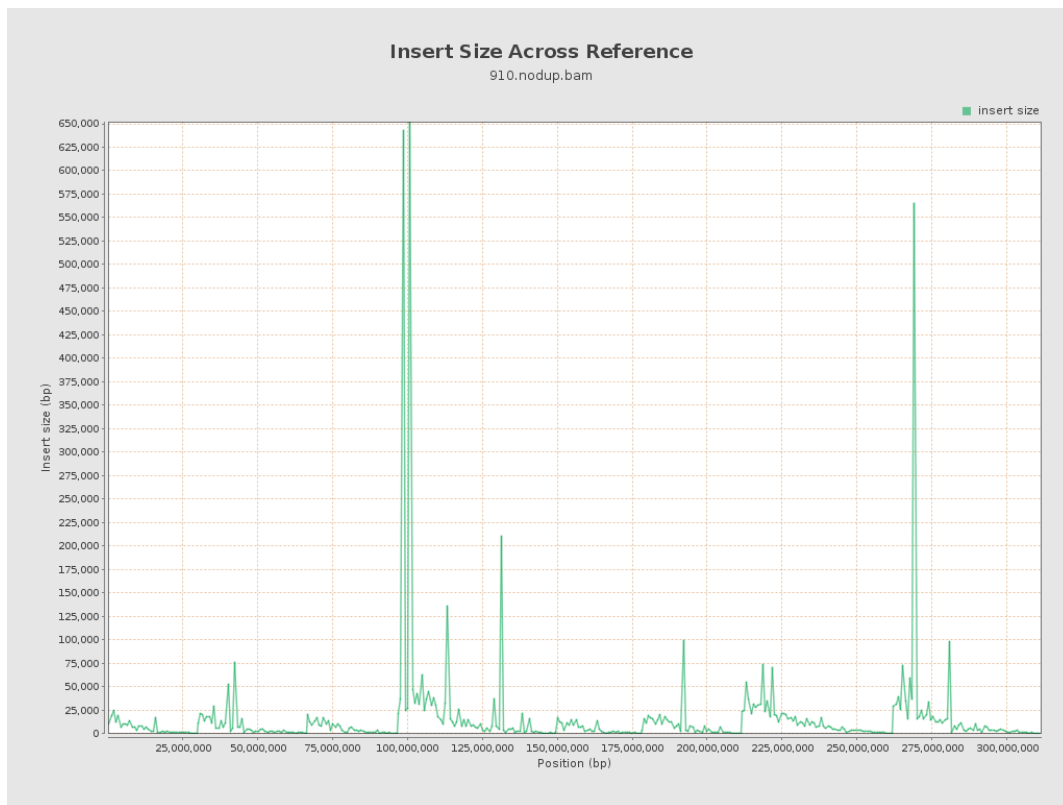




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

