

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:31:37*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/626
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 626 .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_238/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_238_S319_L003 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_238/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_238_S319_L003 _R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:36 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	70,815,233
Mapped reads	63,950,388 / 90.31%
Unmapped reads	6,864,845 / 9.69%
Mapped paired reads	63,950,388 / 90.31%
Mapped reads, first in pair	32,017,383 / 45.21%
Mapped reads, second in pair	31,933,005 / 45.09%
Mapped reads, both in pair	62,410,481 / 88.13%
Mapped reads, singletons	1,539,907 / 2.17%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	9,501,504 / 13.42%
Clipped reads	15,160,223 / 21.41%

### 2.2. ACGT Content

Number/percentage of A's	2,715,136,355 / 30.87%
Number/percentage of C's	1,679,331,694 / 19.1%
Number/percentage of T's	2,720,285,976 / 30.93%
Number/percentage of G's	1,679,224,180 / 19.1%
Number/percentage of N's	32,649 / 0%
GC Percentage	38.19%

### 2.3. Coverage

Mean	28.2918
Standard Deviation	253.4202

## 2.4. Mapping Quality

Mean Mapping Quality	44.12
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## 2.5. Insert size

Mean	234,368.71
Standard Deviation	2,307,909.19
P25/Median/P75	306 / 403 / 524

## 2.6. Mismatches and indels

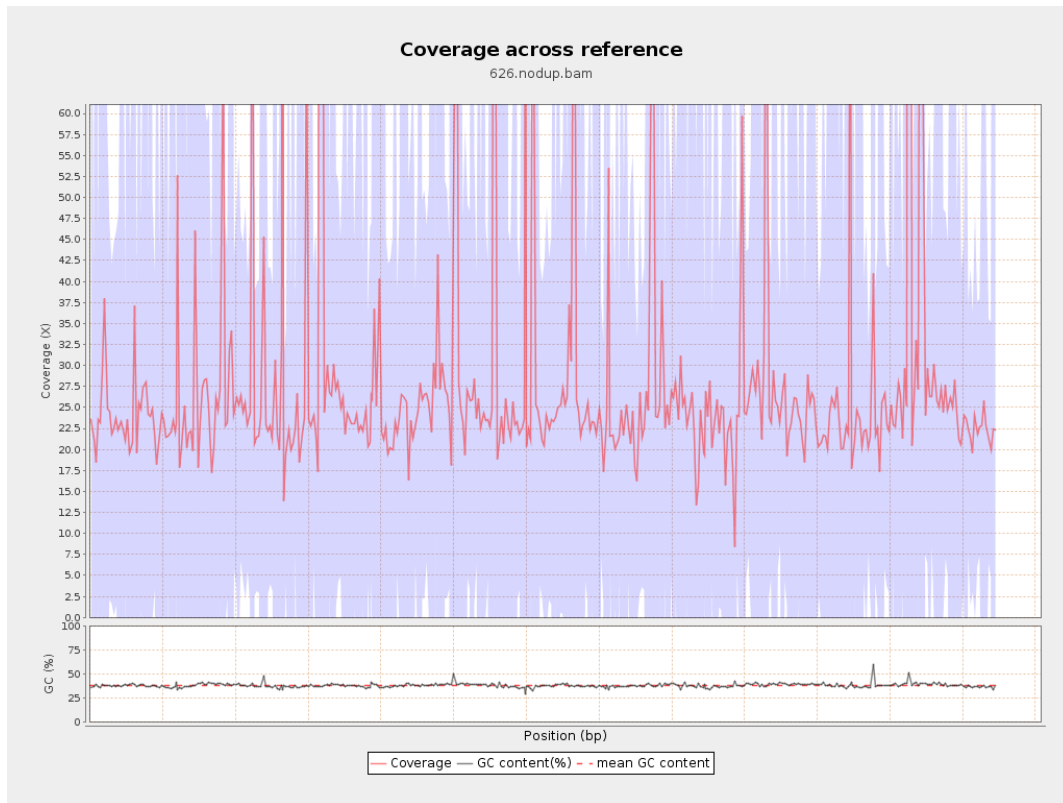
General error rate	2.35%
Mismatches	189,376,473
Insertions	6,179,963
Mapped reads with at least one insertion	8.65%
Deletions	6,130,728
Mapped reads with at least one deletion	8.48%
Homopolymer indels	56.03%

## 2.7. Chromosome stats

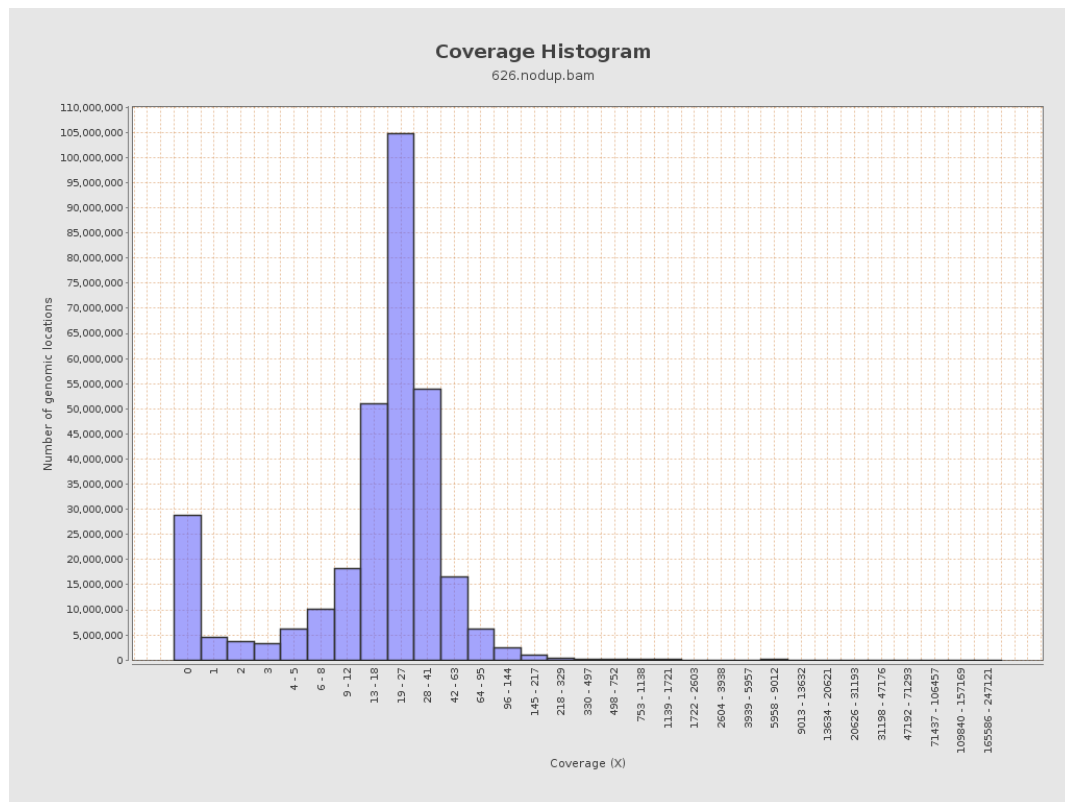
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	706915177	23.7824	93.5972

LT669789.1	36598175	1029932729	28.1416	260.512
LT669790.1	30422129	972508110	31.9671	274.8457
LT669791.1	52758100	1462745386	27.7255	256.0679
LT669792.1	28376109	798888664	28.1536	277.4143
LT669793.1	33388210	876501361	26.2518	165.6566
LT669794.1	50579949	1344521536	26.5821	219.7298
LT669795.1	49795044	1624917034	32.6321	346.2013

### 3. Results : Coverage across reference

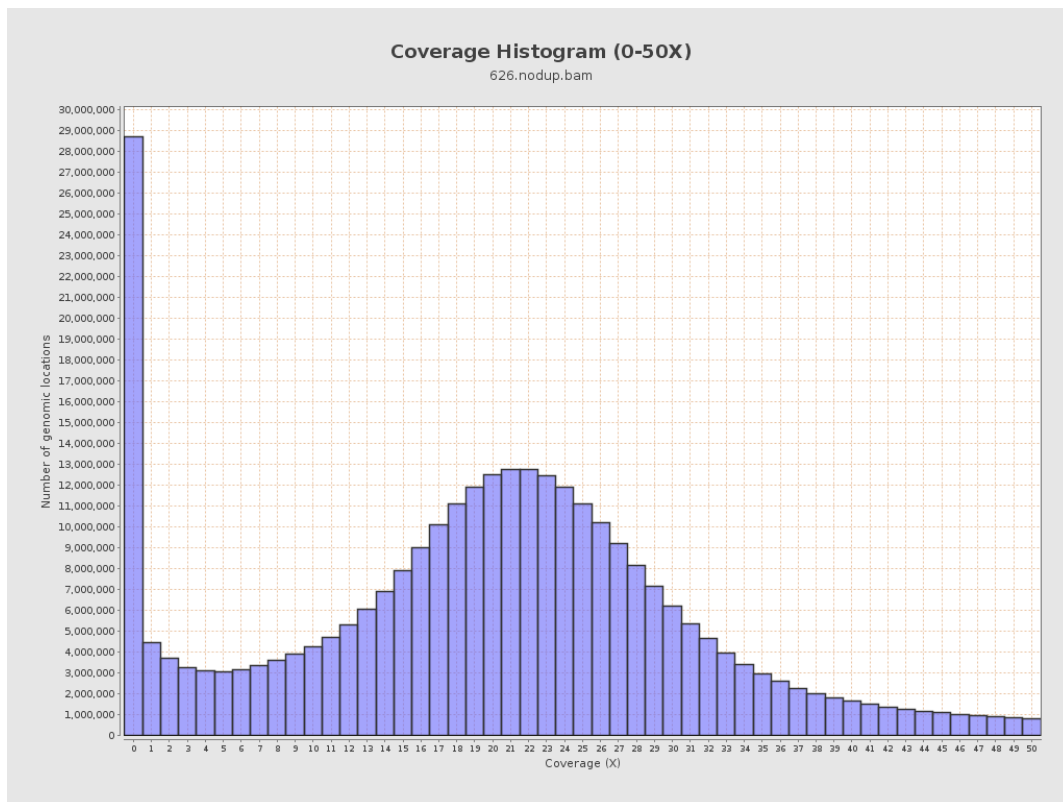


## 4. Results : Coverage Histogram

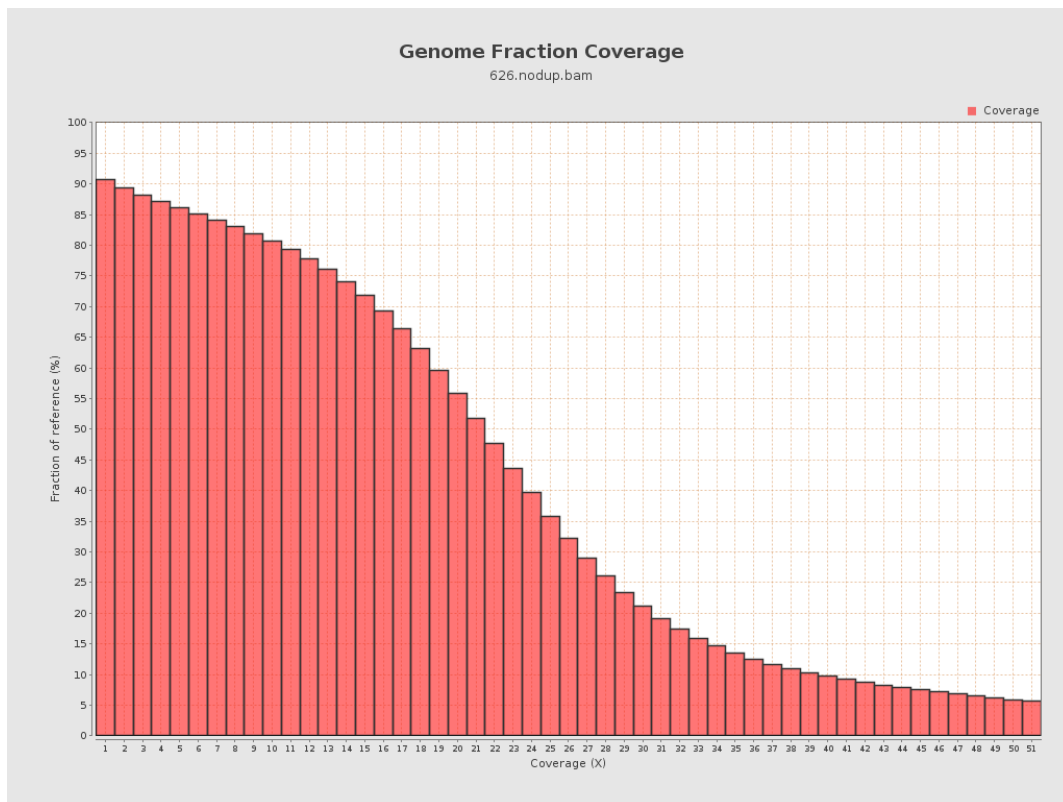




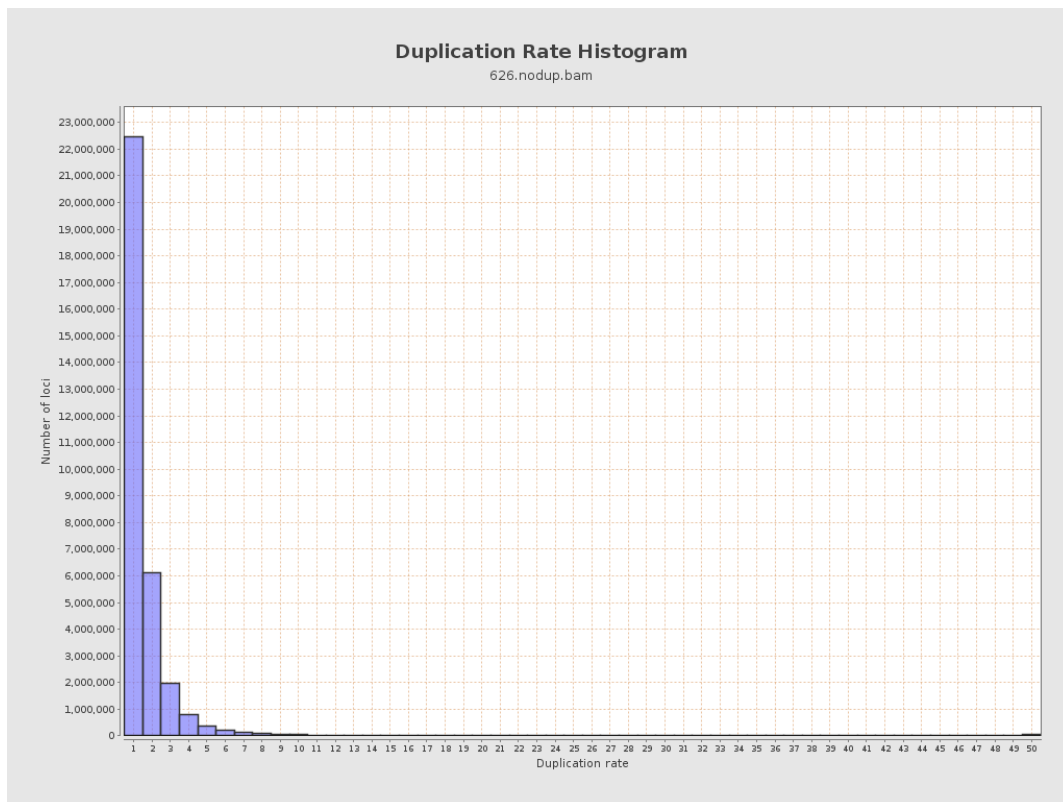
## 5. Results : Coverage Histogram (0-50X)



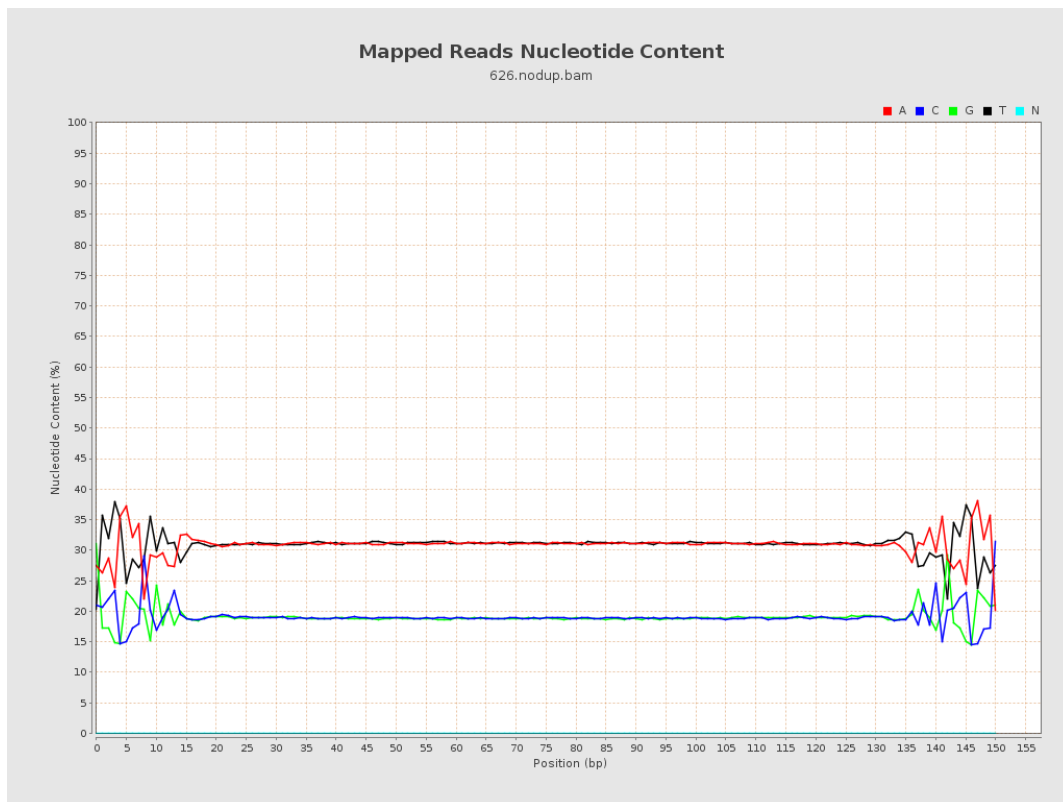
## 6. Results : Genome Fraction Coverage



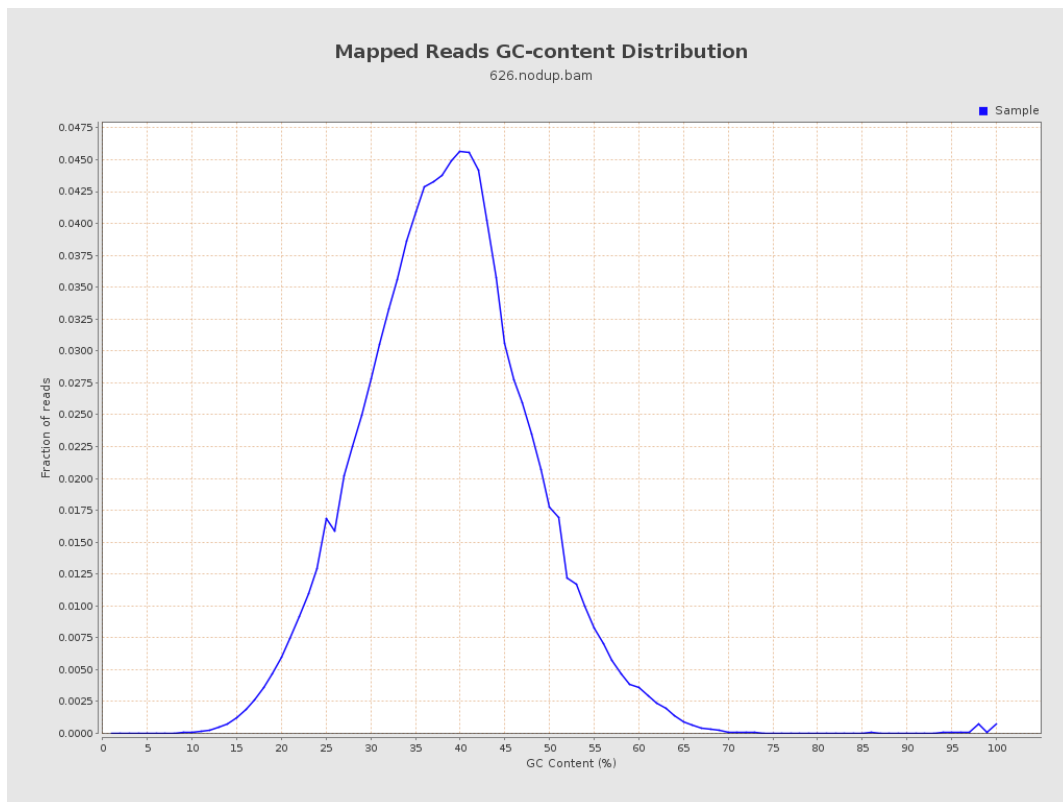
## 7. Results : Duplication Rate Histogram



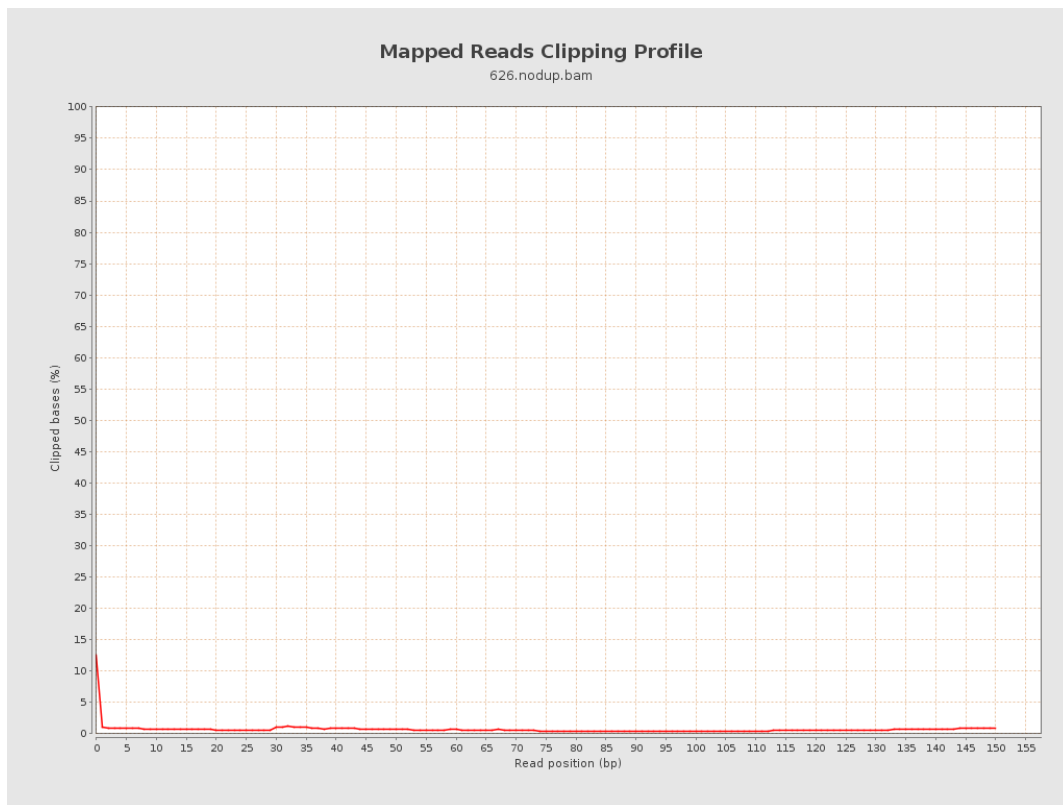
## 8. Results : Mapped Reads Nucleotide Content



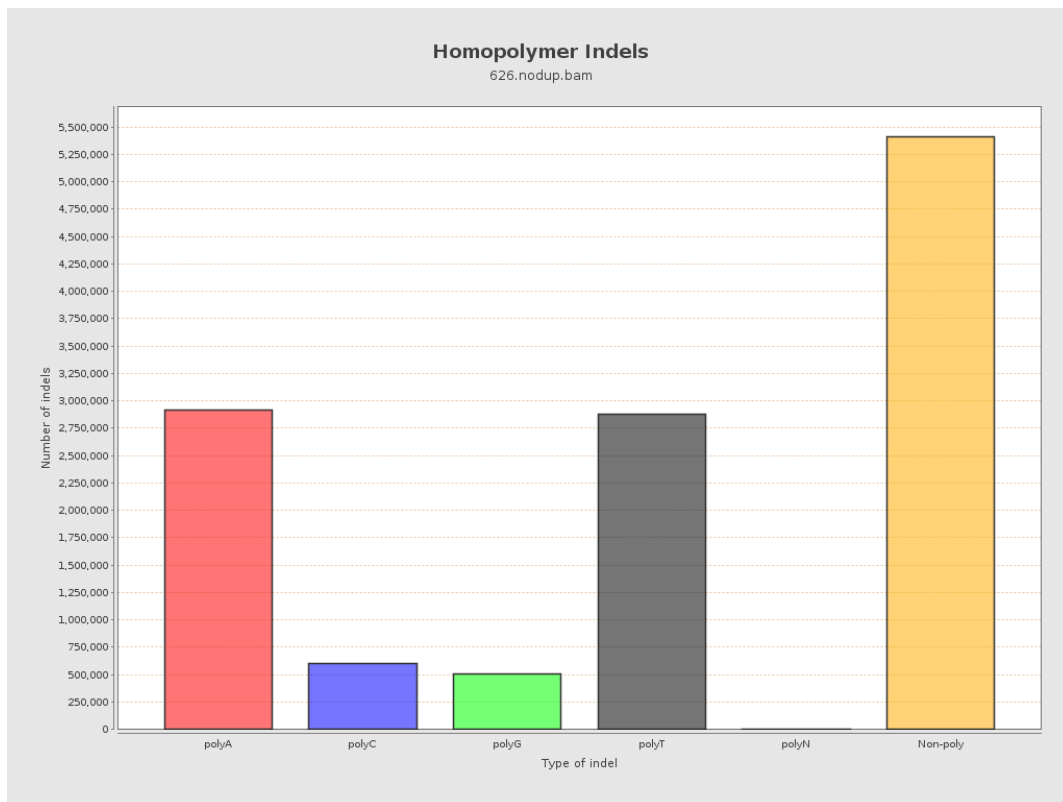
## 9. Results : Mapped Reads GC-content Distribution



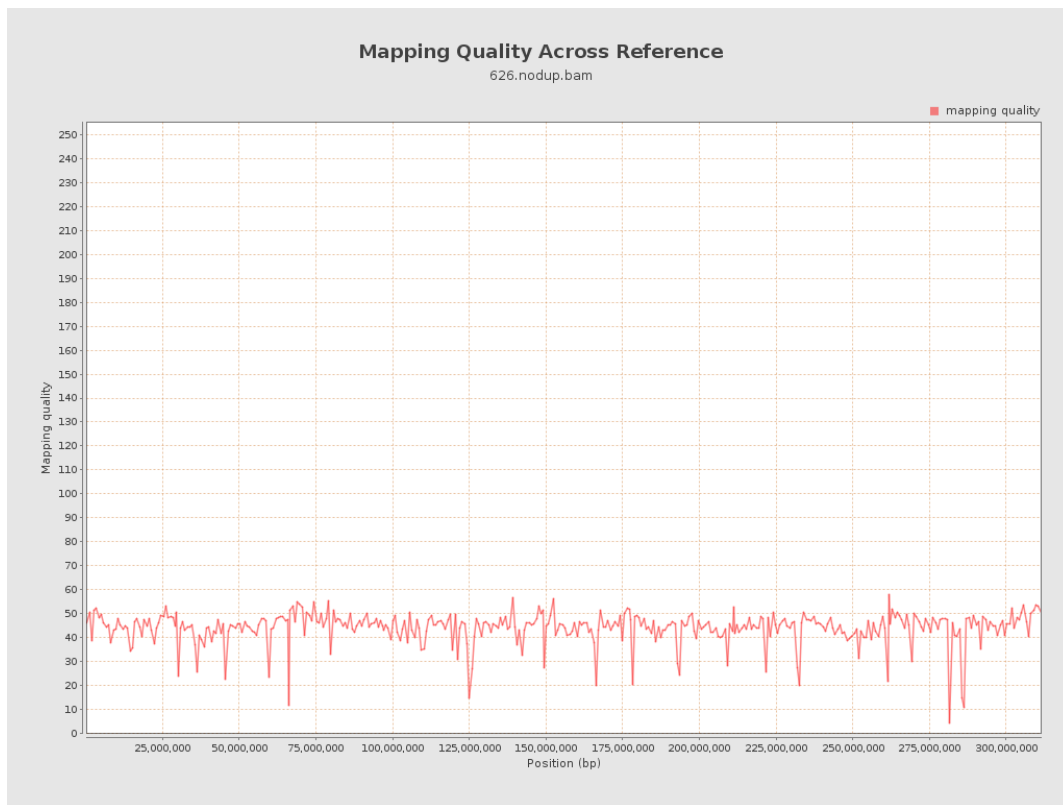
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

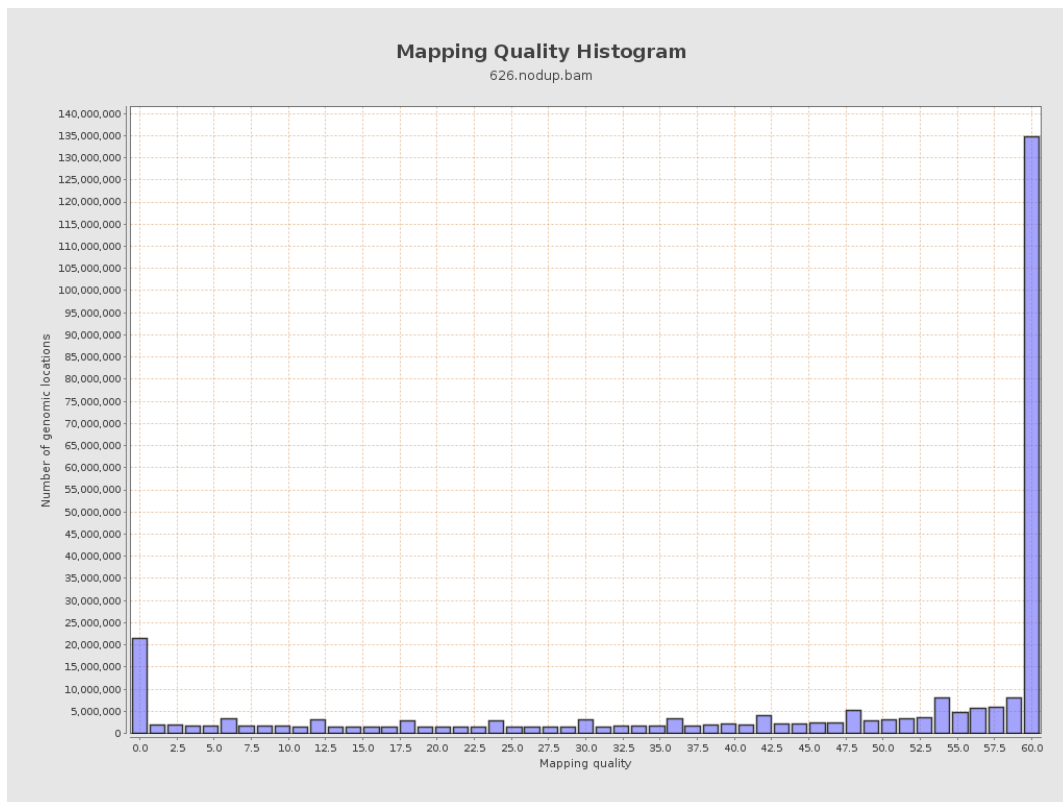


## 12. Results : Mapping Quality Across Reference

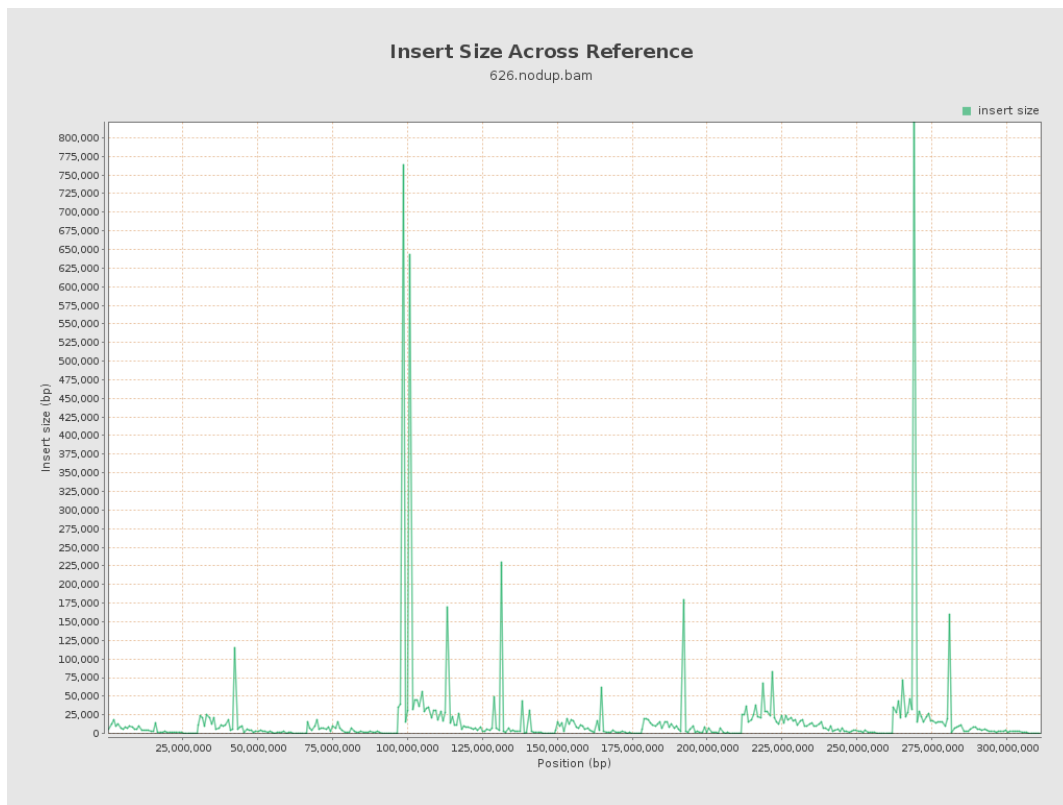




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

